

09/736076

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OM protein - protein search, using sw model

Run on: November 14, 2003, 12:54:54 ; Search time 34.7143 Seconds
(without alignments)
41.151 Million cell updates/sec

Title: US-09-736-076-15
Perfect score: 49
Sequence: 1 MLLGRPPFE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03: *
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT: *
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT: *
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5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT: *
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT: *
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT: *
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT: *
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT: *
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20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT: *
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: *
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT: *
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	AAW74159	HJ loop peptide J-
2	49	100.0	9	AAU98315	Polo kinase serine
3	49	100.0	10	AAW74213	HJ loop peptide K0
4	49	100.0	10	AAU98357	Polo kinase SNK se
5	49	100.0	11	AAW74163	HJ loop peptide J-
6	49	100.0	11	AAU98319	Polo kinase serine
7	49	100.0	469	AAB94717	Human protein sequ
8	49	100.0	469	AAG67426	Amino acid sequenc
9	49	100.0	685	AAU00915	Human serum induci

10	49	100.0	685	20	AAW88432	Disease associated
11	49	100.0	685	23	ABP61474	Human NF-KB activa
12	49	100.0	753	23	ABP41992	Human ovarian anti
13	46	93.9	9	20	AAW74161	HJ loop peptide J-
14	46	93.9	9	23	AAU98317	Polo kinase serine
15	43	87.8	626	21	AAB35805	Protein involved i
16	43	87.8	769	22	ABB63067	Drosophila melanog
17	41	83.7	8	20	AAW74160	HJ loop peptide J-
18	41	83.7	8	23	AAU98316	Polo kinase serine
19	41	83.7	416	17	AAR92176	Sak serine-threoni
20	41	83.7	464	17	AAR92214	SAX-b serine-threo
21	41	83.7	925	17	AAR92177	SAX-a serine-threo
22	41	83.7	925	23	ABB57273	Mouse ischaemic co
23	41	83.7	970	22	AAM78833	Human protein SEQ
24	41	83.7	970	22	AAM39244	Human polypeptide
25	41	83.7	980	22	AAM79817	Human protein SEQ
26	41	83.7	980	22	AAM41030	Human polypeptide
27	40	81.6	9	20	AAW74162	HJ loop peptide J-
28	40	81.6	9	23	AAU98318	Polo kinase serine
29	40	81.6	20	20	AAW74173	HJ loop peptide PO
30	40	81.6	20	23	AAU98306	Peptide sequence o
31	40	81.6	329	21	AAB56690	Human prostate can
32	40	81.6	528	23	ABP73734	Candida albicans e
33	40	81.6	531	23	AAU74656	Mammalian polo-lik
34	40	81.6	603	16	AAR74620	Human lung tumour
35	40	81.6	603	23	AAU79306	Mouse polo-like ki
36	40	81.6	603	23	AAU79308	Mouse polo-like ki
37	40	81.6	603	23	AAU79309	Mouse polo-like ki
38	40	81.6	603	23	AAU79310	Mouse polo-like ki
39	40	81.6	603	23	AAU79311	Mouse polo-like ki
40	40	81.6	603	23	AAU79312	Mouse polo-like ki
41	40	81.6	603	23	AAU79313	Mouse polo-like ki
42	40	81.6	603	23	AAU79314	Mouse polo-like ki
43	40	81.6	603	23	AAU79315	Mouse polo-like ki
44	40	81.6	603	23	AAU79316	Mouse polo-like ki
45	40	81.6	603	23	AAU79317	Mouse polo-like ki

ALIGNMENTS

RESULT 1
AAW74159

ID AAW74159 standard; peptide; 9 AA.

XX AAW74159;

AC AAW74159;

DT 05-MAY-1999 (first entry)

XX HJ loop peptide J-42.

KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.

XX Synthetic.

OS

PH Key Location/Qualifiers

FT Modified-site 1 /note= "acetylated"

FT Modified-site 9 /note= "amidated"

FT Modified-site 9 /note= "benzyl ester of Glu"

XX WO9853050-A2.

PN

XX 26-NOV-1998.

PD

XX 20-MAY-1998; 98WO-US10319.

XX 21-MAY-1997; 97US-0861338.

PA YISSUM RES & DEV CO.
XX
PI Ben-Sasson SA;
XX
DE WPI: 1999-070142/06.
XX
PI New peptides for modulating serine/threonine kinase activity -
XX comprise a sequence corresponding to the HJ loop of a
PI serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Disclosure; Fig 6; 70pp; English.
XX
CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 49; EB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB |||||
2 MLLGRPPPE 10
RESULT 4
AAW98157
ID AAW98157 standard; Peptide; 10 AA.
XX
AC AAW98157;
XX
DT 12-APR-2002 (first entry)
XX
DE Polo kinase SNK serine-threonine kinase HJ loop peptide K038H101.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
KW modulating STK activity; polo kinase; SNK; K038H101.
XX
OS Unidentified.
CS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal myristyl"
FT Modified-site 10 /note= "Benzyl Ester of Glutamic Acid, C-terminal amide"
XX
PR US2002049301-A1.
XX
PD 25 APR 2002.
XX
PF 13 DEC-2000; 2000US-0736076.
XX

PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Ben-Sasson SA;
XX
DR WPI: 2002-462787/49.
XX
PI New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX
PS Disclosure; Fig 6; 41pp; English.
XX
CC The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase SNK
CC serine-threonine kinase HJ loop peptide K038H101. This sequence is one
CC of the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 49; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB |||||
2 MLLGRPPPE 10
RESULT 5
AAW74163
ID AAW74163 standard; peptide; 11 AA.
XX
AC AAW74163;
XX
DT 05-MAY-1999 (first entry)
XX
DE HJ loop peptide J-46.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 11 /note= "amidated"
XX
PN WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10319.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX
PI Ben-Sasson SA;
PI

PT full length cDNAs -

XX Claim 8; SEQ ID 15726; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesising 5602

CC full length cDNAs defined in the specification. Where a primer set
CC comprises (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH33166 to AAH13628 and
CC AAH13629 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB93893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX Sequence 469 AA;

Query Match 100.0%; Score 49; DB 22; Length 469;

Best Local Similarity 100.0%; Pred. NO. 0.66;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

|||||

Db 57 MLLGRPPFE 65

RESULT 8

AAG67426

ID AAG67426 standard; Protein; 469 AA.

XX AAG67426;

UT 26-NOV-2001 (first entry)

DE Amino acid sequence of a human protein kinase/protein phosphatase.

XX Human protein kinase; protein phosphatase; signal transduction;

KW intracellular signalling pathway.

XX Homo sapiens.

XX WC200109345-A1.

PD 08-FEB-2001.

PF 28-JUL-2000; 2000WO-JP05060.

PR 29-JUL-1999; 39JP-0248036.

PR 18-OCT-1999; 99US-0159590.

PR 11-JAN-2000; 2000JP-0118776.

PR 17-FEB-2000; 2000US-0183322.

PR 02-MAY-2000; 2000JP-0183767.

XX (HELIX) HELIX RES INST.

PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Furahashi S;

PI Senoo C, Nezu J;

XX WPI; 2001-564736/63.

DE N-PSDB; AAH78069.

XX New genes encoding protein kinase and protein phosphatase, useful for
PT identifying modulators which can be used to treat human or animal
PT disorders associated with the expression or function of these enzymes -

XX Claim 2; Page 136-139; 336pp; Japanese.

CC The present sequence represents a human protein kinase/protein
CC phosphatase. The polypeptides are expected to participate in signal
CC transduction in cells. The kinase phosphatases are connected with
CC intracellular signalling pathways. Antisense oligonucleotides and
CC compounds identified by screening (agonists or antagonists) can be
CC used to treat human or animal disorders associated with the expression
CC or function of the protein. In addition, the polypeptides may be used
CC as target molecules for drug development.

XX Sequence 469 AA;

Query Match 100.0%; Score 49; DB 22; Length 469;

Best Local Similarity 100.0%; Pred. NO. 0.66;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

|||||

Db 57 MLLGRPPFE 65

RESULT 9

AAAY00915

ID AAAY00915 standard; Protein; 685 AA.

XX AAAY00915;

DT 28-MAY-1999 (first entry)

XX Human serum inducible kinase.

XX Serum inducible kinase; SNK protein; human; proliferative disease;
KW leukaemia; solid tumour cancer; metastasis; chronic inflammatory;
KW psoriasis; rheumatoid arthritis; proliferative cardiovascular disease;
KW restenosis; ocular disorder; diabetic retinopathy; haemangioma;
KW benign hyperproliferative disease; diagnosis.

XX Homo sapiens.

XX WO9909146-A1.

PD 25-FEB-1999.

XX 20-AUG-1998; 98WO-US17248.

PR 20-AUG-1997; 97US-0056112.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PI Anderson KM, Bouzyk M, Hansbury MJ, Jackson JR;

PI Nerurkar SS, Roshak AK;

XX WPI; 1999-181027/15.

DR N-PSDB; AAX27227.

XX New serum inducible kinase (Snk) polypeptides and polynucleotides -
PT useful for treating proliferative diseases

XX Claim 1; Page 39-40; 41pp; English.

XX This sequence is a human serum inducible kinase (SNK) of the
CC invention. The invention relates to diagnostic assays or kits for
CC detecting diseases associated with inappropriate SNK activity or levels.
CC Disease states that can be diagnosed include proliferative diseases such
CC as leukaemia, solid tumour cancers and metastases, chronic inflammatory
CC proliferative diseases such as psoriasis and rheumatoid arthritis,
CC proliferative cardiovascular diseases such as restenosis, proliferative

ocular disorders such as diabetic retinopathy and benign hyperproliferative diseases such as haemangiomas. The polynucleotides can be used as hybridisation probes for cDNA and genomic DNA or as primers for a nucleic acid amplification (PCR) reaction, to isolate full-length cDNAs and genomic clones encoding polypeptides of this invention and to isolate cDNA and genomic clones of other genes which have a high sequence similarity to the SNK coding sequence. The differences between cDNA and genomic sequences can be observed and therefore mutations detected. Any mutations may then be attributed to likely causative agents of disease. The nucleotide sequences are also useful for chromosome identification.

Sequence 685 AA;

Query Match: 100.0%; Score 49; DB 20; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
Db 273 MLLGRPPPE 281

RESULT 10
AAW88432
ID AAW88432 standard; Protein; 685 AA.

AC AAW88432;

DT 26 APR-1999 (first entry)

DE Disease associated protein kinase DAPK-1.

KW DAPK-1; disease associated protein kinase; human; diagnosis; therapy; adult respiratory distress syndrome; allergy; asthma; arteriosclerosis; bronchitis; emphysema; hypereosinophilia; myocardial inflammation; pericardial inflammation; anaemia; rheumatoid arthritis; Addison's disease; AIDS; atherosclerosis; atopic dermatitis; dermatomyositis; diabetes mellitus; glomerulonephritis; gout; Grave's disease; lupus erythematosus; multiple sclerosis; myasthenia gravis; osteoarthritis; osteoporosis; pancreatitis; polycystic kidney disease; polymyositis; scleroderma; Sjorgren's syndrome; autoimmune thyroiditis; cancer; infection; trauma; cell proliferation.

OS Homo sapiens.

PH Key Location/Qualifiers

PT Binding-site 89..96

PT /note= "potential ATP binding site"

PT Peptide 506..511

PT /note= "presumed regulatory sequence common to

PT polo family protein kinases"

XX WC9858052-A2.

XX 21-DEC-1998.

XX 19 JUN-1998; 98WO-US22813.

XX 19 JUN-1997; 97US-0878989.

XX (INCYTE) INCYTE PHARM INC.

PI Bandman G, Corley NC, Golis SK, Guegler KJ, Hillman JL;

PI Lai P, Shah P;

XX WPI; 1999-080952/07.

XX N-PSDB; AAX06831.

XX New disease associated protein kinases used to stimulate cell proliferation and to treat the immune response and cancer

Claim 1; Page 54-56; 93pp; English.

This is the amino acid sequence of human disease associated protein kinase DAPK-1, as deduced from a consensus sequence (see AAX06831) of overlapping cDNA clones from libraries which are immortalised or cancerous and show inflammatory or immune responses. DAPK-1 shows 53% homology to human proliferation-related protein kinase PRK (GI 1488263). The invention provides DAPK-1 to DAPK-7 polypeptides (see AAW88432-38) and cDNA clones encoding them (see AAX06831-36 and AAX06882), as well as expression vectors, host cells, agonists, antagonists and antibodies. The invention further provides uses of such products in the diagnosis, prevention and treatment of diseases associated with cell proliferation, especially cancer or an immune response (claimed). Conditions that may be treated include adult respiratory distress syndrome, allergies, asthma, arteriosclerosis, bronchitis, emphysema, hypereosinophilia, myocardial or pericardial inflammation, rheumatoid arthritis, Addison's disease, AIDS, anaemia, atherosclerosis, various diseases of the digestive system, atopic dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis, gout, Grave's disease, lupus erythematosus, multiple sclerosis, myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis, polycystic kidney disease, polymyositis, scleroderma, Sjorgren's syndrome, autoimmune thyroiditis, complications of cancer, extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal and helminthic infections, and trauma (disclosed).

Sequence 685 AA;

Query Match: 100.0%; Score 49; DB 20; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
Db 273 MLLGRPPPE 281

RESULT 11
ABP61474

ID ABP61474 standard; Protein; 685 AA.

AC ABP61474;

DT 30-SEP-2002 (first entry)

DE Human NF-kB activating protein SEQ ID NO 101.

KW Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory; immunomodulator; cytostatic; antiinfective; osteopathic; nootropic; neuroprotective; anti-HIV; autoimmune disease; cancer; infection; bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

OS Homo sapiens.

XX WO200253737-A1.

XX 11-JUL-2002.

XX 25-DEC-2001; 2001WO-JP11389.

XX 28-DEC-2000; 2000JP-0402288.

XX 26-MAR-2001; 2001JP-0088912.

XX 24-AUG-2001; 2001JP-0254018.

XX (ASAH) ASahi KASEI KOGYO KK.

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

XX WPI; 2002-583617/62.

XX N-PSDB; ABQ91962.

XX NF-approximatelykB activating gene and expressed protein, applicable in

PT diagnosis and screening inhibitors or promoters to control excessive
PT activation or inhibition for treating e.g. inflammations, autoimmune
PT diseases and cancer
XX
PS Claim 1: Page 448-453; 841pp; Japanese.
XX
CC The invention relates to a purified protein (1), comprising one of 90
CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
CC the sequences but with some amino acids deleted, substituted or added and
CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
CC inhibitors or promoters to control excessive activation or inhibition
CC and for treating e.g. inflammations, autoimmune diseases, cancers,
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
CC disorders.
XX
SQ Sequence 685 AA;

Query Match 100.0%; Score 49; DB 23; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
Db |||||
273 MLLGRPPPE 281

RESULT 12
ABP41992
ID ABP41992 standard; Protein; 753 AA.
XX
AC ABP41992;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HAOSM08, SEQ ID NO:3124.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW anti-inflammatory; gynaecological; reproductive; chromosome 5.
XX
OS Homo sapiens.
XX
PN WO200200677-A1.
XX
PD 01-JAN 2002.
XX
EF 07-JUN-2001; 2001WO-US18569.
XX
PR 07-JUN-2000; 2000US-209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Barse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
DR N-PSDB; ABQ55069.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases.
XX
PS Claim 11; SEQ ID No 3124; 2922pp; English.
XX
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-

CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 753 AA;

Query Match 100.0%; Score 49; DB 23; Length 753;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
Db |||||
341 MLLGRPPPE 349

RESULT 13
AAW74161
ID AAW74161 standard; peptide; 9 AA.
XX
AC AAW74161;
XX
DT 05-MAY-1999 (first entry)
XX
DE HJ loop peptide J-43.1.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 9 /note= "amidated"
FT
XX WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10319.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.

XX Ben-Sasson SA;
XX WPI; 1999-070142/06.
XX New peptides for modulating serine/threonine kinase activity -
XX comprise a sequence corresponding to the HJ loop of a
XX serine/threonine kinase, used for treating, e.g. cancers,
XX inflammatory disorders or autoimmune disorders
XX Claim 14; Fig 4; 70pp; English.
XX This sequence represents a peptide of the invention, and is a derivative
XX of the HJ loop of a serine/threonine kinase (STK). The peptides can be
XX used for the treatment of disorders caused by overactivity or
XX underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
XX shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
XX arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
XX hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
XX psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
XX of organ transplant rejection, multiple sclerosis, inflammatory bowel
XX disease and AIDS), central nervous system diseases (e.g. Alzheimer's
XX disease, stroke and trauma), septic shock, Parkinson's disease or
XX hypertension. The peptides can also be used to produce antibodies which
XX can be used to identify cells expressing the STK and to study the
XX intracellular distribution of the STK. In addition, the peptides can be
XX used to identify and quantitate ligands which bind the HJ loop of the STK
XX from which the peptide was derived.
XX Sequence 9 AA;
SQ Query Match 93.9%; Score 46; DB 20; Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB 1 MLLGRPPPE 9
RESULT 14
AAU98317
ID AAU98317 standard; Peptide; 9 AA.
XX AC AAU98317;
XX DT 13-AUG 2002 (first entry)
XX DE Polo kinase serine-threonine kinase HJ loop peptide J-43.1.
XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
KW modulating STK activity; poic kinase; J-43.1.
XX Unidentified.
CS Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 9 /note= "Benzy[ester of Glutamic acid, C-terminal amide"
FT FT
XX US2002049301-A1.
XX 25-APR-2002.
XX 13-DEC 2000; 2000US-0736076.
XX 21 MAY 1997; 97US-0861338.

XX (CHIL-) CHILDRENS MEDICAL CENT.
XX Ben-Sasson SA;
XX WPI; 2002-462787/49.
XX New peptide from the HJ loop of serine-threonine kinase, useful for
XX treating e.g. cancer and for producing diagnostic antibodies -
XX Disclosure; Fig 4; 41pp; English.
XX The present invention relates to new peptides derived from the HJ loop
XX of a serine/threonine kinase (STK). The peptides of the invention are
XX used to modulate STK activity, especially for treating cancer, diabetes,
XX obesity or a wide variety of central nervous system, inflammatory,
XX autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
XX regulating lipid metabolism. The peptides are also used to generate
XX antibodies that bind specifically to the parent STK, used e.g. for
XX identifying STK-expressing cells and to study intracellular distribution
XX of STK, and to identify or quantify ligands that bind to the HJ loop.
XX The present amino acid sequence represents the polo kinase
XX serine-threonine kinase HJ loop peptide J-43.1. This sequence is one of
XX the short peptides of the invention that selectively modulate the
XX activity of STK.
XX Sequence 9 AA;
SQ Query Match 93.9%; Score 46; DB 23; Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB 1 MLLGRPPPE 9
RESULT 15
AAB35805
ID AAB35805 standard; Protein; 626 AA.
XX AC AAB35805;
XX DT 23-FEB-2001 (first entry)
XX DE Protein involved in cell cycle regulation SEQ ID 46.
XX Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
KW cotton; rice; barley; millet.
XX Zea mays.
OS WO200065040-A2.
XX PN WO200065040-A2.
XX PD 02-NOV-2000.
XX PF 13-APR-2000; 2000WO-US09975.
XX PR 22-APR-1999; 99US-0130849.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PI Helentjaris TG, Habben JE, Sun Y;
XX WPI; 2000-687333/67.
XX DR N-PSDB; AAC83112.
XX Nucleic acids useful for producing transgenic plants, preferably maize,
XX with increased cell cycle gene activity, preferably activity of cyclin
XX and/or cyclin-dependent kinase -
XX Claim 16; Page 117-118; 122pp; English.

arteriosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and hypertension), immunosuppressive and inflammatory disorders (e.g. asthma, psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression of organ transplant rejection, multiple sclerosis, inflammatory bowel disease and AIDS), central nervous system diseases (e.g. Alzheimer's disease, stroke and trauma), septic shock, Parkinson's disease or hypertension. The peptides can also be used to produce antibodies which can be used to identify cells expressing the STK and to study the intracellular distribution of the STK. In addition, the peptides can be used to identify and quantitate ligands which bind the HJ loop of the STK from which the peptide was derived.

Sequence 8 AA;
Query Match 83.7%; Score 41; DB 23; Length 8;
Best Local Similarity 87.5%; Pred. No. 9.3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPF 8
Db 1 MLLGKPPF 8

RESULT 18
AAR92176
ID AAR92176 standard; Peptide; 8 AA.
XX
AC AAR92176.
XX
DT 13 AUG-2002 (first entry)
XX
DE Polo kinase serine-threonine kinase HJ loop peptide J-43.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytototoxic; antidiabetic; anorectic; neurological;
KW anti-inflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; J-43.

Unidentified.
OS Synthetic.
XX
EH Key Location/Qualifiers
FT Modified site 1 /note= "N-terminal acetyl"
FT Modified site 8 /note= "C-terminal amide"
XX
FN US2002049302-A1.
PD 25 APR-2002.
XX
PF 13-DEC-2000; 2000US-0736076.
XX
PS 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Ben-Sasson SA;
XX
CR WPI; 2002-462787/49.
XX
PT New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX
PS Disclosure; Fig 4; 41pp; English.

The present invention relates to new peptides derived from the HJ loop of a serine/threonine kinase (STK). The peptides of the invention are used to modulate STK activity, especially for treating cancer, diabetes, obesity or a wide variety of central nervous system, inflammatory, autoimmune or cardiovascular disorders, also haemorrhagic shock, and for

regulating lipid metabolism. The peptides are also used to generate antibodies that bind specifically to the parent STK, used e.g. for identifying STK-expressing cells and to study intracellular distribution of STK, and to identify or quantify ligands that bind to the HJ loop. The present amino acid sequence represents the polo kinase serine-threonine kinase HJ loop peptide J-43. This sequence is one of the short peptides of the invention that selectively modulate the activity of STK.

Sequence 8 AA;
Query Match 83.7%; Score 41; DB 23; Length 8;
Best Local Similarity 87.5%; Pred. No. 9.3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPF 8
Db 1 MLLGKPPF 8

RESULT 19
AAR92176
ID AAR92176 standard; Protein; 416 AA.
XX
AC AAR92176;
XX
DT 25-MAY-1996 (first entry)
XX
DE Sak serine-threonine kinase N-terminus.
XX
KW Sak; serine-threonine kinase; STK; agonist; antagonist;
KW proliferative disease; cancer; tumour; antisense; transgenic animal;
KW therapy.

Mus musculus.
XX
CA2150789-A.
XX
PD 03-DEC-1995.
XX
PF 01-JUN-1995; 95CA-2150789.
XX
PR 02-JUN-1994; 94US-0252995.
XX
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
XX
PI Dennis JW, Fode C, Heffernan M;
XX
DR WPI; 1996-129817/14.
DR N-PSDB; AAT08710.
XX
PT Nucleic acid encoding Sak serine-threonine kinase - useful for
PT identifying modulators potentially useful in treatment or prevention
PT of proliferative disease.

Claim 3; Page 46-48; 73pp; English.
XX
CC 2 Isoforms, sak-a and sak-b, of a novel serine/threonine kinase
CC have an identical N-terminal sequence (AAR92176) that contains the
CC kinase domain and that shows significant homology to the polo
CC subfamily. The C-terminal sequences (each contg. 3 PEST regions)
CC of the 2 isoforms differ (see AAR92177 and AAR92214). Sak-a and Sak-b
CC are associated with mitotic and meiotic cell division, and may be
CC involved in cell proliferation. They can be obtd. in recombinant
CC form by expression of encoding sequences (see AAT08710-12) and used
CC to test for inhibitory or stimulatory cpds. that may be useful
CC in the treatment/diagnosis of proliferative disorders, such as
CC cancer and viral (esp. HIV) infection.

Sequence 416 AA;
Query Match 83.7%; Score 41; DB 17; Length 416;
Best Local Similarity 66.7%; Pred. No. 18;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MLLGRPPFE 9
:|||||:
Db 204 LLIGRPFD 212

RESULT 20
AAR92214
ID AAR92214 standard; Protein: 464 AA.
XX
AC AAR92214;
XX
DT 25-MAY-1996 (first entry)
XX
DE SAK-b serine-threonine kinase.
XX
KW SAK-b; serine-threonine kinase; STK; agonist; antagonist;
KW proliferative disease; cancer; tumour; antisense; transgenic animal;
KW therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
Domain 1..416
FT /label= N-terminal domain
FT /note= "contains the kinase domain"
FT 417..464
FT /label= C-terminal domain
FT /note= "contains 3-PEST regions"
XX
PN CA2150789-A.
XX
PD 03-DEC-1995.
XX
PF 01-JUN-1995; 95CA-2150789.
XX
PR 02-JUN-1994; 94US-0252995.
XX
PA (MOJN) MOUNT SINAI HOSPITAL CORP.
XX
PI Dennis JW, Fode C, Heffernan M;
XX
WP1; 1996-129817/14.
XX
N-PSDB; AAT08712.
XX
Nucleic acid encoding Sak serine-threonine kinase - useful for
identifying modulators potentially useful in treatment or prevention
of proliferative disease.
XX
PS Claim 6; Page 58-61; 73pp; English.
XX
CC 2 Isoforms, SAK-a (AAR92177) and SAK-b (AAR92214), of a novel
serine/threonine kinase are associated with mitotic and meiotic cell
division and are characterized by having a kinase domain at the
N-terminus and 3 PEST sequences (rich in Pro, Ser, Thr, Asp, Glu) at
the C-terminus. The N-terminal regions of the 2 isoforms are
identical (see AAR92176). SAK-a and SAK-b can be obtd. in recombinant
form by expression of encoding sequences (see AAT08711-12), and used
to test for inhibitory or stimulatory cpds. useful in the
treatment/diagnosis of proliferative disorders such as cancer and
and viral (esp. HIV) infection, or used to raise antibodies.
XX
SQ Sequence 464 AA;

Query Match 83.7%; Score 41; DB 17; Length 464;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MLLGRPPFE 9
:|||||:
Db 204 LLIGRPFD 212

RESULT 21
AAR92177
ID AAR92177 standard; Protein: 925 AA.
XX
AC AAR92177;
XX
DT 25-MAY-1996 (first entry)
XX
DE SAK-a serine-threonine kinase.
XX
KW SAK-a; serine-threonine kinase; STK; agonist; antagonist;
KW proliferative disease; cancer; tumour; antisense; transgenic animal;
KW therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
Domain 1..416
FT /label= N-terminal domain
FT /note= "contains the kinase domain"
FT 417..925
FT /label= C-terminal domain
FT /note= "contains 3-PEST regions"
XX
PN CA2150789-A.
XX
PD 03-DEC-1995.
XX
PF 01-JUN-1995; 95CA-2150789.
XX
PR 02-JUN-1994; 94US-0252995.
XX
PA (MOJN) MOUNT SINAI HOSPITAL CORP.
XX
PI Dennis JW, Fode C, Heffernan M;
XX
WP1; 1996-129817/14.
XX
N-PSDB; AAT08711.
XX
Nucleic acid encoding Sak serine-threonine kinase - useful for
identifying modulators potentially useful in treatment or prevention
of proliferative disease.
XX
PS Claim 5; Page 50-55; 73pp; English.
XX
CC 2 Isoforms, SAK-a (AAR92177) and SAK-b (AAR92214), of a novel
serine/threonine kinase are associated with mitotic and meiotic cell
division and are characterized by having a kinase domain at the
N-terminus and 3 PEST sequences (rich in Pro, Ser, Thr, Asp, Glu) at
the C-terminus. The N-terminal regions of the 2 isoforms are
identical (see AAR92176). SAK-a and SAK-b can be obtd. in recombinant
form by expression of encoding sequences (see AAT08711-12), and used
to test for inhibitory or stimulatory cpds. useful in the
treatment/diagnosis of proliferative disorders such as cancer and
and viral (esp. HIV) infection, or used to raise antibodies.
XX
SQ Sequence 925 AA;

Query Match 83.7%; Score 41; DB 17; Length 925;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MLLGRPPFE 9
:|||||:
Db 204 LLIGRPFD 212

RESULT 22
ABB57273
ID ABB57273 standard; Protein: 925 AA.
XX
AC ABB57273;

OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK51966.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 3782-3784; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 970 AA;

Query Match 83.7%; Score 41; DB 23; Length 925;
Best Local Similarity 66.7%; Pred. NO. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db :|||:|:
204 LLGRPPFD 212

RESULT 23
AAM78833
ID AAM78833 standard; Protein; 970 AA.
XX
AC AAM78833;
XX
DT 26-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1495.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.

OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK51966.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 3782-3784; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 970 AA;

Query Match 83.7%; Score 41; DB 23; Length 925;
Best Local Similarity 66.7%; Pred. NO. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db :|||:|:
204 LLGRPPFD 212

RESULT 24
AAM39244
ID AAM39244 standard; Protein; 970 AA.
XX
AC AAM39244;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2389.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK51966.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 3782-3784; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 970 AA;

Query Match 83.7%; Score 41; DB 23; Length 925;
Best Local Similarity 66.7%; Pred. NO. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db :|||:|:
204 LLGRPPFD 212

RESULT 23
AAM78833
ID AAM78833 standard; Protein; 970 AA.
XX
AC AAM78833;
XX
DT 26-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1495.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.

OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK51966.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 3782-3784; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 970 AA;

Query Match 83.7%; Score 41; DB 23; Length 925;
Best Local Similarity 66.7%; Pred. NO. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db :|||:|:
204 LLGRPPFD 212

RESULT 23
AAM78833
ID AAM78833 standard; Protein; 970 AA.
XX
AC AAM78833;
XX
DT 26-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1495.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.
XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000WO-US34263.
XX PR 21-JAN-2000; 2000US-0488725.
XX PR 25-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620322.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.
XX PR 29-NOV-2000; 2000US-0727344.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang C, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX PR WPI; 2001-442253/47.
XX DR N-PSDB; AAI58430.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries -
XX PS Example 4; SEQ ID NO 2389; 10078pp; English.
XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
XX CC the encoded polypeptides (AAM38642 AAM42213) with nootropic,
XX CC immunosuppressant and cytostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activity, chemotactic/chemokinetic activity, haemostatic
XX CC Activin/inhibin activity, cancer diagnosis and therapy, drug screening,
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX CC CNS disorders.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification.
XX SQ Sequence 970 AA;
Query Match 83.7%; Score 41; DP 22; Length 970;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLIGRPPPF 9
:|||||:
Db 204 LLIGRPPFD 212
RESULT 25
AAM79817
ID AAM79817 standard; Protein; 980 AA.
XX AC AAM79817;
XX DT 06-NOV-2001 (first entry)
XX DE Human protein SEQ ID NO 3463.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200157190-A2.
XX PD 09-AUG-2001.
XX PF 05-FEB-2001; 2001WO-US04098.
XX PR 03-FEB-2000; 2000US-0496914.
XX PR 27-APR-2000; 2000US-0560875.
XX PR 20-JUN-2000; 2000US-0598075.
XX PR 19-JUL-2000; 2000US-0620325.
XX PR 01-SEP-2000; 2000US-0654936.
XX PR 15-SEP-2000; 2000US-0663561.
XX PR 20-OCT-2000; 2000US-0693325.
XX PR 30-NOV-2000; 2000US-0728422.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX PR WPI; 2001-476283/51.
XX DR N-PSDB; AAK52950.
XX PT Nucleic acids encoding polypeptides with cytokine-like activities,
XX PT useful in diagnosis and gene therapy -
XX PS Claim 20; Page 345; 6221pp; English.
XX CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
XX CC cytokine, cell proliferation or cell differentiation or which may induce
XX CC production of other cytokines in other cell populations. The
XX CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX CC peptide therapy. The polypeptides have various cytokine-like activities,
XX CC e.g. stem cell growth factor activity, haematopoiesis regulating
XX CC activity, tissue growth factor activity, immunomodulatory activity and
XX CC activin/inhibin activity and may be useful in the diagnosis and/or
XX CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX CC inflammation.
XX CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX CC (AAM80020) are omitted as the relevant pages from the sequence listing
XX CC were missing at the time of publication.
XX SQ Sequence 980 AA;
Query Match 83.7%; Score 41; DB 22; Length 980;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLIGRPPPF 9
:|||||:
Db 214 LLIGRPPFD 222
RESULT 26
AAM41030
ID AAM41030 standard; Protein; 980 AA.
XX AC AAM41030;
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 5961.
XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WC200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue A, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac R;
XX
DR WPI: 2001-442253/47.
DR N-PSDB; AAI60186.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Example 2: SEQ ID NO 5961; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 580 AA;

Query Match 83.7%; Score 41; DB 22; Length 980;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MJLGRPPFE 9
 |||||
DB 214 LJLGRPPFD 222

RESULT 27
AAW74162
ID AAW74162 standard; peptide; 9 AA.
XX
AC AAW74162;
XX
DT 05-MAY-1999 (first entry)
XX
DE HC loop peptide J-45.
XX
KW HC loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;

KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 9 /note= "amidated"
FT
XX WO9853050-A2.
PN
XX 26-NOV-1998.
PD
XX 20-MAY-1998; 98WO-US10319.
PF
XX 21-MAY-1997; 97US-0861338.
PR
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX Ben-Sasson SA;
PI
XX WPI: 1999-070142/06.
DR
XX
PT New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Claim 14; Fig 4; 70pp; English.
XX
CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 9 AA;

Query Match 81.6%; Score 40; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGRPPFE 9
 |||||
DB 1 LGRPPFE 7

RESULT 28
AAU98318
ID AAU98318 standard; Peptide; 9 AA.
XX
AC AAU98318;
XX
DT 13-AUG-2002 (first entry)
XX
DE Polo kinase serine-threonine kinase HJ loop peptide J-45.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;

KW Central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
KW modulating STK activity; polo kinase; J-45.
XX
OS Unidentified.
CS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Modified-site /note= "N-terminal acetyl"
FT Misc difference 7
FT Modified-site 9 /note= "Benzyl ester of Glutamic acid"
FT Modified-site 9 /note= "C-terminal amide"
XX
PN US2002049301 A1.
XX
PD 25-APR-2002.
XX
PF 13-DEC-2003; 2003US-0736C76.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Ben-Sasson SA;
XX
DR WPI; 2002-462787/49.
XX
PT New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX
PS Disclosure; Fig 4; 4lpp; English.
XX
CC The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-45. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
SQ Sequence 9 AA;
Query Match 81.6%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 LGRPPPE 9
DB 1 LGRPPPE 7
RESULT 29
AAW74173
ID AAW74173 standard; peptide; 20 AA.
XX
AC AAW74173;
XX
DI 05-MAY-1999 (first entry)
DT HJ loop peptide POLO.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
PN WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10319.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX
PI Ben-Sasson SA;
XX
DR WPI; 1999-070142/06.
XX
PT New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Claim 41; Fig 3b; 70pp; English.
XX
CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 20 AA;
Query Match 81.6%; Score 40; DB 20; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB 3 LLVGKPPPE 11
RESULT 30
AAU98306
ID AAU98306 standard; Peptide; 20 AA.
XX
AC AAU98306;
XX
DT 13-AUG-2002 (first entry)
XX
DE Peptide sequence of HJ loop of serine-threonine kinase polo kinase.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
KW modulating STK activity; polo kinase.
XX
OS Unidentified.

XX US2002049301-A1.
XX
XX
XX 25-APR 2002.
XX
XX 13 DEC 2000; 2000US-0736076.
XX
XX 21 MAY 1997; 97US-0861338.
XX
XX (CHILD-) CHILDRENS MEDICAL CENT.
XX
XX Ben-Sasson SA;
XX
XX WPI; 2002-462787/49.
XX
XX New peptide from the H3 loop of serine-threonine kinase, useful for
XX treating e.g. cancer and for producing diagnostic antibodies -
XX
XX Claim 33; Fig 3; 41pp; English.
XX
XX The present invention relates to new peptides derived from the H3 loop
XX of a serine/threonine kinase (STK). The peptides of the invention are
XX used to modulate STK activity, especially for treating cancer, diabetes,
XX obesity or a wide variety of central nervous system, inflammatory,
XX autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
XX regulating lipid metabolism. The peptides are also used to generate
XX antibodies that bind specifically to the parent STK, used e.g. for
XX identifying STK-expressing cells and to study intracellular distribution
XX of STK, and to identify or quantify ligands that bind to the H3 loop.
XX The present amino acid sequence represents the peptide sequence of the H3
XX loop of serine-threonine kinase polc kinase. This sequence is one of the
XX short peptides of the invention that selectively modulate the activity
XX of STK.
XX
XX
SQ Sequence 20 AA;
Query Match 81.6%; Score 40; DB 23; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
CY 1 MLLGRPPFE 9
DB 3 LLVGKPPFE 11
RESULT 31
AAB56690
ID AAB56690 standard; Protein; 329 AA.
XX
XX AAB56690;
XX
XX 17-MAR 2001 (first entry)
XX
XX Human prostate cancer antigen protein sequence SEQ ID NO:1268.
XX
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX
XX Homo sapiens.
XX
XX WO2000355174-A1.
XX
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05988.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HJMA-) HJMAN GENOME SCI INC.

PA (ROSE/) ROSEN C A.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-587513/55.
XX N-PSDB; AAF15893.
XX
XX Prostate cancer associated gene sequences, referred to as prostate
XX cancer antigens, useful for treatment, prevention, and diagnosis of
XX disorders such as prostate cancer -
XX
XX Claim 11; Page 1691-1692; 2338pp; English.
XX
XX AAF15566 to AAF16505 encode the human prostate cancer associated
XX proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
XX The prostate cancer antigens can have neuroprotective, cytostatic,
XX cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
XX nephrotropic, antiinfective, gynaecological and antibacterial activities,
XX and can be used in gene therapy. The prostate cancer antigen
XX polynucleotides may be used for detection of prostate cancer, chromosome
XX identification, as chromosome markers, and for numerous other diagnostic
XX or research purposes. The prostate cancer antigens may be used to treat
XX disorders such as neural, immune, muscular, reproductive,
XX gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
XX disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
XX AAB57303 represent sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 329 AA;
Query Match 81.6%; Score 40; DB 21; Length 329;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
CY 1 MLLGRPPFE 9
DB 260 LLVGKPPFE 268
RESULT 32
ABP73734
ID ABP73734 standard; Protein; 528 AA.
XX
XX ABP73734;
XX
XX 30-JAN-2003 (first entry)
XX
XX Candida albicans essential protein SEQ ID NO 7571.
XX
XX Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal.
XX
XX Candida albicans.
XX
XX WO2000253728-A2.
XX
XX 11-JUL-2002.
XX
XX 26-DEC-2001; 2001WO-US49486.
XX
XX 29-DEC-2000; 2000US-259128P.
XX 20-FEB-2001; 2001US-0792024.
XX 22-AUG-2001; 2001US-314050P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX WPI; 2002-566694/60.
XX N-PSDB; ABZ32284.
XX
XX Constructing strains for identifying gene products as effective targets
XX

PT for therapeutic intervention, by inactivating in the strain one allele
PT of a gene and placing other allele of the gene under conditional
PT expression -
XX
PS Claim 44: SEQ ID NO 7571; 167pp - Sequence Listing; English.
XX
CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthesis, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of an
CC essential Candida albicans protein used in the method of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.

SQ Sequence 528 AA;

Query Match 81.6%; Score 40; DB 23; Length 528;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLGKPPFE 9

Db 454 LLVGKPPFE 462

RESULT 33

AAU74656

ID AAU74656 standard; Protein; 531 AA.

XX AC AAU74656;

XX DT 09-APR-2002 (first entry)

XX DE Mammalian polo-like kinase (Plk).

XX KW Polo-like kinase; Plk; polo-box; cytostatic; neoplasm;
KW hyperproliferative disorder; cytokinesis; solid tumour;
KW carcinoma; sarcoma; cancer; small cell carcinoma; adenocarcinoma;
KW Mullerian tumour; squamous cell carcinoma; protein.

XX OS Mammalia.

XX FH Key Location/Qualifiers

FT Misc-difference 130

FT /label= Unknown

FT Misc-difference 131

FT /label= Unknown

FT Misc-difference 132

FT /label= Unknown

FT Misc-difference 133

FT /label= Unknown

FT Misc-difference 134

FT /label= Unknown

FT Misc-difference 135

FT /label= Unknown;

FT Misc-difference 136
FT /label= Unknown
FT Misc-difference 137
FT /label= Unknown
FT Misc-difference 138
FT /label= Unknown
FT Misc-difference 139
FT /label= Unknown
FT Misc-difference 140
FT /label= Unknown
FT Misc-difference 141
FT /label= Unknown
FT Misc-difference 147
FT /label= Unknown
FT Misc-difference 148
FT /label= Unknown
FT Misc-difference 149
FT /label= Unknown
FT Misc-difference 150
FT /label= Unknown
FT Misc-difference 151
FT /label= Unknown
FT Misc-difference 152
FT /label= Unknown
FT Misc-difference 153
FT /label= Unknown
FT Misc-difference 154
FT /label= Unknown
FT Misc-difference 155
FT /label= Unknown
FT Misc-difference 156
FT /label= Unknown
FT Misc-difference 157
FT /label= Unknown
FT Misc-difference 158
FT /label= Unknown
FT Misc-difference 159
FT /label= Unknown
FT Misc-difference 160
FT /label= Unknown
FT Misc-difference 161
FT /label= Unknown
FT Misc-difference 162
FT /label= Unknown
FT Misc-difference 163
FT /label= Unknown
FT Misc-difference 164
FT /label= Unknown
FT Misc-difference 165
FT /label= Unknown
FT Region
FT 410..439
FT /label= Polo-box
FT /note= "Core polo-box consensus sequence"
XX WO200190401-A2.
XX 29-NOV-2001.
XX 23-MAY-2001; 2001WO-US16903.
XX 23-MAY-2000; 2000US-206588P.
XX (HARD) HARVARD COLLEGE.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (USSH) US NAT INST OF HEALTH.
XX Lee KS, Song S, Erikson R;
XX WPI; 2002-106210/14.
XX Identifying polo-like kinase modulators by contacting eukaryotic cells
XX expressing polo-box peptides with test compounds and evaluating changes
XX in dominant negative cytokinesis-defective growth patterns .

XX PS Example 2; Fig 5; 57pp; English.

XX CC The invention describes a novel method of detecting compounds with

CC CC polo-like kinase (PLK) modulating activity. This comprises contacting

CC CC eukaryotic cells expressing polo-box or polo-box related peptides,

CC CC binding peptides comprising 25 contiguous residues from a polo-like

CC CC kinase C-terminal region, with a test compound. Ectopic expression of a

CC CC polo-box in a eukaryotic cell causes a severe cytokinetic defect in the

CC CC cell. These eukaryotic cells can also be tested with the test compound

CC CC used in the method of the invention. The polo-box related peptides and

CC CC polo-like kinase activity modulatory compounds can be used to inhibit or

CC CC enhance cellular proliferation and subsequently for treating

CC CC hyperproliferative disorders including neoplasia, solid tumours,

CC CC carcinomas, sarcomas and cancers e.g. small cell carcinoma,

CC CC adenocarcinoma, Mullerian tumours and squamous cell carcinomas. This

CC CC is the amino acid sequence of a mammalian polo-like kinase (Plk),

CC CC uncontrolled expression of the Plk family is implicated in the

CC CC development of human cancers, discussed in the method of the invention.

XX CC

SQ Sequence 531 AA;

Query Match 81.6%; Score 40; DB 23; Length 531;

Best Local Similarity 66.7%; Pred. No. 36;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

DB 204 LLVGKPPPE 212

RESULT 34

AAR74620

ID AAR74620 standard; Protein; 603 AA.

XX AC AAR74620;

XX AC

DT 25 MAR-2003 (updated)

DT 26-OCT-1995 (first entry)

DE Human lung tumour Polo-like kinase.

XX KW Polo-like kinase; PLK; serine threonine kinase; human; lung tumour;

XX KW autoimmune disease; lymphocyte activity.

XX CS Homo sapiens.

XX CS

EH Key Location/Qualifiers

FT Binding-site 60..86

FT /label= ATP-binding_motif

FT Region 174..177

FT /note= "motif that is highly conserved in protein

FT kinases"

FT Region 194..196

FT /note= "motif that is highly conserved in protein

FT kinases"

XX PN DE4329177-A1.

XX PD 02 MAR-1995.

XX PF 30 AUG-1993; 93DE-4329177.

XX PR 30-AUG-1993; 93DE-4329177.

XX PA (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.

XX PI Holtrich U, Rubsamen-Waigmann H, Strebhardt K;

XX PI Rubsamen-Waigmann H;

XX WPI; 1995-099454/14.

XX N-PSDS; AAC88155.

PT A polo-like serine threonine kinase-protein - isolated from

PT proliferating human tissue, useful in the determn of lymphocyte

PT activity, eg in auto-immune diseases

XX Claim 1; Page 8-10; 11pp; German.

PS

XX A human lung tumour-derived cDNA (AAQ88155) was found to have high

CC homology with sequences from members of the serine/threonine kinase

CC family. Due to the strong homology with the Drosophila polo gene,

CC the protein encoded by the new cDNA (AAR74620) was designated a polo-

CC like kinase (PLK). PLK mRNA is expressed in proliferating cells such

CC as placenta, colon and tumours of the lung, oesophagus, gut and

CC intestine. Resting lymphocytes do not express the PLK gene but after

CC stimulation with phytohaemagglutinin, PLK is expressed and can be

CC used as an indicator of lymphocyte stimulation.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 603 AA;

Query Match 81.6%; Score 40; DB 16; Length 603;

Best Local Similarity 66.7%; Pred. No. 41;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

DB 244 LLVGKPPPE 252

RESULT 35

AAU79306

ID AAU79306 standard; Peptide; 603 AA.

XX AC AAU79306;

XX AC

DT 02-JUL-2002 (first entry)

XX DE Mouse polo-like kinase (Plk).

XX KW Polo box; PBl; cytostatic; fungicide; protozoacide; antihelminthic;

XX KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;

XX KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;

XX KW cancer of the uterus; ovarian cancer; cervical cancer;

XX KW epithelial cancer; brain cancer; retina cancer; prostate cancer;

XX KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;

XX KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;

XX KW arthropod infection; mouse; polo-like kinase; Plk.

XX OS Mus musculus.

XX PN US6358738-B1.

XX PD 19-MAR-2002.

XX PF 13-MAY-1999; 99US-0311311.

XX PR 13-MAY-1998; 98US-085296P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Erikson RL, Lee KS;

XX DR WPI; 2002-314756/35.

XX PT Administering polo kinase inhibitors for the treatment of cancers and

XX PT fungal infections

XX PS Example 1; Column 59-64; 47pp; English.

XX CC The invention describes a method of inhibiting growth of an isolated

CC population of cells by inhibiting a cell polo kinase by administering a

CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a

CC carboxy terminal; domain of the polo kinase which excludes the polo

CC kinase catalytic domain. The method is used for the treatment of cancer

CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of the polo-like kinase (Plk), a
CC protein from which mitotic protein polo kinase inhibitory peptides are
CC derived.

SQ Sequence 603 AA;
Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
:|:|:|:|
Db 244 LLVGKPPPE 252

RESULT 36
AAU79308
ID AAU79308 standard; Peptide; 603 AA.
XX
AC AAU79308;
XX
DT 02 JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T210D mutant.
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.

OS Mus musculus.
OS Synthetic.

FH Key Location/Qualifiers
FT Misc difference 210 /note= "Wild type Thr substituted by Asp"
FT

XX US6358738-B1.

XX 19-MAR-2002.

XX 13-MAY-1999; 99US-0311311.

XX 13-MAY-1998; 98US-085296P.

XX (HARD) HARVARD COLLEGE.

XX Erikson RL, Lee KS;

XX WPI; 2002-314756/35.

XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections -

XX Example 1; Page -; 47pp; English.

XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.

CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.

SQ Sequence 603 AA;
Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
:|:|:|:|
Db 244 LLVGKPPPE 252

RESULT 37
AAU79309
ID AAU79309 standard; Peptide; 603 AA.
XX
AC AAU79309;
XX
DT 02 JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T210E mutant.
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.

OS Mus musculus.
OS Synthetic.

FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Thr substituted by Glu"
FT

XX US6358738-B1.

XX 19-MAR-2002.

XX 13-MAY-1999; 99US-0311311.

XX 13-MAY-1998; 98US-085296P.

XX (HARD) HARVARD COLLEGE.

XX Erikson RL, Lee KS;

XX WPI; 2002-314756/35.

XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections -

XX Example 1; Page -; 47pp; English.

XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.

CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
CY 1 MLLGRPPPE 9
Db 244 LLVGKPPPE 252
:::||||
RESULT 38
AAU79310
ID AAU79310 standard; Peptide; 603 AA.
XX
AC AAU79310;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T210V mutant.
XX
KW Polo box; PBI; cytostatic; fungicide; protozoacide; antihelmintic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Thr substituted by Val"
FT
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13 MAY 1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information

CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
CY 1 MLLGRPPPE 9
Db 244 LLVGKPPPE 252
:::||||
RESULT 39
AAU79311
ID AAU79311 standard; Peptide; 603 AA.
XX
AC AAU79311;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) E206V mutant.
XX
KW Polo box; PBI; cytostatic; fungicide; protozoacide; antihelmintic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Glu substituted by Val"
FT
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information

SQ Sequence 603 AA;
Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
: : : : :
Db 244 LLVGKPPPE 252

RESULT 40
AAU79312
ID AAU79312 standard; Peptide; 603 AA.
XX
AC AAU79312;
XX
ET C2-JUL 2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) E206N mutant.
XX
KW Polo box; P81; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; Helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; tutein.
XX
OS Mus musculus.
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Miscellaneous 206 /note= "Wild type Glu substituted by Asn"
FT
XX
PR US9358738-B1.
XX
PD 19 MAR 2002.
XX
PF 12-MAY 1999; 99US-0311311.
XX
PR 11 MAY 1998; 98US 085296P.
XX
PA CHARD; HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections
XX
PS Example 1; Page 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
: : : : :
Db 244 LLVGKPPPE 252

Search completed: November 14, 2003, 13:25:19
Job time : 34.7143 secs

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CM protein - protein search, using sw model
Run on: November 14, 2003, 13:23:00 ; Search time 11.8286 Seconds
(without alignments)
32.193 Million cell updates/sec

Title: US-09-736-076-15
Perfect score: 49
Sequence: 1 MJJGRPPFE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310838 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
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6: /cgn2_6/ptodata/1/aaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	(9)	3	US-08-861-338-15 Sequence 15, Appl
2	49	100.0	11	3	US-08-861-338-19 Sequence 19, Appl
3	49	100.0	272	1	US-08-252-995D-12 Sequence 12, Appl
4	49	100.0	272	2	US-08-834-108-12 Sequence 12, Appl
5	49	100.0	685	2	US-08-878-989-1 Sequence 1, Appl
6	49	100.0	685	3	US-09-136-282-2 Sequence 2, Appl
7	49	100.0	685	3	US-09-272-796-1 Sequence 1, Appl
8	49	100.0	685	3	US-09-505-744-2 Sequence 2, Appl
9	46	93.9	9	3	US-08-861-338-17 Sequence 17, Appl
10	41	83.7	8	3	US-08-861-338-16 Sequence 16, Appl
11	41	83.7	273	1	US-08-252-995D-10 Sequence 10, Appl
12	41	83.7	273	2	US-08-834-108-10 Sequence 10, Appl
13	41	83.7	416	1	US-08-252-995D-2 Sequence 2, Appl
14	41	83.7	416	2	US-08-834-108-2 Sequence 2, Appl
15	41	93.7	464	1	US-08-252-995D-6 Sequence 6, Appl
16	41	83.7	464	2	US-08-834-108-6 Sequence 4, Appl
17	41	83.7	925	1	US-08-252-995D-4 Sequence 4, Appl
18	41	83.7	925	2	US-08-834-108-4 Sequence 4, Appl
19	40	81.6	9	3	US-08-861-338-18 Sequence 18, Appl
20	40	81.6	20	3	US-08-861-338-6 Sequence 6, Appl
21	40	81.6	272	1	US-08-252-995D-14 Sequence 14, Appl
22	40	81.6	272	2	US-08-834-108-14 Sequence 14, Appl
23	40	81.6	603	3	US-09-198-122-2 Sequence 2, Appl
24	40	81.6	603	4	US-09-311-311C-26 Sequence 26, Appl
25	39	79.6	264	2	US-07-857-224B-17 Sequence 17, Appl
26	39	79.6	271	1	US-08-252-995D-11 Sequence 11, Appl
27	39	79.6	271	2	US-08-834-108-11 Sequence 11, Appl

28	39	79.6	303	4	US-09-739-455-12 Sequence 12, Appl
29	39	79.6	303	4	US-09-739-455-22 Sequence 22, Appl
30	38	77.6	259	4	US-09-252-991A-28679 Sequence 28679, A
31	38	77.6	275	1	US-08-252-995D-13 Sequence 13, Appl
32	38	77.6	275	2	US-08-834-108-13 Sequence 13, Appl
33	38	77.6	344	2	US-08-755-728-3 Sequence 3, Appl
34	38	77.6	344	2	US-08-974-655-3 Sequence 3, Appl
35	38	77.6	344	3	US-09-283-011-3 Sequence 3, Appl
36	38	77.6	347	2	US-09-016-000-1 Sequence 1, Appl
37	38	77.6	403	2	US-08-755-728-4 Sequence 4, Appl
38	38	77.6	403	2	US-08-974-655-4 Sequence 4, Appl
39	38	77.6	403	3	US-09-283-011-4 Sequence 4, Appl
40	38	77.6	737	4	US-09-772-647-4 Sequence 4, Appl
41	37	75.5	20	3	US-08-861-338-3 Sequence 3, Appl
42	37	75.5	182	4	US-09-134-001C-3742 Sequence 3742, Ap
43	37	75.5	220	1	US-08-233-146-2 Sequence 2, Appl
44	37	75.5	220	1	US-08-463-470-2 Sequence 2, Appl
45	37	75.5	264	2	US-07-857-224B-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-861-338-15
; Sequence 15, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861.338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; OTHER INFORMATION: Glutamic Acid-NH2"
US-08-861-338-15

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Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPPE 9
      1 MLLGRPPPE 9

Db      1 MLLGRPPPE 9
      1 MLLGRPPPE 9

RESULT 2
US-08-861-338-19
; Sequence 19, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861-338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CACC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION:
; OTHER INFORMATION: /note= "N Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Serine-NH2"
US-08-861-338-19

Query Match      100.0%; Score 49; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPPE 9
      1 MLLGRPPPE 9

Db      1 MLLGRPPPE 9
      1 MLLGRPPPE 9

RESULT 3
US-08-252-995D-12

```

```

; Sequence 12, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-252-995D-12

Query Match      100.0%; Score 49; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPPE 9
      1 MLLGRPPPE 9

Db      199 MLLGRPPPE 207
      1 MLLGRPPPE 207

RESULT 4
US-08-834-108-12
; Sequence 12, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```



```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-09-834-108-12

Query Match 100.0%; Score 49; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
   |||||
EB 199 MLLGRPPPE 207

RESULT 5
US-09-878-989-1
; Sequence 1, Application US/38878989
; Patent No. 5885803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVEHOB01
; CLONE: 39043
; US-08-878-989-1

Query Match 100.0%; Score 49; DB 2; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
   |||||
DB 273 MLLGRPPPE 281

RESULT 6
US-09-136-282-2
; Sequence 2, Application US/09136282
; Patent No. 6063609
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, KAREN
; APPLICANT: JACKSON, JEFFREY
; APPLICANT: HANSBURY, MICHAEL
; APPLICANT: NERURKAR, SANDHYA
; APPLICANT: ROSHAK, AMY
; APPLICANT: BOUZYK, MARK
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,282
; FILING DATE: 20-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,112
; FILING DATE: 20-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-136-282-2

Query Match 100.0%; Score 49; DB 3; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```
QY      1 MLLGRPPPE 9
      |||||
Db      273 MLLGRPPPE 281

RESULT 7
US-09-272-796-1
; Sequence 1, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Suiya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/078,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-032; US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENOB01
; CLONE: 39043
US-09-272-796-1

Query Match      100.0%; Score 49; DB 3; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPPE 9
      |||||
Db      273 MLLGRPPPE 281

RESULT 8
US-09-505-744-2
; Sequence 2, Application US/09505744
; Patent No. 6245544
; GENERAL INFORMATION:
; APPLICANT: Karen M. Anderson.
```

```
; APPLICANT: Mark M. Bouzyk
; APPLICANT: Michael J. Hansbury
; APPLICANT: Jeffrey R. Jackson
; APPLICANT: Sandhya S. Nerurkar
; APPLICANT: Amy K. Roshak
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; FILE REFERENCE: GH-70231-D1
; CURRENT APPLICATION NUMBER: US/09/505,744
; CURRENT FILING DATE: 2000-02-16
; EARLIER APPLICATION NUMBER: 09/136,282
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/056,112
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 685
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-505-744-2

Query Match      100.0%; Score 49; DB 3; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPPE 9
      |||||
Db      273 MLLGRPPPE 281

RESULT 9
US-08-861-338-17
; Sequence 17, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
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;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; OTHER INFORMATION: Glutamine Acid-NH2"
US-08-861-338-17
Query Match 33.9%; Score 46; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.5e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
| | | | |
Db 1 MLLGKPPPE 9

RESULT 10
US-08-861-338-16
; Sequence 16, Application US/08961338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DCS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861.338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "Phenylalanine-NH2"
US-08-861-338-16
Query Match 83.7%; Score 41; DB 3; Length 8;
Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 8
| | | | |
Db 1 MLLGKPPPE 8

```

```

RESULT 11
US-08-252-995D-10
; Sequence 10, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252.995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdzyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-252-995D-10
Query Match 83.7%; Score 41; DB 1; Length 273;
Best Local Similarity 66.7%; Pred. No. 3.3;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
| | | | |
Db 200 LLIGRPPFD 208

RESULT 12
US-08-834-108-10
; Sequence 10, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

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Db          118 ITGRPPFE 125

RESULT 27
S70964
pkns protein - Myxococcus xanthus
N:Alternate names: serine protein kinase homolog
C:Species: Myxococcus xanthus
C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
C:Accession: S70964
R:Zhang, W.; Inouye, M.; Inouye, S.
Mol. Microbiol. 20, 435-447, 1996
A:Title: Reciprocal regulation of the differentiation of Myxococcus xanthus by Pkn5 and
A:Reference number: S70964; MUID:96310380; PMID:9733241
A:Accession: S70964
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-380 <ZHA>
A:Cross-references: EMBL:U40656; NID:gl113924; PIDN:AAB40049.1; PID:gl113925
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C:Genetics:
A:Gene: pkn5

Query Match          75.5%; Score 37; DB 2; Length 380;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY          1 MLLGRPPFE 9
          |||:|:|:|:
Db          314 LLSGRPPFD 322

RESULT 28
KIHUCA
protein kinase C (EC 2.7.1.1-) alpha - human
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: S09496
R:Finkenzeller, G.; Marne, D.; Hug, H.
Nucleic Acids Res. 18, 2183, 1990
A:Title: Sequence of human protein kinase C alpha.
A:Reference number: S09496; MUID:90245676; PMID:2336401
A:Accession: S09496
A:Molecule type: mRNA
A:Residues: 1-672 <FIN>
A:Cross-references: EMBL:X52479; NID:g35482; PIDN:CAA36718.1; PID:g35483
C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-sp
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters,
C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C:Genetics:
A:Gene: GDB:PRKCA
A:Cross-references: GDB:128015; OMIM:176960
A:Map position: 17q22-17q23.2
C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kin
C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bindi
F:19-29/Region: phospholipid binding #status experimental
F:22-27/Region: pseudophosphorylation motif
F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
F:152-264/Domain: protein kinase C C2 region homology <K2>
F:337-597/Domain: protein kinase C C2 region homology <KIN>
F:345-353/Domain: protein kinase ATP-binding motif
F:368/Active site: Lys #status predicted
F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match          75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY          1 MLLGRPPFE 9
          |||:|:|:|:
Db          314 LLSGRPPFD 322

```

```

QY          1 MLLGRPPFE 9
          |||:|:|:|:
Db          531 MLACQPPFD 539

RESULT 29
KIRTC
protein kinase C (EC 2.7.1.1-) alpha - rat
N:Alternate names: protein kinase C type III
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: S02248; S02620
R:Ono, Y.; Fujii, T.; Igarashi, K.; Kikkawa, U.; Ogita, K.; Nishizuka, Y.
Nucleic Acids Res. 16, 5199-5200, 1988
A:Title: Nucleotide sequences of cDNAs for alpha and gamma subspecies of rat brain p
A:Reference number: S02129; MUID:88262515; PMID:3387228
A:Accession: S02248
A:Molecule type: mRNA
A:Residues: 1-672 <ONO>
A:Cross-references: EMBL:X07286; NID:g56913; PIDN:CAA30266.1; PID:g56914
C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonin
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol est
C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein
C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bi
F:19-29/Region: phospholipid binding #status experimental
F:22-27/Region: pseudophosphorylation motif
F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
F:152-264/Domain: protein kinase C C2 region homology <K2>
F:337-597/Domain: protein kinase C C2 region homology <KIN>
F:345-353/Region: protein kinase ATP-binding motif
F:368/Active site: Lys #status predicted
F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status

Query Match          75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY          1 MLLGRPPFE 9
          |||:|:|:|:
Db          531 MLACQPPFD 539

RESULT 30
KIMSCA
protein kinase C (EC 2.7.1.1-) alpha - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: S07104; JS0078
R:Megidish, T.; Mazurek, N.
Nature 342, 807-811, 1989
A:Title: A mutant protein kinase C that can transform fibroblasts.
A:Reference number: S07104; MUID:90098082; PMID:2601739
A:Accession: S07104
A:Molecule type: mRNA
A:Residues: 1-672 <MEG>
A:Cross-references: GB:X52685; GB:X51603; NID:g49938; PIDN:CAA36908.1; PID:g49939
A:Experimental source: strain Balb/c
R:Rose-John, S.; Dietrich, A.; Marks, F.
Gene 74, 465-471, 1988
A:Title: Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss 3T3 fibr
A:Reference number: JS0078; MUID:89232737; PMID:2469625
A:Accession: JS0078
A:Molecule type: mRNA
A:Residues: 1-146, 'D', 148-217, 'N', 219-276, 'AH', 279-312, 'V', 314-466, 'N', 468-471, 'N', 4
A:Cross-references: GB:M25811
A:Note: the authors translated the codon AAC for residue 141 as Lys; the sequence si
C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonin
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol est
C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membran

```

RESULT 37
JN0548
C:Protein kinase C (EC 2.7.1.1-) gamma - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 18-Jun-1999
C:Accession: JN0548; S20735; S29620
R:Bowers, B.C.; Parham, C.L.; Sikela, J.M.; Wehner, J.M.
Gene 123, 263-265, 1993
A:Title: Isolation and sequence of a mouse brain cDNA coding for protein kinase C-gamma
A:Reference number: JN0548; MUID:93154595; PMID:8428669
A:Accession: JN0548
A:Molecule type: mRNA
A:Residues: 1-697 <BOW>
A:Cross-references: EMBL:X67129; NID:g53696; PIDN:CAA47608.1; PID:g53697
A:Experimental source: Brain
R:Beitges, M.; Proikas, T.; Stabel, S.
Submitted to the EMBL Data Library, April 1992
A:Description: Comparison of the mouse and rat protein kinase C gamma gene promoter.
A:Reference number: S20735
A:Accession: S20735
A:Molecule type: DNA
A:Residues: 1-67 <LEI>
A:Cross-references: EMBL:X65720; NID:g53694; PIDN:CAA46636.1; PID:g53695
C:Genetics:
A:Introns: 57/2
C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C; Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding; F36-85/Domain: protein kinase C zinc-binding repeat homology <K21>
F:101-150/Domain: protein kinase C zinc-binding repeat homology <K22>
F:151-264/Domain: protein kinase C C2 region homology <K2>
F:349-614/Domain: protein kinase C2 region homology <KIN>
F:357-365/Region: protein kinase ATP-binding motif

Query Match 75.5%; Score 37; DB 2; Length 697;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
|||:|:
Db 548 MLAGQPPFD 556

RESULT 39
J24664
C:Protein kinase C (EC 2.7.1.1-) gamma - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1998 #sequence revision 13-May-1996 #text_change 23-Mar-2001
C:Accession: D24664; S31611; S36837
R:Coussens, L.; Parker, P.J.; Rhee, L.; Yang-Feng, T.L.; Chen, E.; Waterfield, M.D.; Fra
Science 233, 859-866, 1986
A:Title: Multiple, distinct forms of bovine and human protein kinase C suggest diversity
A:Reference number: A94291; MUID:86289426; PMID:3755548
A:Accession: D24664
A:Molecule type: mRNA
A:Residues: 1-313, 'VS', 316, 'T', 318 <COU>
A:Note: the authors translated the codon GCA for residue 170 as Ser and AGC for residue
R:Hug, H.
Submitted to the EMBL Data Library, September 1992
A:Description: Partial cDNA sequence of human protein kinase C zeta.
A:Reference number: S25605
A:Accession: S31611
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 162-697 <HUG>
A:Cross-references: EMBL:Z15114; NID:g35496; PIDN:CAA78920.1; PID:g35497
R:Kochs, G.; Hummel, R.; Meyer, D.; Hug, H.; Marne, D.; Sarre, T.F.
Eur. J. Biochem. 216, 597-606, 1993
A:Title: Activation and substrate specificity of the human protein kinase C alpha and ze
A:Reference number: S36836; MUID:93387312; PMID:8375396
A:Accession: S36837
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA

A:Residues: 162-697 <KOC>
A:Cross-references: EMBL:Z15114; NID:g35496; PIDN:CAA78820.1; PID:g35497
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 19
C:Genetics:
A:Gene: GDB:PRKCG
A:Cross-references: GDB:128017; OMIM:176980
A:Map position: 19q13.4-19q13.4
C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/thr
F:36-85/Domain: protein kinase C zinc-binding repeat homology <K21>
F:101-150/Domain: protein kinase C zinc-binding repeat homology <K22>
F:151-264/Domain: protein kinase C C2 region homology <K2>
F:349-614/Domain: protein kinase homology <KIN>
F:357-365/Region: protein kinase ATP-binding motif

Query Match 75.5%; Score 37; DB 2; Length 697;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
|||:|:
Db 548 MLAGQPPFD 556

RESULT 39
S69657
Hypothetical protein YDR490c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 22-Aug-1996 #sequence revision 06-Sep-1996 #text_change 19-Apr-2002
C:Accession: S69657
R:Dietrich, F.S.
Submitted to the EMBL Data Library, August 1995
A:Description: The sequence of S. cerevisiae cosmid 9410, 8035, 8166, and 9787.
A:Reference number: S69554
A:Accession: S69657
A:Molecule type: DNA
A:Residues: 1-766 <DIE>
A:Cross-references: EMBL:U33050; NID:g927726; PIDN:AAB64917.1; PID:g927745; MIPS:YDR
C:Genetics:
A:Gene: SGD:PKH1
A:Cross-references: SGD:S0002898
A:Map position: 4R
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
C:Keywords: ATP
F:123-391/Domain: protein kinase homology <KIN>
F:131-139/Region: protein kinase ATP-binding motif

Query Match 75.5%; Score 37; DB 2; Length 766;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
|||:|:
Db 330 MLAGKPPFK 338

RESULT 40
T15903
Protein kinase C homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text_change 09-Jun-2000
C:Accession: T15903
R:Fulton, B.
Submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid E01H11.
A:Reference number: Z18426
A:Accession: T15903
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-861 <FUL>
A:Cross-references: EMBL:U29376; NID:g868170; PID:g868172; PIDN:AAA68710.1
A:Experimental source: strain Bristol N2
C:Genetics:

AtGene: CHSPK1n-11
A:introns: 79/11; 102/2; 136/1; 163/3; 244/1; 297/3; 377/3; 484/3; 552/3; 623/1; 669/3; 6
C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase
P:104-153/Domain: protein kinase C zinc-binding repeat homology <K2N1>
P:169-218/Domain: protein kinase C zinc-binding repeat homology <K2N2>

Query Match 75.51; Score 37; DB 2; Length 861;
Best Local Similarity 66.78; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy : MLLGRPPPE 9
| | | | |
Db 605 MLAGQPPFD 613

Search completed: November 14, 2003, 13:28:50
Job time : 10.8 secs

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: November 14, 2003, 12:56:44 / Search time 6.68571 Seconds
(without alignments)
63.305 Million cell updates/sec

Title: US-09-736-076-15
Perfect score: 49
Sequence: 1 MLGRPPFE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post processing: Minimum Match 0
Maximum Match 100
Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	score	Query Match	Length	DB ID	Description
1	49	100.0	682	1	SNK_MOUSE
2	49	100.0	682	1	SNK_RAT
3	49	100.0	685	1	SNK_HUMAN
4	40	81.6	282	1	STKD_MOUSE
5	40	81.6	603	1	PLK1_HUMAN
6	40	81.6	603	1	PLK1_MOUSE
7	40	81.6	603	1	PLK1_RAT
8	39	79.6	576	1	POLO_DROME
9	39	79.6	679	1	KPC2_DROME
10	39	79.6	690	1	PKNB_BIFID
11	38	77.6	156	1	STKC_PIG
12	38	77.6	344	1	STKC_HUMAN
13	38	77.6	403	1	STK6_HUMAN
14	38	77.6	407	1	STK6_XENLA
15	38	77.6	408	1	ST6L_XENLA
16	38	77.6	634	1	KPC3_DROME
17	38	77.6	649	1	PLK1_CAEEL
18	38	77.6	660	1	PKNI_COREP
19	39	77.6	683	1	PL01_SCHPO
20	39	77.6	705	1	CDC5_YEAST
21	38	77.6	707	1	KPC2_CAEEL
22	38	77.6	736	1	KPCE_RABIT
23	38	77.6	737	1	KPCE_HUMAN
24	38	77.6	737	1	KPCE_MOUSE
25	38	77.6	737	1	KPCE_RAT
26	38	77.6	743	1	KPC2_APLCA
27	37	75.5	220	1	NHAB_PSECL
28	37	75.5	380	1	PKN5_MYXA
29	37	75.5	632	1	PKC2_CAEEL
30	37	75.5	649	1	KPCL_APLCA
31	37	75.5	658	1	KPC1_LYTF
32	37	75.5	672	1	KPCA_BOVIN
33	37	75.5	672	1	KPCA_HUMAN

34	37	75.5	672	1	KPCA_MOUSE
35	37	75.5	672	1	KPCA_RABIT
36	37	75.5	672	1	KPCA_RAT
37	37	75.5	682	1	KPCG_BOVIN
38	37	75.5	697	1	KPCG_HUMAN
39	37	75.5	697	1	KPCG_MOUSE
40	37	75.5	697	1	KPCG_RABIT
41	36	73.5	217	1	NU2M_MYTED
42	36	73.5	309	1	STKD_HUMAN
43	36	73.5	343	1	STKC_RAT
44	36	73.5	345	1	STKC_MOUSE
45	36	73.5	465	1	KPK1_ARATH

ALIGNMENTS

RESULT 1
SNK_MOUSE STANDARD: PRT; 682 AA.
AC P53351;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.-) (Serum inducible kinase).
DE kinase).
GN SNK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92375085; PubMed=1508211;
RA Simmons D.L., Neel B.G., Stevens R., Evett G., Erikson R.L.;
RT "Identification of an early-growth-response gene encoding a novel putative protein kinase."
RL Mol. Cell. Biol. 12:4164-4169(1992).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA.
CC -!- TISSUE SPECIFICITY: BRAIN, LUNG AND HEART.
CC -!- INDUCTION: BY SERUM AND PHORBOL ESTER.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.

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DR EMBL; M96163; -; NOT_ANNOTATED_CDS.
DR PIR; A44493; A44493;
DR MGD; MGI:1099790; SNK.
DR InterPro; IPR000959; POLO box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00659; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 54 59 POLY-HIS.
FT DOMAIN 79 331 PROTEIN KINASE.
FT NP_BIND 85 93 ATP (BY SIMILARITY).

```

FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 507 570 POLO BOX 1.
FT DOMAIN 603 674 POLO BOX 2.
SQ SEQUENCE 682 AA; 77811 MW; 586DEABFD7208A9D CRC64;

Query Match 100.0%; Score 49; DB 1; Length 682;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 270 MLLGRPPPE 278

RESULT 2
SNK_RAT
ID SNK_RAT STANDARD; PRT; 682 AA.
AC Q9R012;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.1.) (Serum inducible kinase).
DE kinase).
GN SNK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99452760; PubMed=10523297;
RA Kaussmann G., Weiler M., Wulff P., Jessberger S., Konietzko U., Seaidi C., Staubli U., Bereiter-Hahn U., Streibhardt K., Kuhl D.;
RT "The polo like protein kinases Pnk and Snk associate with a Ca(2+)-and integrin-binding protein and are regulated dynamically with synaptic plasticity.";
RT EMBL J. 18:5528-5539(1999).
RL
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLC SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC -----
DR EMBL: AF136583; AAF08366.1; -
DR InterPro: IPR000959; POLO box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00659; POLO box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS50078; POLO BOX; 2.
DR PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding. Repeat.
FT DOMAIN 54 59 POLY-HIS.
FT DOMAIN 79 331 PROTEIN_KINASE.
FT NP_BIND 95 93 ATP (BY SIMILARITY).
FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 507 570 POLO BOX 1.
FT DOMAIN 603 674 POLO BOX 2.
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```

SQ SEQUENCE 682 AA; 77919 MW; 58C50DEBDE83D5F3 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 682;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 270 MLLGRPPPE 278

RESULT 3
SNK_HUMAN
ID SNK_HUMAN STANDARD; PRT; 685 AA.
AC Q9NYJ3; O60679; Q96CV7; Q9UE61;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.1.) (Serum inducible kinase).
DE kinase).
GN SNK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ouyang B., Dai W.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Anderson K.M., Nerurkar S.S., Hansbury M.J., Fornwald J., Scott G., Bouzyk M., Mui P., Imbruglia G.S., Carlson K., Marshall L.A., Roshak A.K.;
RT "Identification and characterization of human serum-inducible kinase (SNK), a novel member of the polo-kinase family of cell cycle regulators: potential implication for regulation of vascular smooth muscle proliferation.";
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22398257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko J., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 110-408 FROM N.A.
RA Fidler C., Boulton J., Wang Jabs E., Wainscoat J.S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLC SUBFAMILY.
```

CC -!- SIMILARITY: Contains 2 POLO box domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF059617; AAC14573.1; --
DR FMBL: AF223574; AAF62897.1; --
DR EMBL: U85755; AAD00575.1; --
DR EMBL: HC013879; AAH13879.1; --
DR MIM: 607023; --
DR InterPro: IPR000959; POLO box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00659; POLO_box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00078; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 57 64 POLY-HIS.
FT DOMAIN 82 334 PROTEIN_KINASE.
FT NP_BIND 88 96 ATP (BY SIMILARITY).
FT BINDING 111 111 ATP (BY SIMILARITY).
FT ACT_SITE 205 205 BY SIMILARITY.
FT DOMAIN 510 573 POLO_BOX_1.
FT DOMAIN 606 677 POLO_BOX_2.
FT CONFLICT 28 28 A -> G (IN REF. 1).
SQ SEQUENCE 685 AA; 78236 MW; 6429F6FE930B333 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 685;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
273 MLLGRPPPE 281

RESULT 4
STKD_MOUSE STANDARD; PRT; 282 AA.
AC Q88445; Q9JLC2;
DT 28-FEB-2003 (Rel. 4); Created)
DT 28-FEB-2003 (Rel. 4); Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Serine/threonine protein kinase 13 (EC 2.7.1.37) (Aurora/Ipl1/Eg2
DE protein 1; (Aurora-C).
GN STK13 OR AIE1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1] -
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=99025616; PubMed=9809744;
Tseng T.C., Chen S.H., Hsu Y.P., Tang T.K.;
"Protein kinase profile of sperm and eggs: cloning and
characterization of two novel testis-specific protein kinases (AIE1,
AIE2) related to yeast and fly chromosome segregation regulators.";
DNA Cell Biol. 17:823-833(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=20551164; PubMed=11098217;

RA Hu H.M., Chuang C.K., Lee M.J., Tseng T.C., Tang T.K.;
RT "Genomic organization, expression, and chromosome localization of a
RT third aurora-related kinase gene, Aie1.";
RL DNA Cell Biol. 19:679-688(2000).
CC -!- FUNCTION: May play a part in organizing microtubules in relation
CC to the function of the centrosome/spindle pole during mitosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to spindle pole from anaphase to
CC cytokinesis (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed only in testis.
CC -!- DEVELOPMENTAL STAGE: Expressed on day 14 dpc in prepubertal
CC testis, expression reached its plateau on day 21 dpc and remained
CC at a high level in adult.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
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CC
CC EMBL: AF054620; AAC25954.1; --
DR EMBL: AF195272; AAF25838.1; --
DR HSSP: Q63450; 1A06.
DR MGD: MGI:132119; Stk13.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 16 266 PROTEIN_KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT CONFLICT 74 74 R -> P (IN REF. 2).
SQ SEQUENCE 282 AA; 32907 MW; 7CB8AEC4984B7883 CRC64;

Query Match 81.6%; Score 40; DB 1; Length 282;
Best Local Similarity 66.7%; Pred. No. 2.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
205 LLVGKPPPE 213

RESULT 5
PLK1_HUMAN STANDARD; PRT; 603 AA.
ID PLK1_HUMAN
AC P53350;
DT 01-OCT-1996 (Rel. 34; Created)
DT 01-OCT-1996 (Rel. 34; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Serine/threonine-protein kinase PLK (EC 2.7.1.-) (PLK-1) (Serine-
DE threonine protein kinase 13) (STPK13).
GN PLK OR PLK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94289293; PubMed=8018557;

RA Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.L.,
RA Ferris D.K.;
RT "Cloning and characterization of human and murine homologues of the
RT Drosophila polo serine-threonine kinase.";
RL Cell Growth Differ. 5:249-257(1994).
RN (2);
RP SEQUENCE FROM N.A.
RX MEDLINE=94067140; PubMed=7902533;
RA Lake R.C., Jeinek W.R.;
RT "Cell cycle and terminal differentiation-associated regulation of
RT the mouse mRNA encoding a conserved mitotic protein kinase.";
RL Mol. Cell. Biol. 13:7793-7801(1993).
RN (3);
RP SEQUENCE FROM N.A.
RX MEDLINE=95051109; PubMed=7962193;
RA Golsteyn R.M., Schultz S.J., Bartek J., Ziemiecki A., Ried T.,
RA Nigg E.A.;
RT "Cell cycle analysis and chromosomal localization of human Plk1, a
RT putative homologue of the mitotic kinases Drosophila polo and
RT Saccharomyces cerevisiae Cdc5.";
RL J. Cell Sci. 107:1509-1517(1994).
RN (4);
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94173904; PubMed=8127874;
RA Holtrich J., Wolf G., Braeuninger A., Karn T., Boehme B.,
RA Ruebsamen-Waigmann H., Strebhardt K.;
RT "Induction and down-regulation of Plk, a human serine/threonine
RT kinase expressed in proliferating cells and tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:1736-1740(1994).
RN (5);
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner J., Shenmen G.M., Schuler G.D.,
RA Aitschui S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farrer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay S.G., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,
RA Biakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: PLACENTA AND COLON.
CC -!- DEVELOPMENTAL STAGE: ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
CC DURING S PHASE.
CC -!- INDUCTION: BY GROWTH-STIMULATING AGENTS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC -----
DR EMBL; U01038; AA56634.1; -
DR EMBL; L19559; AA36659.1; -
DR EMBL; X73458; CAAS1837.1; -
DR EMBL; X75932; CAAS3536.1; -
DR EMBL; BC002369; AAH02369.1; -
DR EMBL; BC003002; AAH03002.1; -
DR EMBL; BC014846; AAH14846.1; -
DR PIR; S34130; S34130;
DR Genew; HGNC:9077; PLK.
DR GK; P53350; -
DR MIM; 602098; -
DR GO; GO:0004674; E:protein serine/threonine kinase activity; TAS.
DR GO; GO:0007067; P:mitosis; TAS.
DR GO; GO:0007048; P:oncogenesis; TAS.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR000959; POLC_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Nuclear protein.
FT DOMAIN 53 305 PROTEIN KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 480 POLO BOX 1.
FT DOMAIN 515 584 POLO BOX 2.
FT CONFLICT 2 2 S -> T (IN REF. 1).
FT CONFLICT 11 11 A -> P (IN REF. 1).
FT CONFLICT 58 58 F -> L (IN REF. 1).
FT CONFLICT 60 60 G -> S (IN REF. 1).
FT CONFLICT 73 73 A -> V (IN REF. 2).
FT CONFLICT 141 141 L -> P (IN REF. 4).
FT CONFLICT 227 227 G -> E (IN REF. 4).
FT CONFLICT 301 301 N -> G (IN REF. 2).
FT CONFLICT 495 495 A -> G (IN REF. 2).
FT CONFLICT 501 501 E -> Q (IN REF. 2).
SQ SEQUENCE 603 AA; 68254 MW; 178C2F13C10E8206 CRC64;
Query Match 81.6%; Score 40; DB 1; Length 603;
Best Local Similarity 66.7%; Pred.No. 4.7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPFE 9
Db 244 LLVGKPPFE 252
RESULT 6
PLK1_MOUSE
ID PLK1_MOUSE STANDARD; PRT; 603 AA.
AC Q07832;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase PLK (EC 2.7.1.-) (PLK-1) (Serine-
DE threonine protein kinase 13) (STPK13).
GN PLK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1] -
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Bone marrow;
RX MEDLINE=93281660; PubMed=8099445;
RA Clay F.J., McEwen S.J., Bertoncello I., Wilks A.F., Dunn A.R.;
RT "Identification and cloning of a protein kinase-encoding mouse gene,
Rf plk, related to the polo gene of Drosophila.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4882-4886(1993).
RW (2).
RE SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=94289293; PubMed=8018557;
RA Hamanaka R., Valoid S., Smith M.R., O'Connell C.D., Longo D.J.,
RA Ferris D.K.;
RT "Cloning and characterization of human and murine homologues of the
Rf Drosophila polo serine-threonine kinase.";
RL Cell Growth Differ. 5:249-257(1994).
RW (3).
RE SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=94067140; PubMed=7902533;
RA Lake R.J., Celinek W.R.;
RT "Cell cycle- and terminal differentiation-associated regulation of
Rf the mouse mRNA encoding a conserved mitotic protein kinase.";
RL Mol. Cell. Biol. 13:7793-7801(1993).
RW (1).
RE FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE.
CC (1).
CC SUBCELLULAR LOCATION: Nuclear.
CC (1).
CC TISSUE SPECIFICITY: NEWBORN AND ADULT SPLEEN, FETAL AND NEWBORN
CC KIDNEY, LIVER, BRAIN, THYMUS AND ADULT BONE MARROW, THYMUS,
CC OVARY AND TESTES.
CC (1).
CC DEVELOPMENTAL STAGE: IN THE THYMUS, LEVELS INCREASED DURING FETAL
CC DEVELOPMENT, WERE HIGHEST IN NEWBORN ANIMALS AND DECREASED IN THE
CC ADULT. IN THE TESTES, THE PLX LEVELS WERE HIGHER IN THE ADULT THAN
CC IN PREPUBESCENT MICE WHILE IN THE OVARY, THE LEVELS WERE HIGHER IN
CC THE PREPUBESCENT MICE. ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
CC DURING S PHASE.
CC (1).
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC (1).
CC SIMILARITY: Contains 2 POLO box domains.
CC (1).
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CC (1).
CC EMBL; L06144; AAA39948.1; .
DR EMBL; U01063; AAA56635.1; .
DR EMBL; L19558; AAA16071.1; .
DR PIR; A47545; A47545.
DR PIR; A54596; A54596.
DR MGD; MG197621; Plk.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Nuclear protein.
KW DOMAIN 53 305 PROTEIN KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 480 POLO BOX 1.

FT DOMAIN 515 584 POLO BOX 2.
FT CONFLICT 4 4 A -> V (IN REF. 1).
FT CONFLICT 15 15 A -> T (IN REF. 1).
FT CONFLICT 23 23 P -> L (IN REF. 1).
FT CONFLICT 27 27 V -> A (IN REF. 1).
FT CONFLICT 29 29 G -> S (IN REF. 1).
FT CONFLICT 41 41 P -> L (IN REF. 1).
FT CONFLICT 54 54 V -> I (IN REF. 1).
FT CONFLICT 495 495 A -> R (IN REF. 1).
SQ SEQUENCE 603 AA; 68300 MW; 1B9806463665FA10 CRC64;

Query Match: 81.6%; Score 40; DB 1; Length 603;
Best Local Similarity 66.7%; Pred. No. 4.7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db 244 LLVGKPPFE 252

RESULT 7
PLK1_RAT
ID PLK1_RAT STANDARD; PRT; 603 AA.
AC Q62673;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase PLK (EC 2.7.1.-) (PLK-1).
GN PLK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1).
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Amstrup J., Hansen J.A., Hxrlis Nielsen J.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBDJ databases.
CC (1).
CC FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE (BY SIMILARITY).
CC (1).
CC SUBCELLULAR LOCATION: Nuclear (By similarity).
CC (1).
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC (1).
CC SIMILARITY: Contains 2 POLO box domains.
CC (1).
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CC or send an email to license@isb-sib.ch).
CC (1).
CC EMBL; U10188; AAA18885.1; .
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Nuclear protein.
KW DOMAIN 53 305 PROTEIN KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 480 POLO BOX 1.
FT DOMAIN 515 584 POLO BOX 2.

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SQ SEQUENCE 603 AA; 68313 MW; 107AFFB3B7EDCC02 CRC64;
Query Match: 81.6%; Score 40; DB 1; Length 603;
Best Local Similarity 66.7%; Pred. No. 4.7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLJGRPPPE 9
Db 244 LLVGKPPPE 252

RESULT 8
PCLO_DROME STANDARD; PRT; 576 AA.
AC P52304; Q9V7B2;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase polo (EC 2.7.1.-).
GN PCLO OR CG12306.
CS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
RN 1;
FP SEQUENCE FROM N.A.
FC STRAIN=Canton-S;
EX MEDLINE=92084090; PubMed=1660828;
RA Liamazares S., Moreira A., Tavares A., Girdham C., Spruce B.A.,
RA Gonzalez C., Kares R.E., Glover D.M., Sunkel C.B.;
RA "Polo encodes a protein kinase homolog required for mitosis in
RA Drosophila.";
RL Genes Dev. 5:2153-2165(1991).
RN 12;
FP SEQUENCE FROM N.A.
FC STRAIN=Berkely;
EX MEDLINE=20156006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champagne M., Effeffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew P.M., Basu A., Baxendale J., Bayraktaroglu T., Beasley E.M.,
RA Benson K.Y., Bernos P.V., Bernier B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotner P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dedson K., Doup L.E., Downes M., Dugan-Rocha S., Durkin B.C., Dunn P.,
RA Durbin K.C., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.C., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McKernson D.,
RA Mervkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.X., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson J.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern J.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheer F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
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RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: MAY PLAY A ROLE IN REGULATING BOTH NUCLEAR AND
CC CYTOPLASMIC ASPECTS OF THE MITOTIC CYCLE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: LARVAL DISCS, BRAIN AND TESTIS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/PCLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 PCLO box domains.
CC -----
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CC -----
DR EMBL; X63361; CAA44963.1; -
DR EMBL; AE003514; AAF49036.1; -
DR PIR; S22127; S22127.
DR HSSP; Q63450; 1A06.
DR FlyBase; FBgn0003124; polo.
DR GO; GO:0005813; C:centrosome; IDA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR GO; GO:0007140; P:male meiosis; IMP.
DR GO; GO:0007067; P:mitosis; IMP.
DR InterPro; IPR000959; PCLO box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002293; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; PCLO box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMC0220; S_TKc; 1.
DR PROSITE; PS00078; PCLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 25 277 PROTEIN KINASE.
FT NP_BIND 31 39 ATP (BY SIMILARITY).
FT BINDING 54 54 ATP (BY SIMILARITY).
FT ACT_SITE 148 148 BY SIMILARITY.
FT DOMAIN 398 461 PCLO_BOX_1.
FT DOMAIN 496 564 PCLO_BOX_2.
FT CONFLICT 187 187 P -> A (IN REF. 1).
SQ SEQUENCE 576 AA; 66973 MW; 5022B9AC0E888FAD CRC64;

Query Match 79.6%; Score 39; DB 1; Length 576;
Best Local Similarity 66.7%; Pred. No. 6.9;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLJGRPPPE 9
Db 216 LLVGQPPPE 224

RESULT 9
KPC1_DROME STANDARD; PRT; 679 AA.
ID KPC1_DROME
AC P05130; Q9V7V6; Q9V7V7;
DT 13-AUG-1987 (Rel. 05, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, brain isozyme (EC 2.7.1.-) (PKC) (dPKC53E(BR)).
GN PKC53E OR PKC1 OR CG6622.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
```

RA PP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=Carton-S, and Oregon-R;
RX MEDLINE=87218499; PubMed=3107983;
RA Rosenthal A., Rhee L., Yadegari R., Paro R., Ullrich A., Goeddel D.V.;
RT "Structure and nucleotide sequence of a Drosophila melanogaster
RL protein kinase C gene";
RN EMBC J. 6:433-441(1987);
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196036; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Cocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale C., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck C., Brockstein P., Brothier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C.,
RA Hostin D., Houston K.A., Howland T.W., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Malshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy J., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacich J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard C., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sider-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhang K.M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RN Science 287:2185-2195(2003);
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=Berkeley; TISSUE=Ovary;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Kronmiller B., Li P.W., Liao G.,
RA Miranda A., Murgali C.J., Nunoo C., Pacieb J.M., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA Celisner S.E.;
RP Submitted (APR-2002) to the EMBL/GenBank/CCDS databases.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P05130-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P05130-2; Sequence=VSP_004743;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: HEAD NEURAL TISSUE.
CC -!- MISCELLANEOUS: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-
CC DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.

CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF OREGON-R.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. PKC
CC SUBFAMILY.
CC -----
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CC -----
CC EMBL: X05076; CAA28736.1; -
CC EMBL: X05279; CAA28890.2; -
CC EMBL: X05280; CAA28890.2; JOINED.
CC EMBL: X05281; CAA28890.2; JOINED.
CC EMBL: X05282; CAA28890.2; JOINED.
CC EMBL: X05283; CAA28890.2; JOINED.
CC EMBL: AE003805; AAF57932.1; -
CC EMBL: AE003805; AAF57933.1; -
CC EMBL: AY095003; AAY11331.1; -
CC HSSP: P05697; ITBN.
CC FlyBase: FBgn0003091; Pkc53E.
CC GO: GO:0004674; F:protein serine/threonine kinase activity; IDA.
CC GO: GO:0006468; P:protein amino acid phosphorylation; IDA.
CC InterPro: IPR000008; C2.
CC InterPro: IPR002219; DAG_PE-bind.
CC InterPro: IPR000961; Pkinase_C.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC InterPro: IPR001245; Tyr_kinase.
CC Pfam: PF00369; pkinase; 1.
CC Pfam: PF00130; DAG_PE-bind; 1.
CC Pfam: PF00168; C2; 1.
CC Pfam: PF00433; pkinase_C; 1.
CC PRINTS: PR00360; C2DOMAIN.
CC PRINTS: PR00008; DAGPEDOMAIN.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00109; C1; 1.
CC SMART: SM00239; C2; 1.
CC SMART: SM00133; S_TK_X; 1.
CC SMART: SM00220; S_TK; 1.
CC SMART: SM00219; TyKc; 1.
CC PROSITE: PS00499; C2_DOMAIN_1; 1.
CC PROSITE: PS50004; C2_DOMAIN_2; 1.
CC PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
CC PROSITE: PS50081; DAG_PE_BIND_DOM_2; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Multigene family; Zinc;
KW Phorbol-ester binding; Alternative splicing.
FT DOMAIN 46 104 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 120 169 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 191 278 C2 DOMAIN.
FT DOMAIN 350 608 PROTEIN KINASE.
FT NP_BIND 356 364 ATP (BY SIMILARITY).
FT BINDING 379 379 ATP (BY SIMILARITY).
FT ACT_SITE 474 474 BY SIMILARITY.
FT VARSPLIC 67 77 CGYQSGYAWMG -> WG (in isoform Short).
FT /FTId=VSP_004743.
FT VARIANT 437 437 M -> I.
FT CONFLICT 608 608 F -> S (IN REF. 1).
FT CONFLICT 634 648 DVSNFDKQFTSEKTD -> MCPTLTSSSHQKQT (IN
FT REF. 1).
FT CONFLICT 649 679 MISSING (IN REF. 1).
SQ SEQUENCE 679 AA; 77695 MW; 3C69AD351E36B7DC CRC64;
Query Match 79.6%; Score 39; DB 1; Length 679;

Best Local Similarity 66.7%; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPF 9
|||
Db 542 MLVGPDPFD 550

RESULT 10
PKNB_BIFLO STANDARD; PRT; 690 AA.
AC Q8G6P9;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine-protein kinase pknB (EC 2.7.1.37).
GN PKNB OR BL0589.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=NC 2705;
RX MEDLINE=22284377; PubMed=12381787;
RA Schell M.A., Karmirantzou M., Snel B., Vilianova D., Berger B.,
Pessi G., Zwielen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: Contains 4 PASTA domains.

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EMBL; AEC14680; AAN24413.1; -
InterPro; IPR005543; PASTA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR022290; Ser_thr_kinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF03793; PASTA; 2.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00740; PASTA; 4.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding; Repeat; Complete proteome.
FT DOMAIN 14 285 PROTEIN KINASE.
FT DOMAIN 399 467 PASTA 1.
FT DOMAIN 468 536 PASTA 2.
FT DOMAIN 539 601 PASTA 3.
FT DOMAIN 602 666 PASTA 4.
FT DOMAIN 667 689 GLY-RICH.
FT NP_BIND 20 28 ATP (BY SIMILARITY).
FT BINDING 43 43 ATP (BY SIMILARITY).
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 690 AA; 72243 MW; 6A439EABCE5D92D CRC64;

Query Match 79.6%; Score 39; DB 1; Length 690;
Best Local Similarity 87.5%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 MLLGRPPPF 8
|||
Db 217 MLTGRPPF 224

RESULT 11
STKC_PIG STANDARD; PRT; 156 AA.
AC Q9N0X0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora-B)
DE (Fragment).
GN STK12.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1].
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=22232338; PubMed=12270437;
RA Braun F., Hosseini S.M., Lorf T., Laabs S., Ringe B.;
RT "Differential gene expression during intestinal ischemia-reperfusion
injury.";
RL Transplant. Proc. 34:2301-2302(2002).
CC -!- FUNCTION: Maybe directly involved in regulating the cleavage of
polar spindle microtubules and is a key regulator for the onset of
cytokinesis during mitosis (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
in late anaphase and concentrated into the midbody in telophase
and cytokinesis. Colocalized with gamma tubulin in the mid-body
(By similarity).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.

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EMBL; AF244364; AAF61735.1; -
InterPro; IPR002052; N6_Mtase.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR0109; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
FT NON_TER 1 1
FT DOMAIN <1 >156 PROTEIN KINASE.
FT ACT_SITE 51 51 BY SIMILARITY.
FT NON_TER 156 156
SQ SEQUENCE 156 AA; 17867 MW; CD23040EDB633FCE CRC64;

Query Match 77.6%; Score 38; DB 1; Length 156;
Best Local Similarity 66.7%; Pred. No. 2.8;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPF 9
|||
Db 117 LLVGNPPFE 125


```
RESULT 12
STKC HUMAN STANDARD; PRT; 344 AA.
AC Q96GD4; O14630; C60446; Q95083; Q96DV5; Q9JQ46;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora- and Ipl1-
DE like midbody-associated protein 1) (AIM-1) (Aurora/IPL1-related kinase
DE 2) (Aurora-related kinase 2) (STK-1) (Aurora-B).
GN STK12 OR AIM1 OR ARK2 OR AIK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=98183439; PubMed=9514916;
RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
RA Gilbert D.J., Jenkins N.A., Cope land N.G., Yagita H., Okumura K.;
RT "cDNA cloning, expression, subcellular localization, and chromosomal
RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
RT 1 and 2.";
RJ Biochem. Biophys. Res. Commun. 244:285-292(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99025855; PubMed=9809983;
RA Tatsuka M., Katayama H., Ota T., Tanaka T., Odashima S., Suzuki F.,
RA Terada Y.;
RT "Multinuclearity and increased ploidy caused by overexpression of the
RT aurora- and Ipl1-like midbody-associated protein mitotic kinase in
RT human cancer cells.";
RJ Cancer Res. 58:4811-4816(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99025855; PubMed=9809983;
RA Tatsuka M., Katayama H., Ota T., Tanaka T., Odashima S., Suzuki F.,
RA Terada Y.;
RT "Multinuclearity and increased ploidy caused by overexpression of the
RT aurora- and Ipl1-like midbody-associated protein mitotic kinase in
RT human cancer cells.";
RJ Cancer Res. 58:4811-4816(1998).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21364697; PubMed=11471245;
RA Prigent C., Gill R., Trower M., Sansseau P.;
RT "In silico cloning of a new protein kinase, AIK2, related to
RT Drosophila aurora using the new tool: EST Blast.";
RJ In Silico Biol. 1:123-128(1999).
RN [5]
RP SEQUENCE FROM N.A.
RA Zhang Q., Yu L., Bi A.;
RT "Cloning of a novel human gene homologous to mouse STK 1.";
RJ Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max A.M., Wang J., Hsieh F.,
RA Diatchenko J., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton V., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.C., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smolius D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RJ Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP REVIEW.
RX MEDLINE=21306577; PubMed=11413462;
RA Nigg B.A.;
RT "Mitotic kinases as regulators of cell division and its checkpoints.";
RJ Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
CC -!- FUNCTION: May be directly involved in regulating the cleavage of
CC polar spindle microtubules and is a key regulator for the onset of
CC cytokinesis during mitosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
CC in late anaphase and concentrated into the midbody in telophase
CC and cytokinesis. Colocalized with gamma tubulin in the mid-body.
CC -!- TISSUE SPECIFICITY: High level expression seen in the thymus. It
CC is also expressed in the spleen, lung, testis, colon, placenta and
CC fetal liver. Expressed during S and G2/M phase and expression is
CC upregulated in cancer cells during M phase.
CC -!- DISEASE: Disruptive regulation of expression is a possible
CC mechanism of the perturbation of chromosomal integrity in cancer
CC cells through its dominant-negative effect on cytokinesis.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC -----
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CC -----
DR EMBL; AF008552; AAC12709.1; -
DR EMBL; AB011450; BAA32136.1; -
DR EMBL; AB011446; BAA82709.1; -
DR EMBL; AF004022; AAB65786.1; -
DR EMBL; AF015254; AAC98891.1; -
DR EMBL; BC000442; AAH00442.1; -
DR EMBL; BC009751; AAH09751.1; -
DR EMBL; BC013300; AAH13300.1; -
DR HSSP; Q63450; IA06.
DR Genew; HGNC:11390; STK12.
DR GK; Q96GD4; -
DR MIM; 604970; -
DR InterPro; IPR002052; N6_Mtase.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 77 327 PROTEIN_KINASE.
FT NP_BIND 83 91 ATP (BY SIMILARITY).
FT BINDING 106 106 ATP (BY SIMILARITY).
FT ACT_SITE 200 200 BY SIMILARITY.
FT CONFLICT 14 15 RQ -> DK (IN REF. 5).
FT CONFLICT 70 70 R -> RR (IN REF. 6; AAH13300).
FT CONFLICT 161 161 E -> M (IN REF. 4 AND 5).
FT CONFLICT 167 169 Q/S -> HKT (IN REF. 4).
FT CONFLICT 179 179 T -> TVRR (IN REF. 4).
FT CONFLICT 180 180 I -> VRVV (IN REF. 5).
FT CONFLICT 226 226 P -> T (IN REF. 3).
FT CONFLICT 249 250 MH -> ID (IN REF. 3).
FT CONFLICT 271 271 MISSING (IN REF. 3).
FT CONFLICT 298 298 T -> M (IN REF. 6; AAH09751/AAH13300).
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SQ SEQUENCE 344 AA; 39280 MW; 8325E3EF5A1FB170 CRC64;
Query Match 77.6%; Score 38; DB 1; Length 344;
Best Local Similarity 66.7%; Pred. No. 6.3;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 XLIGRRPPE 9
D6 266 LLVGNPFFE 274

RESULT 13
STK6_HUMAN
ID STK6_HUMAN STANDARD; PRT; 403 AA.
AC C14965; C60445; C75873; Q9BQD6; Q9UPG5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15 SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine kinase 6 (EC 2.7.1.37) (Serine/threonine kinase 15)
DE (Aurora/IPL1-related kinase 1) (Aurora-related kinase 1) (HARK1)
DE (Aurora-A) (Breast-tumor-amplified kinase)
DE STK6 OR STK15 OR AIK OR ARK1 OR AUKA OR BTAk.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
FP 1.
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=97298083; PubMed=9153231;
RA Kimura M., Kotani S., Hattori T., Sumi N., Yoshioka T., Todokoro K.,
RA Okano Y.;
RT "Cell cycle-dependent expression and spindle pole localization of a
RT novel human protein kinase, Aik, related to Aurora of Drosophila and
RT yeast [p11]";
RL J. Biol. Chem. 272:13766-13771(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98183439; PubMed=9514916;
RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
RT "cDNA cloning, expression, subcellular localization, and chromosomal
RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
RT 1 and 2";
RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=98442657; PubMed=9771714;
RA Zhou H., Kuang J., Zhong L., Kuo W.-L., Gray J.W., Sahin A.,
RA Brinkley B.R., Sen S.;
RT "Tumour amplified kinase STK15/BTAK induces centrosome amplification,
RT aneuploidy and transformation.";
RL Nat. Genet. 20:189-193(1998).
RN [4]
RP SEQUENCE FROM N.A.
RA Wang L., Thibodeau S.N.;
RT "Mutational analysis of the STK15 gene in human tumors.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Ragguely C.L.,
RA Bailey C., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley C.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
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RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivasalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix, Colon, Kidney, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP CELL-CYCLE REGULATION.
RX MEDLINE=21895866; PubMed=11790771;
RA Tanaka M., Ueda A., Kanamori H., Ideguchi H., Yang J., Kitajima S.,
RA Ishigatsubo Y.;
RT "Cell-cycle-dependent regulation of human aurora A transcription is
RT mediated by periodic repression of E4TF1.";
RL J. Biol. Chem. 277:10719-10726(2002).
RN [8]
RP REVIEW.
RX MEDLINE=21306577; PubMed=11413462;
RA Nigg E.A.;
RT "Mitotic kinases as regulators of cell division and its checkpoints.";
RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
CC -!- FUNCTION: May play a role in cell cycle regulation during anaphase
CC and/or telophase, in relation to the function of the
CC centrosome/spindle pole region during chromosome segregation.
CC Maybe involved in microtubule formation and/or stabilization. May
CC play a key role during tumor development and progression.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells
CC and at each spindle pole in mitosis.
CC -!- TISSUE SPECIFICITY: Highly expressed in testis and weakly in
CC skeletal muscle, thymus and spleen. Also highly expressed in
CC colon, ovarian, prostate, neuroblastoma, breast and cervical
CC cancer cell lines. Expression is cell-cycle regulated, low in
CC G1/S, accumulates during G2/M, and decreases rapidly after.
CC -!- PTM: Phosphorylated.
CC -!- DISEASE: Defects in STK6 are responsible for numerical centrosome
CC aberrations including aneuploidy.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
```

CC in positions 105, 125, 129, 235 and 241.
CC -!- CAUTION: Although authors have considered STK6 and STK15 as two
CC different proteins, it is clear that they are the same protein.
CC
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CC
CC -----
DR EMBL; D84212; BAA23592.1; AJT_FRAME.
DR EMBL; AF008551; AAC12708.1; -
DR EMBL; AF011467; AAC23448.1; -
DR EMBL; AF011468; AAC63902.1; -
DR EMBL; AF195947; AAF29508.1; -
DR EMBL; AF195942; AAF29508.1; JOINED.
DR EMBL; AF195943; AAF29508.1; JOINED.
DR EMBL; AF195944; AAF29508.1; JOINED.
DR EMBL; AF195945; AAF29508.1; JOINED.
DR EMBL; AF195946; AAF29508.1; JOINED.
DR EMBL; AL121914; CAC12717.1; -
DR EMBL; BC001280; AAH01280.1; -
DR EMBL; BC002499; AAH02499.1; -
DR EMBL; BC006423; AAH06423.1; -
DR EMBL; BC027464; AAH27464.1; -
DR GK; O14965; -
DR MIM; 602687; -
DR MIM; 603072; -
DR HSSP; P24941; IAHU.
DR Genew; HGNC:11409; STK6.
DR Genew; HGNC:11393; STK15.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0005819; C:spindle; TAS.
DR GO; GO:0007067; P:mitosis; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYRKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 133 383 PROTEIN KINASE.
FT NP_BIND 139 147 ATP (BY SIMILARITY).
FT BINDING 162 162 ATP (BY SIMILARITY).
FT ACT_SITE 256 256 BY SIMILARITY.
FT CONFLICT 31 31 F -> I (IN REF. 3).
FT CONFLICT 57 57 V -> I (IN REF. 2).
SQ SEQUENCE 403 AA; 45809 MW; 125F3594834CD157 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 403;
Best Local Similarity 75.0%; Pred. No. 7.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPFE 9
|:|:|
DB 323 LVGKPPFE 330

RESULT 14
STK6_XENLA
ID STK6_XENLA STANDARD: PRT: 407 AA.
AC Q91820;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serine/threonine protein kinase Eg2 (EC 2.7.1.37) (pEg2) (p46Eg26s).
GN EG2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RX MEDLINE=98122855; PubMed=9454730;
RA Roghi C., Giet R., Uzbekov R., Morin N., Chartrain I., Le Guellec R.,
RA Couturier A., Doree M., Phillippe M., Prigent C.;
RT "The Xenopus protein kinase pEg2 associates with the centrosome in a
RT cell cycle-dependent manner, binds to the spindle microtubules and is
RT involved in bipolar mitotic spindle assembly.";
RL J. Cell Sci. 111:557-572(1998).
CC -!- FUNCTION: Associates with the centrosome in a cell-cycle dependent
CC manner and invades the microtubules at the poles of the spindle
CC during mitosis suggesting that it may be involved in the corect
CC formation of bipolar mitotic spindles.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
CC especially from prophase through anaphase. Partially colocalised
CC with gamma tubulin in the centrosome, from S to M phase.
CC -!- TISSUE SPECIFICITY: Highly expressed in ovary and testis.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC -----

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DR EMBL; Z17207; CAA78915.1; -
DR PIR; S52243; S52243.
DR HSSP; P24941; IAQ1.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 140 390 PROTEIN KINASE.
FT NP_BIND 146 154 ATP (BY SIMILARITY).
FT BINDING 169 169 ATP (BY SIMILARITY).
FT ACT_SITE 263 263 BY SIMILARITY.
SQ SEQUENCE 407 AA; 46372 MW; DE1628A2C6D11277 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 407;
Best Local Similarity 75.0%; Pred. No. 7.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPFE 9
|:|:|
DB 330 LVGKPPFE 337

RESULT 15
ST6L_XENLA
ID ST6L_XENLA STANDARD: PRT: 408 AA.
AC Q91819;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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RE Serine/threonine protein kinase Eg2-like (EC 2.7.1.37) [p46XIEg22].
CS Xenopus laevis (African clawed frog).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
CC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RA Roghi C., Le Guellec R., Paris C., Couturier A., Philippe M.;
RT "Eg2, selected by differential screening encodes a new Xenopus protein
RT kinase family.";
RL Submitted (Oct-1992) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
CC especially from prophase through anaphase. Partially colocalised
CC with gamma tubulin in the centrosome, from S to M phase (by
CC similarity).
CC -!- PTM: Phosphorylated (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC -----
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CC -----
DR EMBL; Z17206; CAA78914.1; ALT_INIT.
DR HSSP; P24943; 1AQ1.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000601; Prot_kinase; 1.
DR SMART; SMC0220; S_TKC; 1.
DR SMART; SMC0219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Cell cycle; transferase; Serine/threonine-protein kinase; ATP binding;
KW Phosphorylation.
FT DOMAIN 140 390 PROTEIN_KINASE.
FT NP_BIND 146 154 ATP (BY SIMILARITY).
FT BINDING 169 169 ATP (BY SIMILARITY).
FT ACT_SITE 263 263 BY SIMILARITY.
SQ SEQUENCE 408 AA; 46461 MW; 5756A69C7357AEE5 (CDS);
Query Match 77.6%; Score 38, DB 1; Length 408;
Best Local Similarity 75.0%; Pred. No. 715;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 LLGRPPE 9
Db 330 LVGKPPPE 337
RESULT 16
KPC3_DROME STANDARD; PRT; 534 AA.
AC P13678; Q9VAQ6;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase C (EC 2.7.1.1-) (PKC) (pPKC98F).
GN PKC98E OR PKC3 OR CG1954.
OS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=89249302; PubMed=2720775;
RA Schaeffer E., Smith D., Mardon G., Quinn W., Zuker C.;
RT "Isolation and characterization of two new Drosophila protein kinase
RT C genes, including one specifically expressed in photoreceptor
RT cells.";
RL Cell 57:403-412(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya P., Brothman P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeter F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- MISCELLANEOUS: THIS IS A CALCIUM-ACTIVATED,
CC PHOSPHOLIPID-DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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DR EMBL; J04848; AAA28818.1; -
DR EMBL; AE003768; AAF56846.1; ALT_INIT.
DR PIR; B32392; B32392.
DR HSSP; P28867; IPTQ.
DR FlyBase; FBgn0003033; PKC98E.
DR InterPro; IPR002219; DAG_PE-bind.
```

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DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00130; DAG_PE_bind; 2.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00433; pkinase_C; 1.
DR PRINTS: PR00008; DAGPECDMAIN.
DR ProDom: PD000032; Prot_kinase; 1.
DR SMART: SMC0109; C1; 2.
DR SMART: SMC0133; S_TK_X; 1.
DR SMART: SY00220; S_TKC; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS00381; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Multigene family; Zinc;
KW Phorbol-ester binding.
FT DOMAIN 72 121 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 147 196 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 303 560 PROTEIN KINASE.
FT NP BIND 309 317 ATP (BY SIMILARITY).
FT BINDING 332 332 ATP (BY SIMILARITY).
FT ACT SITE 422 427 BY SIMILARITY.
SQ SEQUENCE 634 AA; 71156 MW; 3AE3A3D6B7A276BA CRC64;

Query Match 77.6%; Score 35; DB 1; Length 634;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 MLLGRPPPE 9
RL 495 MMAGQPPPE 503

RESULT 17
PUNKI_CAEEL STANDARD; PRT; 649 AA.
AC P34331; O61662; Q76763;
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase plx1; EC 2.7.11.1 (Polo like
kinase-1).
GN PLX1 OR PLC1 OR C14B9.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidea;
OI Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID:6239;
PI 1.
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=99304501; PubMed=10376213;
RA Cuyang B., Wang Y., Dai W.;
RT "Caenorhabditis elegans contains structural homologs of human prk and
plx.";
RL DNA Seq. 10:109-113(1999).
RN 1.
RP SEQUENCE FROM N.A. (ISOFORM A), FUNCTION, AND SUBCELLULAR LOCATION.
RC STRAIN=Bristol N2;
RX MEDLINE=20190108; PubMed=10660671;
RA Chase D., Serafinas C., Ashcroft N., Kosinski M., Longo D.,
RA Ferris D.K., Golden A.;
RT "The polo-like kinase PLX-1 is required for nuclear envelope breakdown
and the completion of meiosis in Caenorhabditis elegans.";
RL Genesis 26:26-41(2000).
RN 13.
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Coysey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
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RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Ropra A., Saunders D., Showkeen R.,
RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
RN 14.
RP REVISIONS, AND ALTERNATIVE SPLICING.
RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Required for oocyte nuclear envelope breakdown before
entry of oocyte into spermatheca. In mitotic cells, plays a role
in spindle organization and centrosome maturation. In meiotic
cells, required for spindle dynamics and probably for spindle
attachment to the chromosomes. Zygotic role in the development of
the germline and nerve cord.
CC -!- SUBCELLULAR LOCATION: In mitosis, remains associated with
centrosomes entering prophase through to anaphase. During
metaphase, found at the chromosomes of the metaphase plate. In
meiosis, detected at centrosomes after pronuclear meeting in post-
meiotic 1-cell embryos. Associated with chromatin during
chromosome segregation of anaphase and in the region between the
dividing chromosomes. Cytoplasmic in mature, unfertilized oocytes.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=b;
CC IsoId=P34331-1; Sequence=Displayed;
CC Name=a;
CC IsoId=P34331-2; Sequence=VSP_004928;
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
EMBL; AF057165; AAC14129.1;
EMBL; AF080581; AAC34661.1;
EMBL; L15188; AAA27947.2;
EMBL; L15188; AAM22025.1;
PIR; T43337; T43337.
HSSP; Q63450; 1A06.
WormPep; C14B9.4a; CE26649.
WormPep; C14B9.4b; CE30602.
GO; GO:0005634; C:nucleus; IEPI.
GO; GO:0005524; F:ATP binding activity; ISS.
GO; GO:0004674; F:protein serine/threonine kinase activity; ISS.
GO; GO:0007417; P:central nervous system development; IMP.
GO; GO:0007098; P:centrosome cycle; IMP.
GO; GO:0007077; P:mitotic nuclear envelope breakdown; IMP.
GO; GO:0007052; P:mitotic spindle assembly; IMP.
GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
InterPro; IPR000959; POLO_box.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00659; POLO_box; 2.
ProDom; PD000001; Prot_kinase; 1.
SMART; SMC0219; TyrKC; 1.
PROSITE; PS50078; POLO_BOX; 2.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
```


KW ATP-binding; Serine/threonine-protein kinase; Transferase; Repeat;
KW Nuclear protein; Alternative splicing.
FT DOMAIN 38 290 PROTEIN_KINASE
FT NP BIND 45 52 ATP (BY SIMILARITY).
FT BINDING 67 67 ATP (BY SIMILARITY).
FT ACT SITE 162 162 BY SIMILARITY.
FT DOMAIN 423 485 POLO BOX 1.
FT DOMAIN 520 589 POLO BOX 2.
FT VARSPLIC 93 89 VNERR:L -> MTQEVQ (in isoform a).
FT /FTID=VSP 004928
SQ SEQUENCE 649 AA; 73633 MW; 54D969F140D7A43B CRC64;

Query Match 77.6%; Score 38; DB 1; Length 649;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db 229 LLFGQPPFE 237

RESULT 18
PKNI_COREF STANDARD; PRT; 660 AA.
AC Q8F0I5;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine protein kinase CE0033 (EC 2.7.1.37).
GN CE0033.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS 314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikee K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS 314."
RU Submitted (MAY-2002) to the EMBL/GenBank/DSJ databases.
-- 1 CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: Contains 3 PASTA domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; APC05214; BAC16843.1; -
DR InterPro; IPR005543; PASTA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF03793; PASTA; 3.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00740; PASTA; 3.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; Transferase; Serine/threonine protein kinase;
KW ATP-binding; Repeat; Complete proteome.
FT DOMAIN 9 278 PROTEIN_KINASE.
FT DOMAIN 377 443 PASTA 1.
FT DOMAIN 444 512 PASTA 2.

FT DOMAIN 513 577 PASTA 3.
FT NP BIND 15 23 ATP (BY SIMILARITY).
FT BINDING 38 38 ATP (BY SIMILARITY).
FT ACT_SITE 136 136 BY SIMILARITY.
SQ SEQUENCE 660 AA; 69646 MW; D33D797EB02D44B1 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 660;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db 207 LVTGRPPFE 215

RESULT 19
PLOI_SCHPO STANDARD; PRT; 683 AA.
ID_PLOI_SCHPO
AC P50528;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase plol (EC 2.7.1.37).
GN PLOI OR SPAC23C11.16.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=95262899; PubMed=7744248;
RA Ohkura H., Hagan I.M., Glover D.M.;
RT "The conserved Schizosaccharomyces pombe kinase plol, required to
RT form a bipolar spindle, the actin ring, and septum, can drive septum
RT formation in G1 and G2 cells."
RL Genes Dev. 9:1059-1073(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -!- FUNCTION: REQUIRED TO FORM A BIPOLAR SPINDLE, THE ACTIN RING AND
CC SEPTUM. FUNCTIONS UPSTREAM OF THE WHOLE SEPTUM FORMATION PATHWAY.
CC INCLUDING ACTIN RING FORMATION (REGULATED BY LATE SEPTATION GENES)
CC AND SEPTAL MATERIAL DEPOSITION (REGULATED BY EARLY SEPTATION
CC GENES). BEHAVES AS A "SEPTUM-PROMOTING FACTOR", AND COULD ALSO BE


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CC INVOLVED IN INDUCING OTHER LATE EVENTS OF CELL DIVISION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC -----
DR EMBL; X85758; CAA59766.1; -
DR EMBL; Z98559; CAB1167.1; -
DR PIR; T38254; T38254.
DR HSSP; Q63450; 1A06.
DR GeneDB SPombe; SPAC23C11.16; -
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PDC00001; Prot_kinase; 1.
DR SMART; SMC0220; S_TKC; 1.
DR PROSITE; PS50078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 41 296 PROTEIN KINASE.
FT NP_BIND 47 55 ATP (BY SIMILARITY).
FT BINDING 69 69 ATP (BY SIMILARITY).
FT ACT_SITE 163 163 BY SIMILARITY.
FT DOMAIN 500 567 POLO BOX 1.
FT DOMAIN 604 670 POLO BOX 2.
SQ SEQUENCE 683 AA; 77301 MW; FALCDDEF9B913917 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 683;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Eb 233 LLIGKPPFQ 241

RESULT 20
CDC5_YEAST STANDARD; PRT; 705 AA.
AC P32562;
DT 01-CCT-1993 (Rel. 27, Created)
DT 01-CCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cell cycle protein kinase CDC5/MSD2 (EC 2.7.11.37).
GN CDC5 OR PKX2 OR MSD2 OR YMR001C OR YMR270.03C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A364A;
RX MEDJINE=93309479; PubMed=8321244;
RA Kitada K., Sugino A., Johnston L.H., Johnson A.L.;
RT "A multicopy suppressor gene of the Saccharomyces cerevisiae G1 cell
RT cycle mutant gene dbf4 encodes a protein kinase and is identified as
RT CDC5."
RJ Mol. Cell. Biol. 13:4445-4457(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
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RX PubMed=9169872;
RA Bowman S., Churher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII."
RL Nature 387:90-93(1997).
RN [3]
RP PHOSPHORYLATION OF SCC1.
RX PubMed=11371343;
RA Alexandru G., Uhlmann F., Mechtler K., Poupard M.-A., Nasmyth K.;
RT "Phosphorylation of the cohesin subunit Scc1 by Polo/Cdc5 kinase
RT regulates sister chromatid separation in yeast."
RL Cell 105:459-472(2001).
CC -!- FUNCTION: Protein kinase required for the cell cycle.
CC Phosphorylates SCC1/MCD1.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
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CC -----
DR EMBL; M84220; AAA02576.1; -
DR EMBL; Z48613; CAA88516.1; -
DR PIR; A48144; A48144.
DR HSSP; Q63450; 1A06.
DR SGD; S0004603; CDC5.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0006261; P:DNA dependent DNA replication; IDA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PDC00001; Prot_kinase; 1.
DR SMART; SMC0220; S_TKC; 1.
DR PROSITE; PS50078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Cell cycle; Cell division; Serine/threonine-protein kinase;
KW Transferase; ATP-binding; Repeat.
FT DOMAIN 82 337 PROTEIN KINASE.
FT NP_BIND 88 96 ATP (BY SIMILARITY).
FT BINDING 110 110 ATP (BY SIMILARITY).
FT ACT_SITE 204 204 BY SIMILARITY.
FT DOMAIN 520 587 POLO BOX 1.
FT DOMAIN 619 692 POLO BOX 2.
SQ SEQUENCE 705 AA; 81030 MW; B5A25F1BBBEAA3DC CRC64;

Query Match 77.6%; Score 38; DB 1; Length 705;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db 274 LLIGKPPFQ 282

RESULT 21
KPC2_CAEEEL STANDARD; PRT; 707 AA.
ID KPC2_CAEEEL
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AC E34885;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein kinase C-like 2 (EC 2.7.1.1) (PKC1B).
GN K1N-13 OR PKC1B.
CS Caenorhabditis elegans.
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
CC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94179345; PubMed=8132661;
RA Land M., Islas-Trejo A., Freedman J.H., Rubin C.S.;
RT "Structure and expression of a novel, neuronal protein kinase C
RT (PKC1B) from Caenorhabditis elegans. PKC1B is expressed selectively
RT in neurons that receive, transmit, and process environmental
RT signals."
RL J. Biol. Chem. 269:9234-9244(1994).
CC 1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC 1- SURCELLULAR LOCATION: ASSOCIATED WITH MEMBRANES AND THE
CC CYTOSKELETON.
CC 1- TISSUE SPECIFICITY: EXPRESSED SELECTIVELY IN NEURONS THAT RECEIVE,
CC TRANSMIT AND PROCESS ENVIRONMENTAL SIGNALS.
CC 1- SIMILARITY: Contains 2 zinc-dependent phorbol ester and DAG
CC binding domains.
CC 1- SIMILARITY: Contains 1 C2 domain.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC
CC EMBL; J00181; AAA18259.1; -;
CC EMBL; J00965; AAA17996.1; -;
CC PIR; A53530; A53530.
CC HSSP; P28867; IPTQ.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000961; Pkinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00168; C2; 1.
CC Pfam; PF00130; DAG_PE-bind; 2.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00433; pkinase_C; 1.
CC PRINTS; PR00008; DAGPEDOMAIN.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00109; C1; 2.
CC SMART; SM00239; C2; 1.
CC SMART; SM00133; S_TK_X; 1.
CC SMART; SM00220; S_TKG; 1.
CC PROSITE; PS50004; C2_DOMAIN_2; 1.
CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
CC PROSITE; PS00381; DAG_PE_BIND_DOM_2; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Zinc;
KW Phorbol-ester binding; Repeat; Membrane; Cytoskeleton.
FT DOMAIN 1 98 C2 DOMAIN.
FT DOMAIN 171 221 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 249 298 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 378 638 PROTEIN KINASE.
FT NP_BIND 384 392 ATP (BY SIMILARITY).

FT BINDING 407 407 ATP (BY SIMILARITY).
FT ACT_SITE 502 502 BY SIMILARITY.
SQ SEQUENCE 707 AA; 80122 MW; 3DC762C8A7A7BA64 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 707;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
I: |||||
Db 570 MMAGQPPPE 578

RESULT 22
KPCE RABIT
ID KPCE_RABIT STANDARD; PRT; 736 AA.
AC P10830;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.1) (nPKC-epsilon).
GN PRKCE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN 11;
RP SEQUENCE FROM N.A.
RX MEDLINE=8823367; PubMed=3370672;
RA Ohno S., Akita Y., Konno Y., Imajoh S., Suzuki K.;
RT "A novel phorbol ester receptor/protein kinase, nPKC, distantly
RT related to the protein kinase C family."
RL Cell 53:731-741(1988).
CC 1- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC 1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC 1- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC 1- SIMILARITY: Contains 1 C2 domain.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M20014; AAA31426.1; -;
CC HSSP; P28867; IPTQ.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000961; Pkinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00168; C2; 1.
CC Pfam; PF00130; DAG_PE-bind; 2.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00433; pkinase_C; 1.
CC PRINTS; PR00008; DAGPEDOMAIN.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00109; C1; 2.
CC SMART; SM00239; C2; 1.
CC SMART; SM00133; S_TK_X; 1.
CC SMART; SM00220; S_TKG; 1.
CC PROSITE; PS50004; C2_DOMAIN_2; 1.
CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
CC PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Repeat; ATP-binding; Transferase; Phosphorylation;
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
 FT DOMAIN 1 99 C2 DOMAIN
 FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 407 667 PROTEIN KINASE.
 FT NP_BIND 421 421 ATP (BY SIMILARITY).
 FT BINDING 436 436 ATP (BY SIMILARITY).
 FT ACT_SITE 531 531 BY SIMILARITY.
 FT MOD_RES 702 702 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 709 709 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 SQ SEQUENCE 736 AA; 83515 MW; 26104FEE59E98FEB CRC64;
 Query Match 77.6%; Score 38; DB 1; Length 736;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGRPPFE 9
 Db 599 MMAGQPPFE 607
 RESULT 23
 KPCE_HUMAN
 ID KPCE_HUMAN STANDARD; PRT; 737 AA.
 AC Q02156; Q9UE81;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 21-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
 GN PRKCE OR PKCE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9300318; PubMed=1382605;
 RA Basta P., Strickland M.B., Holmes W., Locnis C.R., Ballas L.N.,
 Burns D.,
 RT "Sequence and expression of human protein kinase C-epsilon."
 RU Biochim. Biophys. Acta 1132:154-160(1992).
 RN [2]
 RP SEQUENCE OF 1-116 FROM N.A.
 RA Waterston R.;
 RI Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME.
 CC -1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
 CC -1- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -1- SIMILARITY: Contains 1 C2 domain.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC
 CC EMBL; X65293; CAA46388.1;
 CC EMBL; U51244; AAD38855.1;
 CC PIR; S28942; S28942.
 CC HSSP; P28867; IPTQ.
 CC Genbank; HGNC:9401; PRKCE.
 CC MIM; 176975; -.

DR GO; GO:0005624; C:membrane fraction; TAS.
 DR GO; GO:0004697; F:protein kinase C activity; TAS.
 DR GO; GO:0004871; F:signal transducer activity; TAS.
 DR GO; GO:0006917; P:induction of apoptosis; TAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG-PE-bind.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00130; DAG-PE-bind; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS50004; C2 DOMAIN 2; 1.
 DR PROSITE; PS00479; DAG-PE-BIND_DOM_1; 2.
 DR PROSITE; PS00081; DAG-PE-BIND_DOM_2; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Repeat; ATP-binding; Transferase; Phosphorylation;
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
 FT DOMAIN 1 99 C2 DOMAIN
 FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 408 668 PROTEIN KINASE.
 FT NP_BIND 414 422 ATP (BY SIMILARITY).
 FT BINDING 437 437 ATP (BY SIMILARITY).
 FT ACT_SITE 532 532 BY SIMILARITY.
 FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 SQ SEQUENCE 737 AA; 83673 MW; 85032D0A091A1F7F CRC64;
 Query Match 77.6%; Score 38; DB 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGRPPFE 9
 Db 600 MMAGQPPFE 608
 RESULT 24
 KPCE_MOUSE
 ID KPCE_MOUSE STANDARD; PRT; 737 AA.
 AC P16054;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
 GN PRKCE OR PKCE OR PKCEA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89137541; PubMed=2917656;
 RA Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
 RT "Unique substrate specificity and regulatory properties of
 RT PKC-epsilon: a rationale for diversity."
 RL FEBS Lett. 243:351-357(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98127436; PubMed=9467942;
 RA Wang Q.J., Acs P., Goodnight J., Blumberg P.M., Mischak H.,

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RA Mushinski J.F.;
RT "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and -
RT epsilon chimeras, is responsible for conferring tumorigenicity to
RT NIH3T3 cells, whereas both regulatory and catalytic domains of
RT PKC-epsilon contribute to in vitro transformation.";
RJ Cncogene 16:53-60(1998).
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Wheeler D.L.;
RL Submitted (DEC-2000) to the EMBL/GenBank/CCBJ databases.
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL; AF028009; AAB84189.1; -
DR EMBL; AF325507; AAG53692.1; -
DR PIR; S02270; KIMSCE.
DR HSSP; P28567; IPTQ.
DR MGD; MG1197599; Prkce.
DR CC; GO:0004699; F:calcium independent protein kinase C activity; IDA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00220; S_TKG; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 1 99 C2 DOMAIN.
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 408 668 PROTEIN KINASE.
FT NP_BIND 414 422 ATP (BY SIMILARITY).
FT BINDING 437 437 ATP (BY SIMILARITY).
FT ACT_SITE 532 532 BY SIMILARITY.
FT MCD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MCD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 737 AA; 83560 MW; 7AE8B8CC1CC9F57 CRC64;
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Query Match 77.6%; Score 38; DS 1; Length 737;
Best local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MLLGRPPPF 9
Db 600 MMAGQPPFE 608

RESULT 25
KPCE_RAT
ID_KPCE_RAT STANDARD; PRT; 737 AA.
AC P09216;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
GN PKCE OR PKCE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88198270; PubMed=2834337;
RA Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Nishizuka Y.;
RT "Identification of three additional members of rat protein kinase C
RT family: delta-, epsilon- and zeta-subspecies.";
RL FEBS Lett. 226:125-128(1987).
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL; M18331; AAA41872.1; -
DR PIR; B28163; KIRTCE.
DR PDB; 1GMI; 25-OCT-01.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TKG; 1.
DR SMART; SM00220; S_TKG; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
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DR PROSITE; PSS0081; DAG_PE_BIND_DOM_2; 2;
LR PROSITE; PSS0107; PROTEIN_KINASE_ATP; 1;
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1;
DR PROSITE; PSS0018; PROTEIN_KINASE_ST; 1;
KW Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW 3D-structure.
FT DOMAIN 1 99 C2 DOMAIN.
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 408 668 PROTEIN KINASE.
FT NP_BIND 414 422 ATP (BY SIMILARITY).
FT BINDING 437 437 ATP (BY SIMILARITY).
FT ACT_SITE 532 532 BY SIMILARITY.
FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 737 AA; 83478 MW; 6AD6999EFDD2659F CRC64;

Query Match 77.6%; Score 38; DB 1; Length 737;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
Db 600 MWAGQPPPE 608

RESULT 26
KPC2_APLCA
ID KPC2_APLCA STANDARD; PRT; 743 AA.
AC Q16975;
DT 15-JUL-1999 (Rel. 38, Created)
ET 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calcium-independent protein kinase C (EC 2.7.11.-) (APC II).
GN PKC2
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysioidea; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RI SEQUENCE FROM N.A.
RX MEDLINE=91332620; PubMed=1869917;
RA Kruger K.E., Sossin W.S., Sacktor T.O., Beiswenger S.,
RA Schwartz J.H.;
RT "Cloning and characterization of Ca(2+)-dependent and Ca 2+-
RT independent PKCs expressed in Aplysia sensory cells."
RI J. Neurosci. 11:2303-2313(1991).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=93194877; PubMed=8449941;
RA Sossin W.S., Diaz-Arastia R., Schwartz J.H.;
RT "Characterization of two isoforms of protein kinase C in the nervous
RT system of Aplysia californica."
RJ J. Biol. Chem. 268:5763-5768(1993).
RN [3]
RP DOMAIN C2.
RX MEDLINE=93348616; PubMed=8346555;
RA Sossin W.S., Schwartz J.H.;
RT "Ca(2+)-independent protein kinase Cs contain an amino-terminal domain
RT similar to the C2 consensus sequence."
RJ Trends Biochem. Sci. 18:207-208(1993).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=98334636; PubMed=9668085;
RA Pepio A.M., Fan X., Sossin W.S.;
RT "The role of C2 domains in Ca2+-activated and Ca2+-independent protein
RT kinase Cs in aplysia."
RJ J. Biol. Chem. 273:19040-19048(1998).
RN [5]
RP ERRATUM.
RA Pepio A.M., Fan X., Sossin W.S.;
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RL J. Biol. Chem. 273:22856-22856(1998).
RN [6]
RP CHARACTERIZATION.
RX MEDLINE=98138438; PubMed=9477951;
RA Pepio A.M., Sossin W.S.;
RT "The C2 domain of the Ca(2+)-independent protein kinase C Apl I:
RT inhibits phorbol ester binding to the C1 domain in a phosphatidic
RT acid-sensitive manner."
RL Biochemistry 37:1256-1263(1998).
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
CC SIMILARITY).
CC -!- ENZYME REGULATION: REQUIRES HIGH LEVELS OF PHOSPHATIDYL SERINE TO
CC BE ACTIVATED. THE PRESENCE OF THE C2 DOMAIN LOWERS THE AFFINITY OF
CC PROTEIN KINASE C ACTIVATORS FOR THE C1 DOMAINS AND THIS INHIBITION
CC CAN BE REMOVED BY PHOSPHATIDYL SERINE. PHOSPHATIDIC ACID, HOWEVER,
CC IS MUCH MORE POTENT THAN PHOSPHATIDYL SERINE IN REDUCING C2 DOMAIN-
CC MEDIATED INHIBITION, SUGGESTING THAT PHOSPHATIDIC ACID MAY BE A
CC REQUIRED COFACTOR FOR THE ACTIVATION OF APL II.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN NERVOUS TISSUES, OVOTESTIS AND
CC GUT.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL; M94884; AAA27771.1; -
DR HSSP; P28867; IPTQ.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; FALSE_NEG.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Transferase; Serine/threonine-protein kinase;
KW Phorbol-ester binding; Zinc; Repeat.
FT DOMAIN 1 108 C2 DOMAIN.
FT DOMAIN 177 226 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 248 297 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 403 663 PROTEIN KINASE.
FT NP_BIND 409 417 ATP (BY SIMILARITY).
FT BINDING 432 432 ATP (BY SIMILARITY).
FT ACT_SITE 527 527 BY SIMILARITY.
SQ SEQUENCE 743 AA; 84413 MW; 4C982C563CA2B659 CRC64;
```


Query Match 77.6%; Score 38; DB 1; Length 743;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 595 MMAGQPPFE 603

RESULT 27
NHAB_PSECL STANDARD; PRT; 220 AA.
AC P27763;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrile hydratase subunit beta (EC 4.2.1.84) (Nitrilase) (NHase).
GN NTHB.
OS Pseudomonas chlororaphis (Pseudomonas aureofaciens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=333;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-23 AND 158-170.
RC STRAIN=B23;
RX MEDLINE=91193202; PubMed=2013568;
RA Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
RA Beppu T.;
RT "Cloning and characterization of genes responsible for metabolism of
nitrile compounds from Pseudomonas chlororaphis B23.";
RL J. Bacteriol. 173:2465-2472(1991).
CC FUNCTION: NHASE CATALYZES THE HYDRATION OF VARIOUS NITRILE
CC COMPOUNDS TO THE CORRESPONDING AMIDES. INDUSTRIAL PRODUCTION OF
CC ACRYLAMIDE IS NOW BEING DEVELOPED USING SOME OF THESE ENZYMES.
CC CATALYTIC ACTIVITY: An aliphatic amide = a nitrile + H(2)O.
CC SUBUNIT: Heterodimer of an alpha and a beta chain.
CC SIMILARITY: BELONGS TO THE NITRILE HYDRATASE SUBUNIT BETA FAMILY.
CC
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EMBL; D90216; BAA14246.1;
PIR; B42725; B42725.
HSSP; P13449; 2AHJ.
InterPro; IPR003168; NHase_beta.
PFam; PF02211; NHase_beta; 1.
Lyase.
KW
SQ SEQUENCE 220 AA; 24545 MW; 191AE1C5F14D4864 CRC64;
Query Match 75.5%; Score 37; DB 1; Length 220;
Best Local Similarity 75.0%; Pred. No. 6.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLGRPPFE 9
DB 118 LTGRPPFE 125

RESULT 28
PKN5_MYXXA STANDARD; PRT; 360 AA.
AC P54737;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase pkn5 (EC 2.7.1.37).
GN PKN5.

OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DZF1;
RX MEDLINE=96310380; PubMed=8733241;
RA Zhang W., Inouye M., Inouye S.;
RT "Reciprocal regulation of the differentiation of Myxococcus xanthus
by Pkn5 and Pkn6, eukaryotic-like Ser/Thr protein kinases.";
RL Mol. Microbiol. 20:435-447(1996).
CC FUNCTION: Pkn5 and pkn6 may have reciprocal roles in growth and
CC development. Pkn5 may be a kinase that negatively regulates
CC development.
CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC SUBCELLULAR LOCATION: Cytoplasmic.
CC DEVELOPMENTAL STAGE: Expressed constitutively throughout the life
CC cycle, with slight increases at an early stage of development.
CC PTM: Autophosphorylated at serine residues.
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC
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EMBL; U40656; AAB40049.1;
PIR; S70964; S70964.
PhosSite; P54737;
InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 9 378 PROTEIN KINASE.
FT NP_BIND 15 23 ATP (BY SIMILARITY).
FT BINDING 38 38 ATP (BY SIMILARITY).
FT ACT_SITE 244 244 BY SIMILARITY.
SQ SEQUENCE 380 AA; 41924 MW; DC3ADF24420C1F1 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 380;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 314 LLSGRPPFD 322

RESULT 29
PLK2_CAEEL STANDARD; PRT; 632 AA.
ID PLK2_CAEEL
AC Q9N2L7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase plk-2 (EC 2.7.1.-) (Polo-like
DE Kinase-2).
GN PLK-2 OR Y71F9B.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.

```
RX MEDLINE=20541295; PubMed=11092748;
RA Chase D., Golden A., Heidecker G., Ferris D.K.;
RT "Caenorhabditis elegans contains a third polo-like kinase gene.";
RL DNA Seq. 11:327-334(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN: Bristol N2;
RA Bradshaw-Cordum H., Scott K., Graves T.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be required for cell division and may have a role
CC during G1 or S phase (By similarity).
CC ! SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLC SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC -----
DR EMBL; AC024201; AAF36014.1; -
DR EMBL; AF194964; AAF28314.1; -
DR HSSP; G63450; 1AC6.
DR WormPep; Y71F9B.7; CE22877.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:003524; F:ATP binding activity; ISS.
DR GO; GO:0034674; F:protein serine/threonine kinase activity; ISS.
DR GO; GO:0037049; P:cell cycle; NAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR InterPro; IPR000959; POLO box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF03659; POLO box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM02220; S_TKC; 1.
DR PROSITE; PS50078; POLO BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DCM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase; Repeat;
KW Nuclear protein.
FT DOMAIN 36 287 PROTEIN KINASE.
FT NP_BIND 43 50 ATP (By similarity).
FT BINDING 65 65 ATP (By similarity).
FT ACT_SITE 159 159 BY SIMILARITY.
FT DOMAIN 412 476 POLO BOX 1.
FT DOMAIN 511 580 POLO BOX 2.
SQ SEQUENCE 632 AA; 72071 MW; 1B2EB58C15ABED9 CRC64;

Query Match: 75.5%; Score 37; DB 1; Length 632;
Res. Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 1 MLLGRPPPE 9
Db 226 LLEGGPPPE 234

RESULT 30
KPC1 APLCA STANDARD; PRT; 649 AA.
AC Q16974;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calcium-dependent protein kinase C (EC 2.7.11.-) (APL 1).
GN PRKC1.
OS Aplysia californica (California sea hare).
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OC Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysioidea; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91332620; PubMed=1869917;
RA Kruger K.E., Sossin W.S., Sacktor T.C., Bergold P.J., Beushausen S.,
RA Schwartz J.H.;
RT "Cloning and characterization of Ca(2+)-dependent and Ca(2+)-
RT independent PKCs expressed in Aplysia sensory cells.";
RL J. Neurosci. 11:2303-2313(1991).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=93194877; PubMed=8449941;
RA Sossin W.S., Diaz-Arrastia R., Schwartz J.H.;
RT "Characterization of two isoforms of protein kinase C in the nervous
RT system of Aplysia californica.";
RL J. Biol. Chem. 268:5763-5768(1993).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98334636; PubMed=9668085;
RA Pepio A.M., Fan X., Sossin W.S.;
RT "The role of C2 domains in Ca2+-activated and Ca2+-independent protein
RT kinase Cs in aplysia.";
RL J. Biol. Chem. 273:19040-19048(1998).
RN [4]
RP ERRATUM.
RA Pepio A.M., Fan X., Sossin W.S.;
RL J. Biol. Chem. 273:22856-22856(1998).
CC -!- FUNCTION: THIS IS CALCIUM-DEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME. ACTIVATION OF PKC BY
CC SEROTONIN RESULTS IN PRESYNAPTIC FACILITATION OF DEPRESSED
CC SENSORY-TO-MOTOR NEURON SYNAPSES, WHICH IS THOUGHT TO UNDERLIE
CC BEHAVIORAL DISHABITUATION.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
CC SIMILARITY).
CC -!- ENZYME REGULATION: ACTIVATED BY PHOSPHATIDYL SERINE.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC; TRANSLOCATED TO NEURONAL
CC MEMBRANES.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL; M94883; AAA27770.2; -
DR HSSP; P05697; 1TEN.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
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DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00499; C2_DOMAIN 1; 1.
 DR PROSITE; PS00004; C2_DOMAIN 2; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM 1; 2.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM 2; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP binding; Transferase; Serine/threonine-protein kinase.
 KW Phorbol-ester binding; Zinc; Repeat.
 FT DOMAIN 22 71; PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 86 135; PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 157 244; C2 DOMAIN.
 FT DOMAIN 320 578; PROTEIN KINASE.
 FT NP_BIND 326 334; ATP (BY SIMILARITY).
 FT BINDING 349 349; ATP (BY SIMILARITY).
 FT ACT_SITE 444 444; BY SIMILARITY.
 SQ SEQUENCE 649 AA; 74079 MW; A53253399284E33C CRC64;
 Query Match 75.5%; Score 37; DB 1; Length 649;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGRPPFE 9
 DB 512 MLAGQPPFD 520
 RESULT 31
 KPCA_LYTP1
 ID KPCA_LYTP1 STANDARD; PRT; 658 AA.
 AC Q25378;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protein kinase C (EC 2.7.1.-).
 GN PKC1.
 OS Lytechinus pictus (Painted sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinozoa; Euechinozoa; Echinacea; Temnopleurida; Toxopneustidae;
 OC Lytechinus.
 OX NCBI_TaxID=7653;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RA Rakow T.L., Shen S.S.;
 RT Molecular cloning and characterization of protein kinase C from the
 RT sea urchin Lytechinus pictus.;
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME (BY SIMILARITY).
 CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC
 CC -----
 CC EMBL; J02967; AAA03447.1; -.
 CC HSSP; P05697; lTEN.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_PE-bind.

DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00130; DAG_PE-bind; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00499; C2_DOMAIN 1; 1.
 DR PROSITE; PS00004; C2_DOMAIN 2; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM 1; 2.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM 2; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Transferase; Serine/threonine-protein kinase;
 KW Phorbol-ester binding; Zinc; Repeat.
 FT DOMAIN 28 77; PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 93 142; PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 164 251; C2 DOMAIN.
 FT DOMAIN 325 583; PROTEIN KINASE.
 FT NP_BIND 331 339; ATP (BY SIMILARITY).
 FT BINDING 354 354; ATP (BY SIMILARITY).
 FT ACT_SITE 449 449; BY SIMILARITY.
 SQ SEQUENCE 658 AA; 74871 MW; 74B5A27A49C835A2 CRC64;
 Query Match 75.5%; Score 37; DB 1; Length 658;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGRPPFE 9
 DB 517 MLAGQPPFD 525
 RESULT 32
 KPCA_BOVIN
 ID KPCA_BOVIN STANDARD; PRT; 672 AA.
 AC P04409;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
 GN PRKCA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=86289425; PubMed=3755547;
 RA Parker P.J., Coussens L., Totty N., Rhee L., Young S., Chen E.,
 RA Stabel S., Waterfield M.D., Ullrich A.;
 RT "The complete primary structure of protein kinase C -- the major
 RT phorbol ester receptor.";
 RL Science 233:853-859(1986).
 RN [2]
 RP REVIEW.
 RX MEDLINE=88318921; PubMed=30455562;
 RA Nishizuka Y.;
 RT "The molecular heterogeneity of protein kinase C and its implications
 RT for cellular regulation.";
 RL Nature 334:661-665(1988).

CC -! FUNCTION: This is a calcium-activated, phospholipid-dependent,
CC serine- and threonine-specific enzyme.
CC -! FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC -! CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -! SUBUNIT: Interacts with PRKCABP (By similarity).
CC -! SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -! SIMILARITY: Contains 1 C2 domain.
CC -! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL; M33973; AAA30706.1; -;
DR PIR; A00621; KIBOC.
DR HSSP; P05697; ITBN.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; PKinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM0033; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00034; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00091; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00102; PROTEIN_KINASE_ATF; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 369 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 672 AA; 76837 MW; 97BF46DB80FCF21A CRC64;
Query Match 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
Db 531 MLAGQPPED 539
RESULT ??
KPCA_HUMAN
ID KPCA_HUMAN STANDARD; PRT; 672 AA.

AC P17252; Q15137; Q96RE4;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein Kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA OR PKCA OR PRKACA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=90245676; PubMed=2336401;
RA Finkenzeller G., Marne D., Hug H.;
RT "Sequence of human protein kinase C alpha.";
RL Nucleic Acids Res. 18:2183-2183(1990).
RN [2]
RP SEQUENCE OF 15-445 FROM N.A.
RX MEDLINE=91332033; PubMed=1714454;
RA McSwine-Kennick R.L., McKeegan E.M., Johnson M.D., Morin M.J.;
RT "Phorbol diester-induced alterations in the expression of protein
RT kinase C isozymes and their mRNAs. Analysis in wild-type and phorbol
RT diester-resistant HL-60 cell clones.";
RL J. Biol. Chem. 266:15135-15143(1991).
RN [3]
RP SEQUENCE OF 1-57 FROM N.A.
RA Haridasse V., Hackenbruck J., Glazer R.I.;
RT "Homo sapiens protein kinase C alpha 5-flanking sequence.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: This is a calcium-activated, phospholipid-dependent,
CC serine- and threonine-specific enzyme.
CC -! FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC -! CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -! SUBUNIT: Interacts with PRKCABP (By similarity).
CC -! SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -! SIMILARITY: Contains 1 C2 domain.
CC -! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52479; CAA36718.1; -;
DR EMBL; M22199; AAA60098.1; -;
DR EMBL; AF395829; AAK84184.1; -;
DR PIR; S09496; KIHUCA.
DR HSSP; P04410; IA25.
DR Genew; HGNC:9393; PRKCA.
DR MIM; 176960; -;
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0004697; F:protein kinase C activity; TAS.
DR GO; GO:0008624; P:induction of apoptosis by extracellular sig. .; TAS.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; PKinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.


```
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00034; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DCM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CONFLICT 50 50 C -> S (IN REF. 2).
SQ SEQUENCE 672 AA; 76764 MW; 8780DD50388C12DA CSeq64;

Query Match 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLGRRPPE 9
DE 531 NLGRRPPE 539

RESULT 34
KPCA MOUSE STANDARD; PRT; 672 AA.
AC P20444;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.11.37) [PK:alpha] (KRC-A).
GN PRKCA OR PKCA
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232737; PubMed=2469625;
RA Rose John S., Dietrich A., Marks F.;
RT 'Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss
RT 3T3 fibroblasts.';
RU Gene 74:465-471(1988).
RN [2]
RP SEQUENCE FROM N.A.
PC STRAIN=BAJB/C; TISSUE=Brain;
RX MEDLINE=90098082; PubMed=2601719;
RA Megidish T., Mazurek N.;
RT "A mutant protein kinase C that can transform fibroblasts.";
RL Nature 342:807-811(1989).
RN [3]
RP INTERACTION WITH PRKCABP.
RX MEDLINE=95146534; PubMed=7844141;
RA Staudinger G., Zhou J., Burgess R., Elledge S.J., Olson E.N.;
RT "PICK1: A perinuclear binding protein and substrate for protein kinase
RT C isolated by the yeast two-hybrid system.";
RL J. Cell Biol. 128:263-271(1995).
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
CC serine- and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
```

```
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with PRKCABP.
CC -!- DISEASE: Expression of the mutant form UV25 causes malignant
CC transformation of cells.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; M25811; AAA39934.1; ALT_SEQ.
CC EMBL; X52685; CAA36908.1; -.
CC EMBL; X52684; CAA36907.1; -.
CC PIR; S07104; KIMSCA.
CC HSSP; P04410; 1A25.
CC MGD; MGI:97595; Prkca.
CC GO; GO:0004698; F:calcium dependent protein kinase C activity; IDA.
CC InterPro; IPR000308; C2.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000961; Pkinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00168; C2; 1.
CC Pfam; PF00130; DAG_PE-bind; 2.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00433; pkinase_C; 1.
CC PRINTS; PR00360; C2DOMAIN.
CC PRINTS; PR00008; DAGPEDOMAIN.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00109; C1; 2.
CC SMART; SM00239; C2; 1.
CC SMART; SM00133; S_TK_X; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00499; C2_DOMAIN_1; 1.
CC PROSITE; PS00034; C2_DOMAIN_2; 1.
CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
CC PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DCM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARIANT 106 106 I -> V (IN MUTANT FORM UV25).
FT VARIANT 111 111 S -> G (IN MUTANT FORM UV25).
FT VARIANT 240 240 L -> Q (IN MUTANT FORM UV25).
FT VARIANT 339 339 F -> L (IN MUTANT FORM UV25).
FT CONFLICT 147 147 D -> V (IN REF. 2).
FT CONFLICT 218 218 N -> T (IN REF. 2).
FT CONFLICT 277 278 AH -> LL (IN REF. 2).
FT CONFLICT 313 313 V -> A (IN REF. 2).
FT CONFLICT 467 467 N -> D (IN REF. 2).
FT CONFLICT 472 472 N -> D (IN REF. 2).
FT CONFLICT 576 576 Q -> H (IN REF. 2).
```



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SQ SEQUENCE 672 AA; 76852 MW; 394B48C952BB6D50 CRC64;
Query Match 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 531 MLAGQPPED 539

RESULT 35
KPCA_RABIT STANDARD; PRT; 672 AA.
ID KPCA_RABIT STANDARD; PRT; 672 AA.
AC P1C102,
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein Kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87115883; PubMed=3808073;
RA Ohno S., Kawasaki H., Imajoh S., Suzuki K., Inagaki M., Yokokura H.,
RA Sakoh T., Hataka H.;
RT "Tissue-specific expression of three distinct types of rabbit protein
RT kinase C.";
RL Nature 325:161-166(1987).
RN [2]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
RT for cellular regulation.";
RL Nature 334:661-665(1988).
CC 1- FUNCTION: This is a calcium-activated, phospholipid dependent,
CC serine- and threonine-specific enzyme.
CC 2- FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC 3- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC 4- SUBUNIT: Interacts with PRKCABP (By similarity).
CC 5- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC 6- SIMILARITY: Contains 1 C2 domain.
CC 7- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X04796; CAA28483.1; -
CC F01; C26037; KIRBC.
CC HSSP; PC4410; 1A25.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000961; Pkinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00168; C2; 1.
CC Pfam; PF00130; DAG_PE-bind; 2.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00433; pkinase_C; 1.
```

```
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Phorbol-ester binding; Zinc;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 672 AA; 76782 MW; 3D311367D3577A77 CRC64;
Query Match 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 531 MLAGQPPED 539

RESULT 36
KPCA_RAT STANDARD; PRT; 672 AA.
ID KPCA_RAT STANDARD; PRT; 672 AA.
AC P05696;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA OR PKCA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88262515; PubMed=3387228;
RA Ono Y., Fujii T., Igarashi K., Kikkawa U., Ogita K., Nishizuka Y.;
RT "Nucleotide sequences of cDNAs for alpha and gamma subspecies of rat
RT brain protein kinase C.";
RL Nucleic Acids Res. 16:5199-5200(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88030055; PubMed=3666147;
RA Kikkawa U., Ogita K., Ono Y., Asaoka Y., Shearman M.S., Fujii T.,
RA Abe K., Sekiguchi K., Igarashi K., Nishizuka Y.;
RT "The common structure and activities of four subspecies of rat brain
RT protein kinase C family.";
RL FEBS Lett. 223:212-216(1987).
RN [3]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
RT for cellular regulation.";
```

RL Nature 334:661-665(1988).
 CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
 CC serine- and threonine-specific enzyme.
 CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
 CC phosphorylates a range of cellular proteins. PKC also serves as
 CC the receptor for phorbol esters, a class of tumor promoters.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: Interacts with PRKCABP (By similarity).
 CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; X37286; CAA30266.1; -;
 DR PIR; S02248; KIRTC;
 DR PDB; 1DSY; 26-JAN-00.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00130; DAG_PE-bind; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00499; C2_DOMAIN_1; 1.
 DR PROSITE; PS00004; C2_DOMAIN_2; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
 DR PROSITE; PS00081; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Calcium-binding; Repeat; ATP-binding; Transferase.
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
 KW Phosphorylation; 3D-structure.
 FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1;
 FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2;
 FT DOMAIN 172 260 C2 DOMAIN.
 FT DOMAIN 339 597 PROTEIN KINASE.
 FT NP_BIND 345 353 ATP (BY SIMILARITY).
 FT BINDING 368 368 ATP (BY SIMILARITY).
 FT ACT_SITE 463 463 BY SIMILARITY.
 FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 SQ SEQUENCE 672 AA; 76792 MW; 94889E7339C17719 CRC64;
 Query Match 75.5%; Score 37; DB 1; Length 672;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLAGRPPE 9
 Dc 531 MLAGQPPFD 539
 RESULT 37
 KPCG_BOVIN

ID KPCG_BOVIN STANDARD; PRT; 682 AA.
 AC P05128;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma) (Fragment).
 GN PRKCG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86289426; PubMed=3755548;
 RA Coussens L., Parker P.J., Rhee L., Yang-feng T.L., Chen E.,
 RA Waterfield M.D., Francke U., Ullrich A.;
 RT "Multiple, distinct forms of bovine and human protein kinase C
 RT suggest diversity in cellular signaling pathways.";
 RL Science 233:859-866(1986).
 RN [2]
 RP REVIEW.
 RX MEDLINE=88318921; PubMed=3045562;
 RA Nishizuka Y.;
 RT "The molecular heterogeneity of protein kinase C and its implications
 RT for cellular regulation.";
 RL Nature 334:661-665(1988).
 CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME.
 CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; M13976; AAA30704.1; -;
 DR PIR; C24664; KIBOGC.
 DR HSSP; P05697; ITBN.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00130; DAG_PE-bind; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00499; C2_DOMAIN_1; 1.
 DR PROSITE; PS00004; C2_DOMAIN_2; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
 DR PROSITE; PS00081; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT NON_TER 1 1
FT DOMAIN 21 70 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 96 135 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 155 245 C2 DOMAIN.
FT DOMAIN 336 599 PROTEIN KINASE.
FT NP_BIND 342 350 ATP (BY SIMILARITY).
FT BINDING 365 365 ATP (BY SIMILARITY).
FT ACT_SITE 465 465 BY SIMILARITY.
FT MOD_RES 633 633 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 640 640 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 682 AA; 77156 MW; 20392011188C731C CRC64;

Query Match 75.5%; Score 37; DB 1; Length 692;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 MLJGRPPPE 9
|||
DB 533 MLAGQPPFD 541

RESULT 38

KPCG HUMAN STANDARD; PRT; 697 AA.
AC PC5129;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma).
GN PRKCG OR PKCG.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RF SEQUENCE FROM N.A.
RA Cui W.C., Yu L., Chu Y.Y., Wang J., Zheng L.H., Zhou G.J., Zhao S.Y.;
RL Submitted (FEB-2001) to the EMBL/GenBank/EBJ databases.
RN [2]
RP SEQUENCE OF 1-318 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=86289426; PubMed=3755548;
RA Coussens L., Parker P.J., Rhee L., Yang-Feng T.L., Chen E.,
RA Waterfield M.D., Francke U., Ulrich A.;
RT "Multiple, distinct forms of bovine and human protein kinase C
suggest diversity in cellular signaling pathways."
RL Science 233:859-866(1986).
RN [3]
RP SEQUENCE OF 162-697 FROM N.A.
RC TISSUE=Hippocampus;
RX MEDLINE=93387312; PubMed=8375336;
RA Kochs G., Meyer D., Hug H., Marre D., Sarre T.F.;
RT "Activation and substrate specificity of the human protein kinase C
alpha and zeta isoenzymes."
RL Eur. J. Biochem. 216:597-606(1993).
RN [4]
RP VARIANTS CYS-141; GLN-415; ASP-523 AND SER-659.
RX MEDLINE=98213587; PubMed=9545390;
RA Al-Maghteth M., Vithana E.N., Inglehearn C.F., Moore T., Bird A.C.,
RA Bhattacharya S.S.;
RT "Segregation of a PKCG mutation in two Rpl1 families."
RL Am. J. Hum. Genet. 62:1248-1252(1998).
RN [5]
RE SHOWS THAT THE VARIANTS ARE NOT A CAUSE OF RPL1.
RX MEDLINE=99375047; PubMed=10441600;
RA Dryja T.P., McEvoy J., McGee T.L., Berson E.L.;
RT "No mutations in the coding region of the PRKCG gene in three families
with retinitis pigmentosa linked to the RPL1 locus on chromosome

RT 19q.";
RL Am. J. Hum. Genet. 65:926-928(1999).
CC FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC SIMILARITY: Contains 1 C2 domain.
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC DATABASE: NAME=Mutations of the PRKCG gene;
CC NOTE=Retina International's Scientific Newsletter;
CC WWW="http://www.retina-international.com/sci-news/prkcgmut.htm".

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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

DR EMBL; AF345987; AAK13533.1; --
DR EMBL; M13977; AAA60102.1; ALT_TERY.
DR EMBL; Z15114; CAA78820.1; --
DR PIR; D24664; D24664.
DR HSSP; P05697; ITBN.
DR Genew; HGNC:9402; PRKCG.
DR MIM; 176980; --
DR GO; GO:0004697; F:protein kinase C activity; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
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DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMC0109; C1; 2.
DR SMART; SMC0239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation; Polymorphism.
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT DOMAIN 351 614 PROTEIN KINASE.
FT NP_BIND 357 365 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARIANT 141 141 R -> C.
FT /FTId=VAR_008755.

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FT VARIANT 415 415 H -> Q.
FT VARIANT 523 523 /FTID=VAR_008756.
FT VARIANT 523 523 A -> D.
FT VARIANT 659 659 /FTID=VAR_008757.
FT VARIANT 659 659 R -> S.
FT SEQUENCE 697 AA: 78447 MW: 3F91B55EF713C41 CRC64:
SQ
Query Match 75.5%; Score 37; DB 1; Length 697;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
Db 548 MLAGQPPFD 556
RESULT 39
ID_KPCG_MOUSE STANDARD; PRT; 697 AA.
AC P05697;
DT 01-NOV-1998 (Rel. 09, Created)
DT 01-NOV-1998 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma).
GN PKCG OR PKCG OR PRKCC OR PKCC.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090, 10116;
RN 1;
SEQUENCE FROM N.A.
RC SPECIES=Rat; TISSUE=Brain;
RX MEDLINE=88262515; PubMed=3387228;
RA Cuo Y., Fujii T., Igarashi K., Kikkawa U., Ogita K., Nishizuka Y.;
RT "Nucleotide sequences of cDNAs for alpha and gamma subtypes of rat
RL brain protein kinase C";
RN 12;
SEQUENCE FROM N.A.
RC SPECIES=Rat;
RX MEDLINE=86272097; PubMed=3755379;
PA Knopf C.L., Lee M.-H., Sultzman L.A., Kriz R.W., Iloomis C.R.,
RT Hewick R.M., Bell R.M.;
RT "Cloning and expression of multiple protein kinase C genes";
RL Cell 46:491-502(1986);
RN 13;
SEQUENCE OF 1-56 FROM N.A.
RC SPECIES=Rat;
RX MEDLINE=91060619; PubMed=2246272;
RA Chen K.H., Widen S.G., Wilson S.H., Huang K.P.;
RT "Characterization of the 5'-flanking region of the rat protein kinase
RT C gamma gene";
RL J. Biol. Chem. 265:19961-19965(1990);
RN 14;
SEQUENCE FROM N.A.
RC SPECIES=Mouse; TISSUE=Brain;
RX MEDLINE=93154595; PubMed=8428669;
RA Bowers B.J., Parham C.L., Sikela J.M., Wehner J.M.;
RT "Isolation and sequence of a mouse brain cDNA coding for protein
RT kinase C-gamma isozyme.";
RL Gene 123:263-265(1993);
RN 15;
SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=BALB/c; TISSUE=Brain;
RA Tseng C.P., Verma A.;
RT Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN 16;
STRUCTURE BY NMR OF 91-172.
RC SPECIES=Rat;
RX MEDLINE=97419134; PubMed=9271531;
RA Xu R.X., Pawlaczek T., Xia T.-H., Brown S.C.;
```

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RT "NMR structure of a protein kinase C-gamma phorbol-binding domain and
RT study of protein-lipid micelle interactions.";
RL Biochemistry 36:10709-10717(1997).
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains : C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC
CC EMBL; X07287; CAA30267.1; -
CC EMBL; M13707; AAA41874.1; -
CC EMBL; M55417; AAA41873.1; -
CC EMBL; X67129; CAA47608.1; -
CC EMBL; L28035; AAA39939.1; -
CC PIR; A05105; KIRTGC.
CC PIR; JN0548; JN0548.
CC PDB; 1TBN; 29-APR-98.
CC PDB; 1TBO; 29-APR-98.
CC MGD; MGI:97597; Prkcc.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000961; Pkinase C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC Pfam; PFC0168; C2; 1.
CC Pfam; PFC0130; DAG_PE-bind; 2.
CC Pfam; PFC0069; pkinase; 1.
CC Pfam; PFC0433; pkinase C; 1.
CC PRINTS; PR00360; C2DOMAIN.
CC PRINTS; PR00038; DAGPEDOMAIN.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000031; Prot_kinase; 1.
CC SMART; SM00109; C1; 2.
CC SMART; SM00239; C2; 1.
CC SMART; SM00133; S_TK_X; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00499; C2_DOMAIN_1; 1.
CC PROSITE; PS50004; C2_DOMAIN_2; 1.
CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
CC PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation; 3D-structure.
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT DOMAIN 351 614 PROTEIN KINASE.
FT NP_BIND 357 365 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT STRAND 103 105
FT STRAND 113 113
FT STRAND 120 120
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FT TURN 123 124
FT STRAND 129 131
FT TURN 132 134
FT STRAND 137 138
FT TURN 140 145
SQ SEQUENCE 697 AA; 78357 MW; E6E2F7A3B93C42FF CRC64;

Query Match: 75.5%; Score 37; DB 1; Length 697;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 548 MLAGQPPFD 556

RESULT 40
KPCG_RABIT STANDARD; PRT; 697 AA.
AC P10829;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28 FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma) (PKC-delta).
GN PRKCG.
CS Oryctolagus cuniculus (Rabbit).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CX NCB: TaxID=9986;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=88241036; PubMed=2837282;
RA Cano S., Kawasaki H., Konno Y., Inagaki M., Hidaka H., Suzuki K.;
RT "A fourth type of rabbit protein kinase C";
RL Biochemistry 27:2083-2087(1988).
CC ! FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC ! SERINE AND THREONINE-SPECIFIC ENZYME.
CC ! FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS.
CC -- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated
CC -- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -- SIMILARITY: Contains 1 C2 domain.
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.

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or send an email to license@isb-sib.ch).

EMBL: M19338; AAA31449.1; --
PIR: A28708; KIRRGK.
HSSP: P05697; ITBN.
InterPro: IPR000008; C2.
InterPro: IPR002219; DAG_PE-bind.
InterPro: IPR000961; Pkinase_C.
InterPro: IPR00719; Prot_kinase.
InterPro: IPR002290; Ser_thr_kinase.
InterPro: IPR001245; Tyr_pkinase.
Pfam: PF00168; C2; 1.
Pfam: PF00130; DAG_PE-bind; 2.
Pfam: PF00069; pkinase; 1.
Pfam: PF00433; pkinase_C; 1.
PRINTS: PR00360; C2DOMAIN.
PRINTS: PR00008; DAGPEDOMAIN.
PRINTS: PR00109; TYRKINASE.
ProDom: PD000001; Prot_kinase; 1.
SMART: SM00109; C1; 2.

DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT DOMAIN 352 614 PROTEIN KINASE.
FT NP_BIND 357 365 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 697 AA; 78371 MW; 925D22221F78E5BF CRC64;

Query Match: 75.5%; Score 37; DB 1; Length 697;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 548 MLAGQPPFD 556

Search completed: November 14, 2003, 13:25:57
Job time : 6.68571 secs

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CM protein - protein search, using sw model

Run on: November 14, 2003, 13:18:40 ; Search time 27 Seconds
(without alignments)
86.018 Million cell updates/sec

Title: US-09-736-076-15
Perfect score: 49
Sequence: 1 MLLGRPPFE 9

Scoring table: SLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	316	Q9BDK4	Q9BDK4 sus scrofa
2	49	100.0	372	Q8N7M6	Q8N7M6 homo sapien
3	49	100.0	666	Q90XS4	Q90XS4 xenopus lae
4	49	100.0	682	Q8K226	Q8K226 mus musculus
5	43	87.8	673	Q62567	Q62567 suberites d
6	43	87.8	677	Q96997	Q96997 geodia cydo
7	43	87.8	769	Q97143	Q97143 drosophila
8	42	85.7	456	Q8MYF1	Q8MYF1 dictyosteli
9	41	83.7	324	Q9CVR6	Q9CVR6 mus musculus
10	41	83.7	568	Q8MXG6	Q8MXG6 caenorhabdi
11	41	83.7	749	Q8MXG7	Q8MXG7 caenorhabdi
12	41	83.7	780	Q76360	Q76360 caenorhabdi
13	41	83.7	925	Q8R015	Q8R015 mus musculus
14	41	83.7	925	Q64702	Q64702 mus musculus
15	41	83.7	970	Q96Q95	Q96Q95 homo sapien
16	41	83.7	970	Q00444	Q00444 homo sapien

17	41	83.7	970	4	Q8IYF0	Q8IYF0 homo sapien
18	40	81.6	526	6	Q9BDP8	Q9BDP8 sus scrofa
19	40	81.6	582	5	Q9GRB7	Q9GRB7 hemacentrot
20	40	81.6	598	13	P70032	P70032 xenopus lae
21	40	81.6	623	5	Q8IU35	Q8IU35 asterina pe
22	39	79.6	235	5	Q9GP07	Q9GP07 leishmania
23	39	79.6	358	5	OC0872	OC0872 leishmania
24	39	79.6	690	16	Q8G6P9	Q8G6P9 bifidobacte
25	39	79.6	1337	2	Q9KJN7	Q9KJN7 myxococcus
26	38	77.6	80	13	Q91891	Q91891 xenopus lae
27	38	77.6	240	11	Q63432	Q63432 rattus norv
28	38	77.6	305	5	O01427	O01427 caenorhabdi
29	38	77.6	332	16	Q9AJZ9	Q9AJZ9 streptomyce
30	38	77.6	554	5	Q95T78	Q95T78 drosophila
31	38	77.6	660	16	Q8FUI5	Q8FUI5 corynebacte
32	38	77.6	661	5	O01669	O01669 hydra atten
33	38	77.6	707	5	Q20953	Q20953 caenorhabdi
34	38	77.6	754	5	Q8MXB6	Q8MXB6 limulus poi
35	38	77.6	769	10	Q9LLJ1	Q9LLJ1 chlamydomon
36	37	75.5	178	16	Q8CR93	Q8CR93 staphylococ
37	37	75.5	301	8	Q950L6	Q950L6 rhizophydia
38	37	75.5	484	11	Q91YI6	Q91YI6 mus musculu
39	37	75.5	622	4	Q9H9T2	Q9H9T2 homo sapien
40	37	75.5	670	5	O01715	O01715 hydra atten
41	37	75.5	670	13	Q8JFZ9	Q8JFZ9 fugu rubrip
42	37	75.5	674	5	O01716	O01716 hydra atten
43	37	75.5	675	3	P87248	P87248 collettotric
44	37	75.5	680	5	P90980	P90980 caenorhabdi
45	37	75.5	680	5	Q8MQ88	Q8MQ88 caenorhabdi

ALIGNMENTS

RESULT 1
Q9BDK4
ID Q9BDK4 PRELIMINARY; PRT: 316 AA.
AC Q9BDK4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Serum-inducible kinase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Anger M., Kues W.A., Klima J., Motlik J., Carnwath J.W., Niemann H.;
RT "Porcine serum-inducible kinase."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF348424; AAK27154.1; -
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00659; pkinase; 1.
DR Pfam; PF00659; POLO_box; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50078; POLO_BOX; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER 1
FT NON_TER 316
SQ SEQUENCE 316 AA; 35330 MW; F63BBE4A2691D62F CRC64;

Query Match 100.0%; Score 49; DB 6; Length 316;
Best Local Similarity 100.0%; Pred.No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
|||||
DB 25 MLLGRPPFE 33

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RESULT 2
Q8N7M6          PRELIMINARY;          PRT;      372 AA.
AC  Q8N7M6;
DT  01-OCT-2002 (TrEMBLrel. 22, Created)
DT  01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Hypothetical protein FLJ40844.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  1;
RP  SEQUENCE FROM N.A.
RC  TISSUE=Trachea;
RA  Suzuki C., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
RA  Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA  Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,
RA  Kaeriyama S., Satoh N., Matsunawa H., Takatashi E., Kataoka R.,
RA  Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,
RA  Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,
RA  Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K.,
RA  Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
RA  Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K.,
RA  Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA  Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isegai T.,
RA  "NEDO human cDNA sequencing project.";
RT  Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AK098163; BAC05247.1; -.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR002290; Ser_thr_kinase.
DR  InterPro; IPR001245; Tyr_pkinase.
DR  Pfam; PF00069; pkinase; 1.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00220; S_TKC; 1.
DR  SMART; SM00219; TyrKC; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW  Hypothetical protein; ATP-binding; Transferase.
SQ  SEQUENCE 372 AA; 42632 MW; 7E3C33F65020A0C9 CRC64;

Query Match      100.0%; Score 49; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 MLLGRPPPE 9
DB  266 MLLGRPPPE 274

RESULT 3
Q90XS4          PRELIMINARY;          PRT;      666 AA.
AC  Q90XS4;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Polo-like kinase 2.
GN  PLX2.
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;
RN  1;
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21481843; PubMed=11597129;
RA  Durcan P.I., Pollet N., Niehrs C., Nigg E.A.;
RT  "Cloning and Characterization of Plx2 and Plx3, Two Additional Polo-
RT  like Kinases from Xenopus laevis.";
RL  Exp. Cell Res. 270:78-87(2001).
CC  -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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DR  EMBL; AF357840; AAL30175.1; -.
DR  InterPro; IPR000959; POLO_box.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR002290; Ser_thr_pkinase.
DR  Pfam; PF00069; pkinase; 1.
DR  Pfam; PF00659; POLO_box; 2.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00220; S_TKC; 1.
DR  PROSITE; PS00078; POLO_BOX; 2.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW  ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ  SEQUENCE 666 AA; 76322 MW; AB4D8F8BDFB5D4FC CRC64;

Query Match      100.0%; Score 49; DB 13; Length 666;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 MLLGRPPPE 9
DB  254 MLLGRPPPE 262

RESULT 4
Q8K226          PRELIMINARY;          PRT;      682 AA.
AC  Q8K226;
DT  01-OCT-2002 (TrEMBLrel. 22, Created)
DT  01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Serum-inducible kinase.
GN  SNK.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  1;
RP  SEQUENCE FROM N.A.
RA  Strausberg R.;
RL  Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC034513; AAH34513.1; -.
DR  MGD; MGI:1099790; Snk.
DR  InterPro; IPR000959; POLO_box.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR002290; Ser_thr_pkinase.
DR  InterPro; IPR001245; Tyr_pkinase.
DR  Pfam; PF00069; pkinase; 1.
DR  Pfam; PF00659; POLO_box; 2.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00220; S_TKC; 1.
DR  SMART; SM00219; TyrKC; 1.
DR  PROSITE; PS00078; POLO_BOX; 2.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW  ATP-binding; Kinase; Transferase.
SQ  SEQUENCE 682 AA; 77777 MW; 89BA65C8DFAFFD95 CRC64;

Query Match      100.0%; Score 49; DB 11; Length 682;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 MLLGRPPPE 9
DB  270 MLLGRPPPE 278

RESULT 5
O62567          PRELIMINARY;          PRT;      673 AA.
ID  O62567
AC  O62567;
DT  01-AUG-1998 (TrEMBLrel. 07, Created)
```

01-AUG-1998 (TrEMBLrel. 07, last sequence update)
01-MAR-2003 (TrEMBLrel. 23, last annotation update)
Serine/threonine protein kinase.
Suberites domuncula (Sponge).
Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
Hadromerida; Suberitidae; Suberites.
NCBI_TaxID=55567;
[1]
SEQUENCE FROM N.A.
Mueller W.E.G.;
Submitted (APR-1997) to the EMBL/GenBank/CDRJ databases.
[2]
SEQUENCE FROM N.A.
MEDLINE=96394698; PubMed=8798342;
Krusse M., Gamulin V., Cetkovic H., Pancer Z., Mueller I.M.,
Mueller W.E.G.;
"Molecular evolution of the Metazoan protein kinase C multigene
family."
J. Mol. Evol. 43:374-383(1996).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
EMBL; Y13099; CAA73553.1; -.
HSSP; P28867; IPTQ.
InterPro; IPR000008; C2.
InterPro; IPR001064; Crystallin.
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00168; C2; 1.
Pfam; PF00130; DAG_PE-bind; 2.
Pfam; PF00069; pkinase; 1.
Pfam; PF00433; pkinase_C; 1.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00008; DAGPEDOMAIN.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00109; C1; 2.
SMART; SM00239; C2; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00133; S_TKC_X; 1.
PROSITE; PS00499; C2_DOMAIN_1; 1.
PROSITE; PS00004; C2_DOMAIN_2; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding, Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 673 AA; 77344 MW; 86D24F55497C293 CRC64;

Query Match 87.8%; Score 43; DB 5; Length 673;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLVGRPPPE 9
|:|||||
Db 535 MLVGRPPPD 543

RESULT 6

O96997
ID O96997 PRELIMINARY; PRT; 673 AA.
AC O96997;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein kinase C.
GN PKC2.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Asciophorida; Geodiidae; Geodia.
NCBI_TaxID=6047;

[1]
SEQUENCE FROM N.A.
MEDLINE=99147839; PubMed=10023072;
Seack J., Kruse M., Mueller I.M., Mueller W.E.G.;
"Promoter and exon-intron structure of the protein kinase C gene from
the marine sponge Geodia cydonium: Evolutionary considerations and
promoter activity."
Biochim. Biophys. Acta 1444:241-253(1999).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
EMBL; Y17882; CAA76911.1; -.
HSSP; P28867; IPTQ.
InterPro; IPR000008; C2.
InterPro; IPR001064; Crystallin.
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00168; C2; 1.
Pfam; PF00130; DAG_PE-bind; 2.
Pfam; PF00069; pkinase; 1.
Pfam; PF00433; pkinase_C; 1.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00008; DAGPEDOMAIN.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00109; C1; 2.
SMART; SM00239; C2; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00133; S_TKC_X; 1.
PROSITE; PS00499; C2_DOMAIN_1; 1.
PROSITE; PS00004; C2_DOMAIN_2; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 677 AA; 76787 MW; 8D0025C81B3DBA33 CRC64;

Query Match 87.8%; Score 43; DB 5; Length 677;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLVGRPPPE 9
|:|||||
Db 539 MLVGRPPPD 547

RESULT 7

O97143
ID O97143 PRELIMINARY; PRT; 769 AA.
AC O97143;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SAK protein.
GN SAK OR CG7186.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhardani D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry C.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos E., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup E.E., Downes M., Dugan-Rocha S., Gunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Geibart W.M., Glasser K.,
RA Gloddek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris M.B., Harvey D., Heiman T.C., Hernandez J.P., Houck J.,
RA Hostin D., Houston K.A., Howland T.C., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Miushina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.B.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Poirard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman C.A., Weinstein G.M., Weissenbach C.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster";
RA Science 287:185-2195(2000);
RA [2]
RA SEQUENCE FROM N.A.
RA Hudson J.W., Dennis J.W.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RA EMBL; AEO33594; AAF51737.1; -
RA EMBL; AF166952; AAC19607.1; -
RA HSSP; P00518; IPHK.
RA FlyBase; FBgn026371; SAK.
RA InterPro; IPR000959; POLO_box.
RA InterPro; IPR000719; Prot_kinase.
RA InterPro; IPR002290; Ser_thr_kinase.
RA InterPro; IPR001245; Tyr_kinase.
RA Pfam; PF00069; pkinase; 1.
RA PRINTS; PR0109; TYRKINASE.
RA ProDom; PD000001; Prot_kinase; 1.
RA SMART; SM00220; S_TKC; 1.
RA PROSITE; PS00078; POLO_BOX; 1.
RA PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
RA PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
RA PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
RA ATP binding; Kinase; Transferase.
RA SEQUENCE 769 AA; 85886 MW; F05CBF60A5D94AA4 CRC64;
Query Match 87.8%; Score 43; DB 5; Length 769;
Best Local Similarity 77.8%; Pred. No. 719;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY : MLLGRPPPE 9 PRT; 456 AA.
DB 206 LLVGRPPPE 214
RESULT 8
Q8MYF1
ID Q8MYF1 PRELIMINARY; PRT; 456 AA.
AC Q8MYF1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RAC-family serine/threonine kinase homolog.
OS Dictyostelium discoideum (Slime mold);

OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gloeckner G., Eichinger J., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RA "Sequence and Analysis of Chromosome 2 of Dictyostelium";
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC117081; AM43765.1; -
DR InterPro; IPR000961; pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR0109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; Ty_KC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 456 AA; 51154 MW; EB8749EC64C89309 CRC64;
Query Match 85.7%; Score 42; DB 5; Length 456;
Best Local Similarity 66.7%; Pred. No. 7.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY : MLLGRPPPE 9
DB 319 MMIGKPPPE 327
RESULT 9
Q9CVR6
ID Q9CVR6 PRELIMINARY; PRT; 324 AA.
AC Q9CVR6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serine/threonine kinase 18 (Fragment).
GN STK18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";


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RC Nature 409:685-690(2001).
CR EMBL: AK006827; BAB24759.1; -.
DR HSSP: Q00534; iB18.
DR MGD: MGI:101783; Stk18.
DR InterPro: IPR000719; Prot_kinase.
CR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
CR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
CR ProDom: PDC00001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Transferase.
KW NON_TER 324 324
SQ SEQUENCE 324 AA; 36568 MW; C4247065DFB198CC CRC64;

Query Match: 83.7%; Score 41; DB 1; Length 324;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGRPPPF 9
Db 204 LLLGRPPPF 212

RESULT 10
Q8MXG6
ID Q8MXG6 PRELIMINARY; PRT; 568 AA.
AC Q8MXG6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE EGL-4 protein (corresponding sequence F55A8.2d).
GN F55A8.2 OR EGL-4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Langston Y., Wohldmann P., Duckels G.;
RT "The sequence of C. elegans cosmid F55A8."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Langston Y., Wohldmann P., Duckels G.;
RT "The sequence of C. elegans cosmid F55A8."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF067612; AAM98011.1; -.
DR WormPep; F55A8.2d; CE31542.
DR InterPro: IPR002373; CAMP_kin.
DR InterPro: IPR002374; CGMP_kin.
DR InterPro: IPR000595; cNMP_binding.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00103; CAMPKINASE.
DR PRINTS; PR00104; CGMPKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00103; CAMPKINASE.
DR PRINTS; PR00104; CGMPKINASE.
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DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00100; cNMP; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS00442; cNMP_BINDING_3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 568 AA; 65094 MW; 423AB3BD6E52ACF4 CRC64;

Query Match: 83.7%; Score 41; DB 5; Length 568;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGRPPPF 9
Db 448 LMLGRPPPF 456

RESULT 11
Q8MXG7
ID Q8MXG7 PRELIMINARY; PRT; 749 AA.
AC Q8MXG7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE EGL-4 protein (corresponding sequence F55A8.2c).
GN F55A8.2 OR EGL-4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Langston Y., Wohldmann P., Duckels G.;
RT "The sequence of C. elegans cosmid F55A8."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Langston Y., Wohldmann P., Duckels G.;
RT "The sequence of C. elegans cosmid F55A8."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF067612; AAM98010.1; -.
DR WormPep; F55A8.2c; CE31541.
DR InterPro: IPR002373; CAMP_kin.
DR InterPro: IPR002374; CGMP_kin.
DR InterPro: IPR000595; cNMP_binding.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00103; CAMPKINASE.
DR PRINTS; PR00104; CGMPKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00103; CAMPKINASE.
DR PRINTS; PR00104; CGMPKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00100; cNMP; 2.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
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DR SMART; SMO0219; TyrKc; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 2.
DR PROSITE; PS00889; CNMP_BINDING_2; 2.
DR PROSITE; PS00442; CNMP_BINDING_3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 749 AA; 84497 MW; ADE0B9F6354D93C6 CRC64;

Query Match 83.7%; Score 41; DB 5; Length 749;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGRPPPE 9
DB 629 LMLGRPPPFQ 637

RESULT 12
O76360
ID O76360 PRELIMINARY; PRT; 780 AA.
AC O76360;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 86.7 kDa protein F55A8.2 in chromosome IV.
GN F55A8.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Langston Y., Wolldmann P., Duckels G.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
FN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; MAY BE
PRODUCED BY ALTERNATIVE SPLICING.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF067612; AAD36954.1; -.
DR EMBL; AF067612; AAD36953.1; -.
DR HSSP; PCS132; 1APM.
DR WormPep; F55A8.2a; CE19897.
DR WormPep; F55A8.2b; CE19898.
DR InterPro; IPR002374; CGMP_kin.
DR InterPro; IPR000595; CNMP_binding.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00027; CNMP_binding; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR PRINTS; PR00104; CGMPKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0100; CNMP; 2.
DR SMART; SMO0220; S_TKc; 1.
DR SMART; SMO0133; S_TK_X; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 2.
DR PROSITE; PS00889; CNMP_BINDING_2; 2.
DR PROSITE; PS00442; CNMP_BINDING_3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Alternative splicing; Kinase;
KW Serine/threonine-protein kinase; Transferase.
FT VARSPJC 1 52 MSSGRPSGGGGGASGAGGAPGGGGGIRGFFSKL
RKPSDQPNQ -> MKQPPRIY (IN ISOFORM B).
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SQ SEQUENCE 780 AA; 86741 MW; 55E036AF50626DD2 CRC64;

Query Match 83.7%; Score 41; DB 5; Length 780;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 660 LMLGRPPPFQ 668

RESULT 13
Q8R015
ID Q8R015 PRELIMINARY; PRT; 925 AA.
AC Q8R015;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 103.9 kDa protein.
GN STK18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026785; AAH26785.1; -.
DR MGD; MGI:101783; Stk18.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0220; S_TKc; 1.
DR PROSITE; PS00078; POLO_BOX; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 925 AA; 103861 MW; 844AFF8C9AAC54C1 CRC64;

Query Match 83.7%; Score 41; DB 11; Length 925;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 204 LMLGRPPPFQ 212

RESULT 14
Q64702
ID Q64702 PRELIMINARY; PRT; 925 AA.
AC Q64702;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SMK/PLK-AKIN kinase (Protein kinase SMK/PLK-AKIN) (EC 2.7.1.-).
GN STK18 OR SAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2; TISSUE=Lymphoma;
RX MEDLINE=94294387; PubMed=8022793;
RA Fode C., Motro B., Yousefi S., Heffernan M., Dennis J.W.;
RT "Sak, a murine protein-serine/threonine kinase that is related to the
Drosophila polo kinase and involved in cell proliferation.";
```

Proc. Natl. Acad. Sci. U.S.A. 91:6388-6392(1994).
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SAK-A (SHOWN HERE) AND SAK-B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
DR EMBL; L29479; AAC37648.1; -;
DR EMBL; J29480; AAC37649.1; -;
DR HSSP; QCC534; 1B18.
DR MGC; MGI:101783; Stk18.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50078; POLO_BOX; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Alternative splicing; Serine/threonine-protein kinase;
KW transferase.
FT VARSPLIC 417 464 SSNHCLGKTPFPFADQTPQWYQWFGNLOVNAHLGETN
FT EHHTVSP -> RYSPKSNVNVLTSLNTKQPIVKDLKDR1
FT MTEQYKDNLLNLLNKFR (IN ISOFORM SAK-B).
FT MISSING (IN ISOFORM SAK-B).
SQ SEQUENCE 925 AA; 103685 MW; D868A76BR7343E81 CRC64;

Query Match 83.7%; Score 41; DB 11; Length 925;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 204 LLIGRPPFD 212

RESULT 15
Q96Q95 PRELIMINARY; PRT; 970 AA.
AC Q96Q95;
DT 01-DEC-2001 (TREMBLrel. 19, Created;
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Sak.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE=21486437; PubMed=11489307;
RA Varashita Y., Kajigaya S., Yoshida K., Ueno S., Ota J., Ohmine K.,
RA Ueda M., Miyazato A., Ohya K., Kitamura T., Ozawa K., Mano H.;
RT "Sak Serine Threonine Kinase Acts as an Effector of Tec Tyrosine
RT Kinase.";
RL J. Biol. Chem. 276:39012-39020(2001).
DR EMBL; AB006972; BAB69958.1; -;
DR HSSP; P24941; 1BUH.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50078; POLO_BOX; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 970 AA; 109084 MW; 1F431FA6C7A355CA CRC64;

Query Match 83.7%; Score 41; DB 4; Length 970;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 204 LLIGRPPFD 212

RESULT 16
O00444 PRELIMINARY; PRT; 970 AA.
AC O00444;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Serine/threonine protein kinase.
GN SAK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Karn T., Holtrich U., Wolf G., Hock B., Streibhardt K.,
RA Ruebsamen-Waigmann H.;
RT "Human SAK related to the PLK/polo family of cell cycle kinases shows
RT high mRNA expression in testis.";
RL Oncol. Rep. 4:505-510(1997).
DR EMBL; Y13115; CAA73575.1; -;
DR HSSP; Q63450; 1A06.
DR Genew; HGNC:11397; STK18.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50078; POLO_BOX; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 970 AA; 108955 MW; 552535615F8BE8DF CRC64;

Query Match 83.7%; Score 41; DB 4; Length 970;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 204 LLIGRPPFD 212

RESULT 17
Q8IYF0 PRELIMINARY; PRT; 970 AA.
AC Q8IYF0;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Similar to serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;

ML Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 UR EMBL; BC036023; AAH36023.1; -;
 KW Kinase; Serine/threonine-protein kinase.
 SQ SEQUENCE 970 AA; 10897 MW; 4D56F5FD983211A6 CRC64;

Query Match 83.7%; Score 41; DB 4; Length 970;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGRPPPE 9

Db 204 LLIGRPPPD 212

RESULT 18

Q9BDP8 PRELIMINARY; PRT; 526 AA.

AC Q9BDP8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created;
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
 DE Polo like protein kinase (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN 1;
 RP SEQUENCE FROM N.A.
 RA Anger M., Kues W.A., Klima J., Mielenz M., Motlik J., Carnwath J.W.,
 RA Niemann H.;
 RT "Expression Of Polo-like Kinase In Cell Cycle Synchronized Porcine
 RT Fetal Fibroblasts";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AF339021; AAK28550.1; -;
 DR HSSP; Q63450; 1A06.
 DR InterPro; IPR000959; POLO_BOX; 2.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00659; POLO_BOX; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SMO0220; S_TKC; 1.
 DR PROSITE; PS00078; POLO_BOX; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER 1
 FT NON_TER 526
 SQ SEQUENCE 526 AA; 60399 MW; 1AF1E5E09B2CBB3 CRC64;

Query Match 81.6%; Score 40; DB 6; Length 526;
 Best Local Similarity 66.7%; Pred. No. 23;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGRPPPE 9

Db 199 LLVGKPPPE 207

RESULT 19

Q9GRB7 PRELIMINARY; PRT; 582 AA.

AC Q9GRB7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created;
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update);
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
 DE Polo-like kinase.
 GN UPK.

OS Hemacentrotus pulcherrimus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;

OC Hemacentrotus.
 OX NCBI_TaxID=7650;
 RN 1;
 RP SEQUENCE FROM N.A.
 RA Yonemura I., Fujimoto H., Mabuchi I.;
 RT "Cloning of sea urchin plk.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AB043897; BAB18588.1; -;
 DR InterPro; IPR001395; Aldo/ket_red.
 DR InterPro; IPR000959; POLO_BOX.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00659; POLO_BOX; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00063; ALDO-KETO_REDUCTASE_3; 1.
 DR PROSITE; PS00078; POLO_BOX; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 582 AA; 66429 MW; A3774A0CAACFDE5D CRC64;

Query Match 81.6%; Score 40; DB 5; Length 582;
 Best Local Similarity 66.7%; Pred. No. 23;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGRPPPE 9

Db 218 LLVGKPPPE 226

RESULT 20

P70032 PRELIMINARY; PRT; 598 AA.

AC P70032;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Plx1.

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;

RN 1;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96355660; PubMed=8703070;
 RA Kumagai A., Dunphy W.G.;

RT "Purification and molecular cloning of Plx1, a Cdc25-regulatory kinase
 RT from Xenopus egg extracts";
 RL Science 273:1377-1380(1996).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; U58205; AAC60017.1; -;
 DR HSSP; Q63450; 1A06.

DR InterPro; IPR000959; POLO_BOX.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00659; POLO_BOX; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00078; POLO_BOX; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 598 AA; 68211 MW; 2467195911F225E6 CRC64;

Query Match 81.6%; Score 40; DB 13; Length 598;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
|||
Db 235 LLVGKPPPE 243

RESULT 21

Q8IU35 PRELIMINARY; PRT; 623 AA.
AC Q8IU35;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Polio-like kinase.
GN PLK.
OS Asterina pectinifera (Starfish).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
OX NCBI_TaxID=7594;
RN [1]
RP SEQUENCE FROM N.A.
RA Uchida T.O., Tachibana K., Kishimoto T.;
RT "Starfish Plk."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB084465; BAC22692.1; --
KW Kinase.
SQ SEQUENCE 623 AA; 70929 MW; CFCD1903602D724A CRC64;

Query Match 81.6%; Score 40; DB 5; Length 623;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
|||
Db 220 LLVGKPPPE 228

RESULT 22

Q8G6P9 PRELIMINARY; PRT; 235 AA.
AC Q8G6P9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative mitogen-activated protein kinase (Fragment).
GN MPK1.
OS Leishmania amazonensis.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5659;
RN [1]
RP SEQUENCE FROM N.A.
RA Wieso M., Goercke I.;
RT "Homologues of LMPK, a mitogen-activated protein kinase from
Leishmania mexicana, in different Leishmania species."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ298021; CAC17612.1; --
DR HSSP; P24941; 1HCL.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
FT NON_TER 235 235
SQ SEQUENCE 235 AA; 26792 MW; 7F5DF167C0FBD3B7 CRC64;

Query Match 79.6%; Score 39; DB 5; Length 235;
Best Local Similarity 88.9%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
|||
Db 192 MLLGRPLFE 200

RESULT 23

O00872 PRELIMINARY; PRT; 358 AA.
ID O00872
AC O00872;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MAP-kinase homologue.
GN LMPK.
OS Leishmania mexicana.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MNYC/BZ/62/M379;
RX MEDLINE=98232507; PubMed=9564044;
RA Wieso M.;
RT "A mitogen-activated protein (MAP) kinase homologue of Leishmania
mexicana is essential for parasite survival in the infected host."
RL EMBO J. 17:2619-2628(1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; Z95887; CAB09307.1; --
DR HSSP; Q00534; 1BI8.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 358 AA; 41151 MW; 7D2D43C6057D8D4F CRC64;

Query Match 79.6%; Score 39; DB 5; Length 358;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
|||
Db 212 MLLGRPLFE 220

RESULT 24

Q8G6P9 PRELIMINARY; PRT; 690 AA.
ID Q8G6P9
AC Q8G6P9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Probable serine/threonine-protein kinase pknB.
GN PKNB OR BL0589.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]

```
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Scheil M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422 14427(2002).
DR EMBL: AE014680; AAN24413.1; -.
KW Kinase; Complete proteome.
SQ SEQUENCE 690 AA; 72243 MW; 6A419EA8CED592D CRC64;

Query Match 79.6%; Score 39; DB 16; Length 690;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 MLJGRPPF 8
DB 217 MLTGRPPF 224

RESULT 25
Q9KJN7
ID Q9KJN7 PRELIMINARY; PRT; 1337 AA.
AC Q9KJN7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created);
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Putative serine/threonine protein kinase.
GN PKND2.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=14;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=D22;
RX MEDLINE=20032045; PubMed=10564511;
RA Cho K., Zusman D.R.;
RT "Sporulation timing in Myxococcus xanthus is controlled by the espAB
RT locus.";
RL Mol. Microbiol. 34:714-725(1999).
RN 2;
RP SEQUENCE FROM N.A.
RC STRAIN=D22;
RA Cho K., Zusman D.R.;
RL Submitted (JUL-2000) to the EMBL/GenBank/CCPC databases.
DR EMBL: AF183841; AAF87930.1; -.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR01440; TPR.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF0515; TPR; 4.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00028; TPR; 3.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1337 AA; 144738 MW; 6086E8CA4C92499D CRC64;

Query Match 79.6%; Score 39; DB 2; Length 1337;
Best Local Similarity 87.5%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 MLJGRPPF 8
DB 242 MLTGRPPF 249

RESULT 26
Q91891
ID Q91891 PRELIMINARY; PRT; 60 AA.
AC Q91891;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 9.4 kDa protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN 1;
RP SEQUENCE FROM N.A.
RA Bouvet P., Omilli F., ARLOT-BONNEMAIN Y., Legagneux V., Roghi C.,
RA Bassez T., OSBORNE H.;
RT "Deadenylation conferred by the 3' untranslated region of a
RT developmentally controlled mRNA in xenopus embryos is switched to
RT polyadenylationby deletion of a short sequences element.";
RL Mol. Cell. Biol. 14:1893-1900(1995).
DR EMBL: Z24453; CAA80826.1; -.
DR InterPro: IPR000719; Prot_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; ATP-binding; Transferase.
FT NON_TER 1
SQ SEQUENCE 80 AA; 9388 MW; 8DFCEDBA14BE14FB CRC64;

Query Match 77.6%; Score 38; DB 13; Length 80;
Best Local Similarity 75.0%; Pred. No. 8;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPF 9
DB 3 LVGRPPPF 10

RESULT 27
Q63432
ID Q63432 PRELIMINARY; PRT; 240 AA.
AC Q63432;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Rat protein kinase C-family related (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=87147193; PubMed=3469647;
RA Housley G.M., O'Brian C.A., Johnson M.D., Kirschmeier P.,
RA Weinstein I.B.;
RT "Isolation of cDNA clones encoding protein kinase C: Evidence for a
RT protein kinase C-related gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:1065-1069(1987).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: M15523; AAA41877.1; -.
DR HSSP: Q63450; 1A06.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 26848 MW; 289934FE257E4682 CRC64;

Query Match 77.6%; Score 38; DB 11; Length 240;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 MLLGRPPFE 9
|:|:|:|:|
204 MMAGQPPFE 212

RESULT 28
001427 PRELIMINARY; PRT; 305 AA.

ID 001427
AC 001427;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE C. ELEGANS AURORA/IPL1-related protein KINASE 2 (AIR-2) (GB:AF071207),
DE CONTAINS SIMILARITY TO PFAM domain PF00069 (PKINASE), SCORE=295.1,
DE E-VALUE=2.8E-85, N=1 (AIR-2) (PKINASE).
GN AIR-2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Henkhaus J., Wohldmann P.;
RT "The sequence of C. elegans cosmid B0207.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=N2 BRISTOL;
RA Schumacher J.M., Golden A., Donovan P.J.;
RT "Air-2: An autora/Ipl1-related protein kinase associated with
RT chromosomes and midbody microtubules is required for polar body
RT extrusion and cytokinesis in C. elegans embryos.";
RL J. Cell Biol. 0:0-0(1998).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U97196; AAB52459.2; -.
DR EMBL; AF071207; AAC70945.1; -.
DR HSSP; P24941; 1A01.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMC0220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 305 AA; 34749 MW; 1635EB60D2E14011 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 305;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPFE 9
|:|:|:|:|
220 LVGKPPFE 227

Db 220 LVGKPPFE 227

RESULT 29
Q9AJZ9 PRELIMINARY; PRT; 332 AA.

ID Q9AJZ9
AC Q9AJZ9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SCO7729.
GN SCO7729 OR SC8D11.20.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D.C., Harris D.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Regendach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939132; CAC22737.1; -.
DR InterPro; IPR003829; DUF209.
DR Pfam; PF02678; DUF209; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 332 AA; 35974 MW; 7E05869A9386B0ED CRC64;

Query Match 77.6%; Score 38; DB 16; Length 332;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
|:|:|:|:|

Db 262 LLLGPPPE 270

RESULT 30

Q95T78 PRELIMINARY; PRT; 554 AA.

AC Q95T78;

DT 01-DEC-2001 (TrEMBLrel. 19, Created);

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update);

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);

DE GH13631P;

GN PKC98E CR C01954.

OS Drosophila melanogaster (Fruit fly);

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

CC Neoptera; Endopterygota; Diptera; Brachycera; Musco-orpha;

CC Ephydroidea; Drosophilidae; Drosophila.

CX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkley;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Yungall C.J.,

RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL: AY060293; AAL25332.1; ..

DR FlyBase: FBgn003093; PKC98E.

DR InterPro: IPR002219; DAG_PE-bind.

DR InterPro: IPR000961; PKinase_C.

DR InterPro: IPR000719; Prot_kinase.

DR InterPro: IPR002290; Ser_thr_kinase.

DR Pfam: PF00130; DAG_PE-bind; 1.

DR Pfam: PF00069; pkinase; 1.

DR Pfam: PF00433; pkinase_C; 1.

DR PRINTS: PR00008; DAGPEDOMAIN.

DR ProDom: PD000001; Prot_kinase; 1.

DR SMART: SM00109; C1; 1.

DR SMART: SM02220; S_TKC; 1.

DR SMART: SM0133; S_TK_X; 1.

DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.

DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 554 AA; 61598 MW; 30CFA0599AB3F4 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 554;

Best Local Similarity 66.7%; Pred. No. 52;

Matches 6; Conservative 2; Mismatches 1; Indels 3; Gaps 0;

QY 1 MLLGPPPE 9

Db 415 VMAGPPPE 423

RESULT 31:

Q8FU15 PRELIMINARY; PRT; 660 AA.

AC Q8FU15;

DT 01-MAR-2003 (TrEMBLrel. 23, Created);

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);

DE Putative serine/threonine-protein kinase.

GN CEC033.

OS Corynebacterium efficiens.

CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

CC Corynebacterineae; Corynebacteriaceae; Corynebacterium.

CX NCBI_TaxID=152794;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

RA Kwarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,

RA Ikeo K., Suzuki M., Mashima C., Itoh T., Yamagishi A., Nishio Y.,

RA Usuda Y., Sugimoto S.,

RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AP005214; BAC16843.1; ..

KW Kinase; Complete proteome.

SQ SEQUENCE 660 AA; 69646 MW; D33D797EB02D44B1 CRC64;

Query Match 77.6%; Score 38; DB 16; Length 660;

Best Local Similarity 66.7%; Pred. No. 62;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGPPPE 9

Db 207 LVTGPPPE 215

RESULT 32

O01669 PRELIMINARY; PRT; 661 AA.

ID O01669;

AC O01669;

DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Protein kinase C (Fragment).

OS Hydra attenuata (Hydra) (Hydra vulgaris).

OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;

OC Hydridae; Hydra.

OX NCBI_TaxID=6087;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Zuerich;

RX MEDLINE=98179225; PubMed=9510545;

RA Hassel M., Bridge D.M., Stover N.A., Kleinholz H., Steele R.E.;

RT "The level of expression of a protein kinase C gene may be an

RT important component of the patterning process in Hydra.";

RL Dev. Genes Evol. 207:502-514(1998).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.

DR EMBL: Y12237; CAA72926.1; ..

DR HSSP: P05697; ITEN.

DR InterPro: IPR000008; C2.

DR InterPro: IPR002219; DAG_PE-bind.

DR InterPro: IPR000961; pkinase_C.

DR InterPro: IPR000719; Prot_kinase.

DR InterPro: IPR002290; Ser_thr_kinase.

DR Pfam: PF00168; C2; 1.

DR Pfam: PF00130; DAG_PE-bind; 2.

DR Pfam: PF00069; pkinase; 1.

DR Pfam: PF00433; pkinase_C; 1.

DR PRINTS: PR00008; DAGPEDOMAIN.

DR ProDom: PD000001; Prot_kinase; 1.

DR SMART: SM00109; C1; 2.

DR SMART: SM00239; C2; 1.

DR SMART: SM00220; S_TKC; 1.

DR SMART: SM00133; S_TK_X; 1.

DR PROSITE: PS50004; C2_DOMAIN_2; 1.

DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.

DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 2.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

FT NON TER 661

SQ SEQUENCE 661 AA; 75054 MW; 3346BD6EE4A2B2D5 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 661;

Best Local Similarity 66.7%; Pred. No. 62;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGPPPE 9

Db 1 MLLGPPPE 9

Db 561 MMAGQPPFE 569

RESULT 33

Q20953

ID Q20953 PRELIMINARY; PRT; 707 AA.

AC Q20953;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE F57F5.5 protein.

GN F57F5.5.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1];

RP SEQUENCE FROM N.A.

RA Harris B.R.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RN [2];

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

RT investigating biology."

RL Science 282:2012-2018(1998).

RN [3];

RP SEQUENCE FROM N.A.

RA White S.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.

DR EMBL; Z75953; CAB00101.2;

DR EMBL; Z81497; CAB00101.2; JOINED.

DR EMBL; Z81497; CAC70080.1;

DR EMBL; Z75953; CAC70080.1; JOINED.

DR HSSP; P28867; IPTQ.

DR WormPep; F57F5.5; CE29092.

DR InterPro; IPR000008; C2.

DR InterPro; IPR002219; DAG_PE-bind.

DR InterPro; IPR000961; Pkinase_C.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00168; C2; 1.

DR Pfam; PF00130; DAG_PE-bind; 2.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00433; pkinase_C; 1.

DR PRINTS; PR00008; DAGPEDOMAIN.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00109; C1; 2.

DR SMART; SM00239; C2; 1.

DR SMART; SM00220; S_TK_X; 1.

DR SMART; SM00133; S_TK_X; 1.

DR SMART; SM00219; TyKc; 1.

DR PROSITE; PS50004; C2_DOMAIN_2; 1.

DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.

DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Hypothetical protein; ATP-binding; Transferase.

SQ SEQUENCE 707 AA; 80151 MW; 08C1ED1B7A911B49 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 707;

Best Local Similarity 66.7%; Pred. No. 66;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

Db 570 MMAGQPPFE 578

RESULT 34

Q8MXB6

ID Q8MXB6 PRELIMINARY; PRT; 754 AA.

AC Q8MXB6;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical protein.

OS Limulus polyphemus (Atlantic horseshoe crab).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;

OC Limulidae; Limulus.

OX NCBI_TaxID=6850;

RN [1];

RP SEQUENCE FROM N.A.

RX MEDLINE=20356442; PubMed=10901270;

RA Wang Y., Cao Z., Reid E.A., Newkirk R.F., Ivy M.T., Townsend J.G.;

RT "The use of competitive PCR mimic to evaluate a Limulus lambda phage

RT genomic DNA library."

RL Cell. Mol. Neurobiol. 20:539-520(2000).

CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.

DR EMBL; AF289084; AAM90321.1;

DR InterPro; IPR000008; C2.

DR InterPro; IPR002219; DAG_PE-bind.

DR InterPro; IPR000961; Pkinase_C.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00168; C2; 1.

DR Pfam; PF00130; DAG_PE-bind; 2.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00433; pkinase_C; 1.

DR PRINTS; PR00008; DAGPEDOMAIN.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00109; C1; 2.

DR SMART; SM00239; C2; 1.

DR SMART; SM00220; S_TK_X; 1.

DR SMART; SM00133; S_TK_X; 1.

DR SMART; SM00219; TyKc; 1.

DR PROSITE; PS50004; C2_DOMAIN_2; 1.

DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.

DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Hypothetical protein; ATP-binding; Transferase.

SQ SEQUENCE 754 AA; 85488 MW; BF16A40497E2BB40 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 754;

Best Local Similarity 66.7%; Pred. No. 70;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

Db 607 MMAGQPPFE 615

RESULT 35

Q9LLJ1

ID Q9LLJ1 PRELIMINARY; PRT; 769 AA.

AC Q9LLJ1;

DT 01-OCT-2003 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE CALK protein.

OS Chlamydomonas reinhardtii.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

OC Chlamydomonadaceae; Chlamydomonas.

OX NCBI_TaxID=3055;

RN [1];

RP SEQUENCE FROM N.A.

RX MEDLINE=20379056; PubMed=10807915;

RA Pan J., Snell W.J.;

RT "Regulated targeting of a protein kinase into an intact flagellum. An

RT aurora/Iplip-like protein kinase translocates from the cell body into

RT the flagella during gamete activation in Chlamydomonas.";
 RL J. Biol. Chem. 275:24106-24114(2000).
 CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL: AF199021; AAF97501.1; ..
 DR HSSP: C63450; IAC6.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 769 AA; 80250 MW; DBC37FFCD424510; CRC64;

Query Match 77.6%; Score 38; DB 10; Length 269;
 Best Local Similarity 55.6%; Pred. No. 72;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRPPPE 9

Db 241 LIVGRPPFD 249

RESULT 36

Q8CR93
 ID Q8CR93 PRELIMINARY; PRT; 178 AA.
 AC Q8CR93;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Conserved hypothetical protein.
 GI1984.
 OS Staphylococcus epidermidis.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia C., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.
 RJ Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB016750; AA005625.1; ..
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 178 AA; 20507 MW; F78C1D39DC4B7298 CRC64;

Query Match 75.5%; Score 37; DB 16; Length 178;
 Best Local Similarity 85.7%; Pred. No. 27;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 8

Db 172 ILGRPPPE 178

RESULT 37

Q950L6
 ID Q950L6 PRELIMINARY; PRT; 301 AA.
 AC Q950L6;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE NADH dehydrogenase subunit 1 (EC 1.6.5.3) (NADH ubiquinone
 oxidoreductase chain 1).
 GN NAD1.
 OS Rhizoglyphus sp. 136.
 OG Mitochondrion.
 CC Rhizoglyphus.
 CC Eukaryota; Fungi; Chytridiomycota; Chytridiales; Chytridiaceae;
 OX NCBI_TaxID=60187;
 RN [1]
 RP SEQUENCE FROM N.A.

QY 2 LLGRPPPE 8

Db 172 ILGRPPPE 178

RA Forget L., Ustinova J., Wang Z., Huss V.A.R., Lang F.B.F.;
 RT "Hyaloraphidium curvatum: a linear mitochondrial genome, tRNA editing,
 RT and an evolutionary link to lower fungi.";
 RL Mol. Biol. Evol. 0:0-0(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=136;
 RA Lang F.B.F.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC - CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 CC - SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
 DR EMBL: AF404306; AAK84292.1; ..
 DR InterPro: IPR001694; Resp_NADH_dh1.
 DR Pfam: PF00146; NADHdh; 1.
 KW NAD; Oxidoreductase; Transmembrane; Ubiquinone; Mitochondrion.
 SQ SEQUENCE 301 AA; 33286 MW; DD58195953EF41D5 CRC64;

Query Match 75.5%; Score 37; DB 8; Length 301;
 Best Local Similarity 85.7%; Pred. No. 45;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGRPPPE 9

Db 194 LGRPPFD 200

RESULT 38

Q91Y16
 ID Q91Y16 PRELIMINARY; PRT; 484 AA.
 AC Q91Y16;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Hypothetical 55.9 kDa protein.
 GN A1649009.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC016629; AAH16629.1; ..
 DR MGD; MGI:2140950; A1649009.
 DR InterPro: IPR001201; PAP_25A_core.
 DR InterPro: IPR002058; PAP_assoc.
 DR Pfam: PF03828; PAP_assoc; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 484 AA; 55933 MW; C60D799AA5F14CB6 CRC64;

Query Match 75.5%; Score 37; DB 11; Length 484;
 Best Local Similarity 85.7%; Pred. No. 71;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 8

Db 6 ILGRPPPE 12

RESULT 39

Q9H9T2
 ID Q9H9T2 PRELIMINARY; PRT; 622 AA.
 AC Q9H9T2;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Hypothetical protein FLC12565.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuka T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakanatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.,
RT "NEDO human cDNA sequencing project";
RL Submitted (AUG-2000) to the EXBL/GenBank/CCBJ databases.
DR EMBL; AK022627; BAB14139.1; -;
DR InterPro; IPR001841; Znf_ring.
DR SMART; SMC0184; RING; 1;
DR PROSITE; PS50089; ZF_RING_2; 1;
KW Hypothetical protein.
SQ SEQUENCE 622 AA; 70366 MW; B837A8389163B5B8 CRC64;

Query Match 75.5%; Score 37; DB 4; Length 622;
Best Local Similarity 77.8%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
|||
DB 37 LLLGRPPPE 45

RESULT 40
CG1715 PRELIMINARY; PRT; 670 AA.
AC CG1715;
DT 01-JUL-1997 (TRENDELrel. 04, Created)
DI 01-JUL-1997 (TRENDELrel. 04, Last sequence update)
DT 01-MAR-2003 (TRENDELrel. 23, Last annotation update)
DE Protein kinase C.
GN PKC1A.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Hydrozoa; Hydroids; Anthomedusae;
OC Hydrozoa; Hydra.
OX NCBI TaxID=6087;
RN (1)
RF SEQUENCE FROM N.A.
RC STRAIN=Zuerich;
RX MEDLINE=98179224; PubMed=9510544;
RA Rasae, M.;
RT "Upregulation of a Hydra vulgaris cdk2 gene is tightly coupled to the
RT differentiation of head structures";
RJ Dev. Genes Evol. 203:489-501 (1998)
CC 1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1 SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; Y12858; CAA73363.1; -;
DR HSSP; PCS697; ITEN.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00169; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PDC00001; Prot_kinase; 1.
DR SMART; SMC0109; C1; 2.
DR SMART; SMC0239; C2; 1.
DR SMART; SMC0220; S_TKC; 1.
DR SMART; SMC0133; S_TK_X; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 670 AA; 76642 MW; EBFC370229065878 CRC64;

Query Match 75.5%; Score 37; DB 5; Length 670;
Best Local Similarity 66.7%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
|||
DB 534 MLAGQPPFD 542

Search completed: November 14, 2003, 13:27:56
Job time : 28 secs

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OM protein - protein search, using sw model

Run on: November 14, 2003, 12:54:54 / Search time 30.5571 Seconds
(without alignments)
41.151 Million cell updates/sec

Title: US-09-736-076-16
Perfect score: 44
Sequence: : MLGKPPF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	8	AAW74160	HJ loop peptide J-
2	44	100.0	8	AAU98316	Polo kinase serine
3	44	100.0	9	AAW74161	HJ loop peptide J-
4	44	100.0	9	AAU98317	Polo kinase serine
5	41	93.2	9	AAW74159	HJ loop peptide J-
6	41	93.2	9	AAU98315	Polo kinase serine
7	41	93.2	10	AAW74213	HJ loop peptide K0
8	41	93.2	10	AAU98357	Polo kinase SNK se
9	41	93.2	11	AAW74163	HJ loop peptide J-

10	41	93.2	11	23	AAU98319	Polo kinase serine
11	41	93.2	469	22	AAB94717	Human protein sequ
12	41	93.2	469	22	AAG67426	Amino acid sequenc
13	41	93.2	685	20	AAU00915	Human serum induci
14	41	93.2	685	20	AAW88432	Disease associated
15	41	93.2	585	23	ABP61474	Human NF-kB activa
16	41	93.2	753	23	ABP41992	Human ovarian anti
17	39	88.6	304	21	AAG36347	Arabidopsis thalia
18	39	88.6	304	21	AAG37267	Arabidopsis thalia
19	39	88.6	305	21	AAG38660	Arabidopsis thalia
20	39	88.6	329	21	AAG36346	Arabidopsis thalia
21	39	88.6	329	21	AAG37266	Arabidopsis thalia
22	39	88.6	330	21	AAG38659	Arabidopsis thalia
23	39	88.6	465	21	AAG36345	Arabidopsis thalia
24	39	88.6	465	21	AAG37265	Arabidopsis thalia
25	39	88.6	466	21	AAG38658	Arabidopsis thalia
26	39	88.6	592	21	AAU93500	Amino acid sequenc
27	39	88.6	604	23	AAU74657	Yeast cyciin depen
28	39	88.6	766	21	AAU93498	Amino acid sequenc
29	38	86.4	8	20	AAW74211	HJ loop peptide K0
30	38	86.4	8	23	AAU98355	Polo kinase Plk se
31	38	86.4	20	20	AAW74173	HJ loop peptide PO
32	38	86.4	20	23	AAU98306	Peptide sequence o
33	38	86.4	329	21	AAB56690	Human prostate can
34	38	86.4	419	23	AAU83127	Novel secreted pro
35	38	86.4	528	23	ABP73734	Candida albicans e
36	38	86.4	531	23	AAU74656	Mammalian polo-lik
37	38	86.4	603	16	AAR74620	Human lung tumour
38	38	86.4	603	23	AAU79306	Mouse polo-like ki
39	38	86.4	603	23	AAU79308	Mouse polo-like ki
40	38	86.4	603	23	AAU79309	Mouse polo-like ki
41	38	86.4	603	23	AAU79310	Mouse polo-like ki
42	38	86.4	603	23	AAU79311	Mouse polo-like ki
43	38	86.4	603	23	AAU79312	Mouse polo-like ki
44	38	86.4	603	23	AAU79313	Mouse polo-like ki
45	38	86.4	603	23	AAU79314	Mouse polo-like ki

ALIGNMENTS

RESULT 1
AAW74160
ID AAW74160 standard; peptide; 8 AA.
XX
AC AAW74160;

DT 05-MAY-1999 (first entry)

DE HJ loop peptide J-43.

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "acetylated"

FT Modified-site 8 /note= "amidated"

XX WO9853050-A2.

XX 26-NOV-1998.

XX 20-MAY-1998; 98WO-US-0319.

XX 21-MAY-1997; 97US-0861338.

XX (CHIL-) CHILDREN'S MEDICAL CENT.

PA (YISS) YISSUM RES & DEV CO.
XX
PI Ben-Sasson SA;
XX
XX WPI; 1999-070142/06.
XX
XX New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Claim 14; Fig 4; 70pp; English.
XX
CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 44; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db : MLLGKPPF 8

RESULT 2
AAU98316
ID AAU98316 standard; Peptide; 8 AA.
XX
AC AAU98316;
XX
DT 13-AUG-2002 (first entry)
XX
DE Polo kinase serine-threonine kinase HJ loop peptide J 43.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; J-43.
XX
OS Unidentified.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 8 /note= "C-terminal amide"
FT
XX
PN US2002049301-A1.
XX
PD 25-APR-2002.
XX
PF 13-DEC-2000; 2000US-0736076.
XY

PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Ben-Sasson SA;
XX
DR WPI; 2002-462787/49.
XX
PT New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX
PS Disclosure; Fig 4; 41pp; English.
XX
CC The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders. The peptides are also used to generate
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-43. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 44; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db : MLLGKPPF 8

RESULT 3
AAW74161
ID AAW74161 standard; peptide; 9 AA.
XX
AC AAW74161;
XX
DT 05-MAY-1999 (first entry)
XX
DE HJ loop peptide J-43.1.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 9 /note= "amidated"
FT
XX
PN WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10319.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX
PI Ben-Sasson SA;

XX WPI, 1999-070142/36.
DR New peptides for modulating serine/threonine kinase activity -
XX comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Claim 14; Fig 4; 70pp; English.
XX
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CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 9 AA;
Query Match: 100.0%; Score 44; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 1 MLLGKPPF 8
RESULT 4
AAU98317
ID AAU98317 standard; Peptide; 9 AA.
XX
AC AAU98317;
XX
DT 12-AUG-2002 (first entry)
XX
DE Polo kinase serine-threonine kinase HJ loop peptide J-43.1.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haerostatic;
KW modulating STK activity; polo kinase; J-43.1.
XX
CS Unidentified.
CS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 9 /note= "Benzyl ester of Glutamic acid, C-terminal amide"
FT Modified-site 9 /note= "Benzyl ester of Glu"
XX
PN US2002049301-A1.
XX
PD 25-APR-2002.
XX
PF 13-DEC-2000; 2000US-0736076.
XX
PR 21 MAY-1997; 97US-0861338.
XX
PA (CHILD- CHILDRENS MEDICAL CENT

XX Ben-Sasson SA;
PI
XX WPI; 2002-462787/49.
DR
XX New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
PT
XX
PS Disclosure; Fig 4; 41pp; English.
XX
CC The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-43.1. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
SQ Sequence 9 AA;
Query Match: 100.0%; Score 44; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 1 MLLGKPPF 8
RESULT 5
AAW74159
ID AAW74159 standard; peptide; 9 AA.
XX
AC AAW74159;
XX
DT 05-MAY-1999 (first entry)
XX
DE HJ loop peptide J-42.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 9 /note= "amidated"
FT Modified-site 9 /note= "benzyl ester of Glu"
XX
PN WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10319.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHILD- CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX
PI Ben-Sasson SA;
XX

DR WPI: 1999-070142/06.

XX New peptides for modulating serine/threonine kinase activity -

PT comprise a sequence corresponding to the HJ loop of a

PT serine/threonine kinase, used for treating, e.g. cancers,

PT inflammatory disorders or autoimmune disorders

XX Claim 14: Fig 4; 70pp; English.

XX This sequence represents a peptide of the invention, and is a derivative

CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be

CC used for the treatment of disorders caused by overactivity or

CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic

CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,

CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and

CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,

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CC of organ transplant rejection, multiple sclerosis, inflammatory bowel

CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's

CC disease, stroke and trauma), septic shock, Parkinson's disease or

CC hypertension. The peptides can also be used to produce antibodies which

CC can be used to identify cells expressing the STK and to study the

CC intracellular distribution of the STK. In addition, the peptides can be

CC used to identify and quantitate ligands which bind the HJ loop of the STK

CC from which the peptide was derived.

XX

SQ Sequence 9 AA;

Query Match 93.2%; Score 41; DB 20; Length 9;

Best Local Similarity 87.5%; Pred. No. 9.3e+05;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGKPPF 8

Db 1 MLLGRPPF 8

RESULT 6

AAU98315

ID AAU98315 standard; Peptide: 9 AA.

XX

AC AAU98315;

XX

DT 13-AUG 2002 (first entry)

XX

DE Polo kinase serine-threonine kinase HJ loop peptide J-42.

XX

KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;

KW central nervous system disorder; inflammatory disorder;

KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;

KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;

KW antiinflammatory; immunosuppressive; cardiac; haemostatic;

KW modulating STK activity; polo kinase; J-42.

XX

OS Unidentified.

OS Synthetic.

XX

PH Key Location/Qualifiers

FT Modified site 1 /note= "N-terminal acetyl"

FT

FT Modified site 9 /note= "Benzyl ester of Glutamic acid"

FT /note= "C-terminal amide"

XX

PN US2002049301-A1.

XX

PD 25-APR-2002.

XX

PF 13 DEC-2000; 2000US-0736076.

XX

PR 21 MAY-1997; 97US-0861338.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.

XX Ben-Sasson SA;

PI

XX WPI: 2002-462787/49.

DR

XX New peptide from the HJ loop of serine-threonine kinase, useful for

PT treating e.g. cancer and for producing diagnostic antibodies -

XX

PS Disclosure; Fig 4; 41pp; English.

XX

CC The present invention relates to new peptides derived from the HJ loop

CC of a serine/threonine kinase (STK). The peptides of the invention are

CC used to modulate STK activity, especially for treating cancer, diabetes,

CC obesity or a wide variety of central nervous system, inflammatory,

CC autoimmune or cardiovascular disorders. The peptides are also used to generate

CC regulating lipid metabolism. The peptides are also used to generate

CC antibodies that bind specifically to the parent STK, used e.g. for

CC identifying STK-expressing cells and to study intracellular distribution

CC of STK, and to identify or quantify ligands that bind to the HJ loop.

CC The present amino acid sequence represents the polo kinase

CC serine-threonine kinase HJ loop peptide J-42. This sequence is one of

CC the short peptides of the invention that selectively modulate the

CC activity of STK.

XX

SQ Sequence 9 AA;

Query Match 93.2%; Score 41; DB 23; Length 9;

Best Local Similarity 87.5%; Pred. No. 9.3e+05;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGKPPF 8

Db 1 MLLGRPPF 8

RESULT 7

AAW74213

ID AAW74213 standard; peptide; 10 AA.

XX

AC AAW74213;

XX

DT 05-MAY-1999 (first entry)

XX

DE HJ loop peptide K038H101.

XX

KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;

KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

KW inflammatory disorder; central nervous system disease; septic shock;

KW Parkinson's disease; hypertension.

XX

OS Synthetic.

XX

PH Key Location/Qualifiers

FT Modified-site ; /note= "myristylated"

FT Modified-site 10

FT /note= "amidated"

XX

PN W09853050-A2.

XX

PD 26-NOV-1998.

XX

PF 20-MAY-1998; 98WO-US10319.

XX

PR 21-MAY-1997; 97US-0861338.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.

PA (YISS) YISSUM RES & DEV CO.

XX

PI Ben-Sasson SA;

XX

DR WPI: 1999-070142/06.

PT New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders

XX Disclosure; Fig 6; 70pp; English.

XX This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.

XX Sequence 10 AA;

Query Match 93.2%; Score 41; DB 20; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.43;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB |||:|:
2 MLLGRPPF 9

RESULT 8

AAU98157
ID AAU98157 standard; Peptide; 10 AA.

XX AC AAU98357;

DT 13 AUG-2002 (first entry)

XX Polo kinase SNK serine-threonine kinase HJ loop peptide K038H101.

XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; metabolic;
KW modulating STK activity; polo kinase; SNK; K038H101.

XX Unidentified.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal myristyl"

FT Modified-site 10

FT /note= "Benzyl Ester of Glutamic Acid, C-terminal amide"

XX US2002049301-A1.

XX 25-APR-2002.

XX 13-DEC-2000; 2000US-0736076.

XX 21-MAY-1997; 97US-0861338.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Ben-Sasson SA;

XX

DR WPI; 2002-462787/49.

XX New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -

PS Disclosure; Fig 6; 41pp; English.

XX The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
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CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase SNK
CC serine-threonine kinase HJ loop peptide K038H101. This sequence is one
CC of the short peptides of the invention that selectively modulate the
CC activity of STK.

XX Sequence 10 AA;

Query Match 93.2%; Score 41; DB 23; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.43;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB |||:|:
2 MLLGRPPF 9

RESULT 9

AAW74163
ID AAW74163 standard; peptide; 11 AA.

XX AC AAW74163;

DT 05-MAY-1999 (first entry)

XX HJ loop peptide C-46.

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "acetylated"

FT Modified-site 11

FT /note= "amidated"

XX W09853050-A2.

XX 26-NOV-1998.

XX 20-MAY-1998; 98WO-US10319.

XX 21-MAY-1997; 97US-0861338.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX (YISS) YISSUM RES & DEV CO.

XX Ben-Sasson SA;

XX WPI; 1999-070142/06.

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CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
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CC disease, stroke and trauma), septic shock, Parkinson's disease or
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CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 11 AA;
Query Match 93.2%; Score 41; DB 20; Length 11;
Best Local Similarity 87.5%; Pred. No. 0.47;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 1 MLLGRPPF 8
RESULT 10
AAU98319
ID AAU98319 standard; Peptide; 11 AA.
XX
AC AAU98319;
XX
DT 13 AUG-2002 (first entry)
XX
DE polo kinase serine-threonine kinase HJ loop peptide J 46.
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase, J 46.
XX
OS Unidentified.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Misc difference 9 /note= "Benzyl ester of Glutamic acid"
FT Modified-site 11 /note= "C-terminal amide"
FT
XX US2002049301-A1.
PN
XX
FD 25-APR-2002.
XX
PF 13-DEC-2000; 2000US-0736076.
XX
PR 21-MAY-1997; 97US-0861338.
XX (CHIL-); CHILDRENS MEDICAL CENT.
PA Ben-Sasson SA;
XX
PI
XX WPI: 2002-462787/49.

XX New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX
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CC of a serine/threonine kinase (STK). The peptides of the invention are
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CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-46. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
SQ Sequence 11 AA;
Query Match 93.2%; Score 41; DB 23; Length 11;
Best Local Similarity 87.5%; Pred. No. 0.47;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 1 MLLGRPPF 8
RESULT 11
AAB94717
ID AAB94717 standard; Protein; 469 AA.
XX
AC AAB94717;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:15726.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX Homo sapiens.
OS
XX EP1074617-A2.
PN
XX 07-FEB-2001.
PD
XX 28-JUL-2000; 2000EP-0116126.
PF
XX 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99CP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI: 2001-318749/34.
DR
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 15726; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX SQ Sequence 469 AA;

Query Match 93.2%; Score 41; DB 22; Length 469;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
Db 57 MLLGRPPF 64

RESULT 13
AAG67426
ID AAG67426 standard; Protein: 469 AA.

XX AC AAG67426;

XX DT 26-NOV-2001 (first entry)

XX DE Amino acid sequence of a human protein kinase/protein phosphatase.

XX KW Human; protein kinase; protein phosphatase; signal transduction;

XX KW intracellular signalling pathway.

XX OS Homo sapiens.

XX PN WO200109345-A1.

XX PD 08 FEB-2001.

XX PF 28 JUL-2000; 2000WO-JP05360.

XX PR 29 JUL-1999; 99JP-0248036.

XX PR 18 OCT-1999; 99US-0159590.

XX PR 11 JAN-2000; 2000JP-0118776.

XX PR 17 FEB-2000; 2000US-0183322.

XX PR 22 MAY-2000; 2000JP-0183767.

XX PA (HELI-) HELIX RES INST.

XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;

XX PI Senoo C, Nezu J;

XX WPI; 2001-564736/63.

XX DR N-PSDB; AAH78069.

XX PT New genes encoding protein kinase and protein phosphatase, useful for
XX PT identifying modulators which can be used to treat human or animal
XX PT disorders associated with the expression or function of these enzymes -

XX PS Claim 2; Page 136-139; 336pp; Japanese.

XX

CC The present sequence represents a human protein kinase/protein
CC phosphatase. The polypeptides are expected to participate in signal
CC transduction in cells. The kinase phosphatases are connected with
CC intracellular signalling pathways. Antisense oligonucleotides and
CC compounds identified by screening (agonists or antagonists) can be
CC used to treat human or animal disorders associated with the expression
CC or function of the protein. In addition, the polypeptides may be used
CC as target molecules for drug development.

XX SQ Sequence 469 AA;

Query Match 93.2%; Score 41; DB 22; Length 469;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8

|||:|

Db 57 MLLGRPPF 64

RESULT 13
AAY00915

ID AAY00915 standard; Protein: 685 AA.

XX AC AAY00915;

XX DT 28-MAY-1999 (first entry)

XX DE Human serum inducible kinase.

XX KW Serum inducible kinase; SNK protein; human; proliferative disease;
XX KW leukaemia; solid tumour cancer; metastasis; chronic inflammatory;
XX KW psoriasis; rheumatoid arthritis; proliferative cardiovascular disease;
XX KW restenosis; ocular disorder; diabetic retinopathy; haemangioma;
XX KW benign hyperproliferative disease; diagnosis.

XX OS Homo sapiens.

XX PN WO9909146-A1.

XX PD 25-FEB-1999.

XX PF 20-AUG-1998; 98WO-US17248.

XX PR 20-AUG-1997; 97US-0056112.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Anderson KM, Bouzyk M, Hansbury MJ, Jackson JR;

XX PI Nerurkar SS, Roshak AK;

XX WPI; 1999-181027/15.

XX DR N-PSDB; AAX27227.

XX PT New serum inducible kinase (Snk) polypeptides and polynucleotides -
XX PT useful for treating proliferative diseases

XX PS Claim 1; Page 39-40; 41pp; English.

XX CC This sequence is a human serum inducible kinase (SNK) of the
XX CC invention. The invention relates to diagnostic assays or kits for
XX CC detecting diseases associated with inappropriate SNK activity or levels.
XX CC Disease states that can be diagnosed include proliferative diseases such
XX CC as leukaemia, solid tumour cancers and metastases, chronic inflammatory
XX CC proliferative diseases such as psoriasis and rheumatoid arthritis,
XX CC proliferative cardiovascular diseases such as restenosis, proliferative
XX CC ocular disorders such as diabetic retinopathy and benign
XX CC hyperproliferative diseases such as haemangiomas. The polynucleotides can
XX CC be used as hybridisation probes for cDNA and genomic DNA or as primers
XX CC for a nucleic acid amplification (PCR) reaction, to isolate full-length
XX CC cDNAs and genomic clones encoding polypeptides of this invention and to
XX CC isolate cDNA and genomic clones of other genes which have a high sequence

CC similarity to the SNK coding sequence. The differences between cDNA and
CC genomic sequences can be observed and therefore mutations detected. Any
CC mutations may then be attributed to likely causative agents of disease.
CC The nucleotide sequences are also useful for chromosome identification.
XX
SQ Sequence 685 AA;
Query Match 93.2%; Score 41; DB 20; Length 685;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
Db 273 MLLGRPPF 280
RESULT 14
AAW88432
ID AAW88432 standard; Protein; 685 AA.
AC AAW88432;
XX
DT 26-APR-1999 (first entry)
DE Disease associated protein kinase DAPK-1.
XX
KW DAPK-1; disease associated protein kinase; human; diagnosis;
KW therapy; adult respiratory distress syndrome; allergy; asthma;
KW arteriosclerosis; bronchitis; emphysema; hyper eosinophilia;
KW myocardial inflammation; pericardial inflammation; anaemia;
KW rheumatoid arthritis; Addison's disease; AIDS; atherosclerosis;
KW atopic dermatitis; dermatomyositis; diabetes mellitus;
KW glomerulonephritis; gout; Grave's disease; lupus erythematosus;
KW multiple sclerosis; myasthenia gravis; osteoarthritis;
KW osteoporosis; pancreatitis; polycystic kidney disease;
KW polymyositis; scleroderma; Sjorgren's syndrome;
KW autoimmune thyroiditis; cancer; infection; trauma;
KW cell proliferation.
XX
CS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Binding-site 89..96
FH /note= "potential ATP binding site"
FH Peptide 506..511
FH /note= "presumed regulatory sequence common to
FH polo family protein kinases"
XX
FN WC9559052.A2.
XX
PD 23 DEC-1998.
XX
PF 19-JUN-1999; 98WO-US12813.
XX
PR 19-JUN-1997; 97US-0878989.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Corley NC, Goli SK, Giegler RJ, Hillman JL;
PI Lai P, Shah P;
XX
DR WPI: 1999-080952/07.
DR N-PSDB; AAXC6831.
XX
PT New disease associated protein kinases - used to stimulate cell
PT proliferation and to treat the immune response and cancer
XX
PS Claim 1; Page 54-56; 93pp; English.
XX
CC This is the amino acid sequence of human disease associated protein
CC kinase DAPK-1, as deduced from a consensus sequence (see AAXC6831;
CC of overlapping cDNA clones from libraries which are immortalised
CC or cancerous and show inflammatory or immune responses. DAPK-1

CC shows 53% homology to human proliferation-related protein kinase
CC PRK (GI 1488263). The invention provides DAPK-1 to DAPK-7
CC polypeptides (see AAW88432-38) and cDNA clones encoding them (see
CC AAX06831-36 and AAXC6882), as well as expression vectors, host cells,
CC agonists, antagonists and antibodies. The invention further
CC provides uses of such products in the diagnosis, prevention and
CC treatment of diseases associated with cell proliferation,
CC especially cancer or an immune response (claimed). Conditions
CC that may be treated include adult respiratory distress syndrome,
CC allergies, asthma, arteriosclerosis, bronchitis, emphysema,
CC hyper eosinophilia, myocardial or pericardial inflammation,
CC rheumatoid arthritis, Addison's disease, AIDS, anaemia,
CC atherosclerosis, various diseases of the digestive system, atopic
CC dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis,
CC gout, Grave's disease, lupus erythematosus, multiple sclerosis,
CC myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis,
CC polycystic kidney disease, polymyositis, scleroderma, Sjorgren's
CC syndrome, autoimmune thyroiditis, complications of cancer,
CC extracorporeal circulation, viral, bacterial, fungal, parasitic,
CC protozoal and helminthic infections, and trauma (disclosed).
XX
SQ Sequence 685 AA;
Query Match 93.2%; Score 41; DB 20; Length 685;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
Db 273 MLLGRPPF 280
RESULT 15
ABP61474
ID ABP61474 standard; Protein; 685 AA.
XX
AC ABP61474;
XX
DT 30-SEP-2002 (first entry)
XX
DE Human NF-kB activating protein SEQ ID NO 101.
XX
KW Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
KW immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;
KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
XX
OS Homo sapiens.
XX
PN WO200253737-A1.
XX
PD 11-JUL-2002.
XX
PF 25-DEC-2001; 2001WO-JP11389.
XX
PR 28-DEC-2000; 2000JP-0402288.
PR 26-MAR-2001; 2001JP-0088912.
PR 24-AUG-2001; 2001JP-0254018.
XX
PA (ASAH) ASAH KASEI KOGYO KK.
XX
PI Matsuda A, Honda G, Muramatsu S, Nagano Y;
XX
DR WPI: 2002-583617/62.
DR N-PSDB; ABQ91962.
XX
PT NF-approximatelykB activating gene and expressed protein, applicable in
PT diagnosis and screening inhibitors or promoters to control excessive
PT activation or inhibition for treating e.g. inflammations, autoimmune
PT diseases and cancer -
XX
PS Claim 1; Page 448-453; 841pp; Japanese.
XX

CC The invention relates to a purified protein (I), comprising one of 90
CC fully defined sequences (ABP61424 ABP61513) or a protein based on any of
CC the sequences but with some amino acids deleted, substituted or added and
CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
CC inhibitors or promoters to control excessive activation or inhibition
CC and for treating e.g. inflammations, autoimmune diseases, cancers,
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
CC disorders.
XX
SQ Sequence 685 AA;

Query Match 93.2%; Score 41; DB 23; Length 685;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 273 MLLGRPPF 280
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RESULT 16
ABP41992
ID ABP41992 standard; Protein; 753 AA.
XX
AC ABP41992;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HAOSM08, SEQ ID NO:3124.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; chromosome 5.
XX
XX Homo sapiens.
XX
XX WO200200677-A1.
XX
XX 03 JAN-2002.
XX
XX 07 JUN-2002; 2001WO-US18569.
XX
XX 07 JUN-2002; 2000US-209467P.
XX
XX HUNYA-1 HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
XX WP1; 2002-147878/19.
XX
XX N-PSDB; ABQ55069.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g.
XX ovarian cancer), immune disorders, cardiovascular disorders and
XX neurological diseases -
XX
XX Claim 11; SEQ ID No 3124; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (APP41054-
XX ABP41228) and to cDNAs encoding them (ABQ54131-ABQ56105), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,

CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 753 AA;

Query Match 93.2%; Score 41; DB 23; Length 753;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 341 MLLGRPPF 348
|||||
|||

RESULT 17
AAG36347
ID AAG36347 standard; Protein; 304 AA.
XX
AC AAG36347;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44530.
XX
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 23-APR-1999; 99US-0130891.
XX 28-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 26-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142330.
PR 06-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.

PR	21-OCT-1999;	99US-0160768.	PR	14-MAY-1999;	99US-0134219.
PR	21-OCT-1999;	99US-0160770.	PR	14-MAY-1999;	99US-0134221.
PR	21-OCT-1999;	99US-0160814.	PR	14-MAY-1999;	99US-0134370.
PR	21-OCT-1999;	99US-0160815.	PR	18-MAY-1999;	99US-0134768.
PR	22-OCT-1999;	99US-0160980.	PR	19-MAY-1999;	99US-0134941.
PR	22-OCT-1999;	99US-0160981.	PR	20-MAY-1999;	99US-0135124.
PR	22-OCT-1999;	99US-0160989.	PR	21-MAY-1999;	99US-0135353.
PR	25-OCT-1999;	99US-0161404.	PR	24-MAY-1999;	99US-0135629.
PR	25-OCT-1999;	99US-0161405.	PR	25-MAY-1999;	99US-0136021.
PR	25-OCT-1999;	99US-0161406.	PR	27-MAY-1999;	99US-0136392.
PR	26-OCT-1999;	99US-0161359.	PR	28-MAY-1999;	99US-0136782.
PR	26-OCT-1999;	99US-0161360.	PR	01-JUN-1999;	99US-0137222.
PR	26-OCT-1999;	99US-0161361.	PR	03-JUN-1999;	99US-0137528.
PR	28-OCT-1999;	99US-0161920.	PR	04-JUN-1999;	99US-0137502.
PR	28-OCT-1999;	99US-0161992.	PR	07-JUN-1999;	99US-0137724.
PR	28-OCT-1999;	99US-0161993.	PR	08-JUN-1999;	99US-0138094.
PR	29 OCT-1999;	99US-0162142.	PR	10-JUN-1999;	99US-0138540.
			PR	10-JUN-1999;	99US-0138847.
			PR	14-JUN-1999;	99US-0139119.
			PR	16-JUN-1999;	99US-0139452.
			PR	16-JUN-1999;	99US-0139453.
			PR	17-JUN-1999;	99US-0139492.
			PR	18-JUN-1999;	99US-0139454.
			PR	18-JUN-1999;	99US-0139455.
			PR	18-JUN-1999;	99US-0139456.
			PR	18-JUN-1999;	99US-0139457.
			PR	18-JUN-1999;	99US-0139458.
			PR	18-JUN-1999;	99US-0139459.
			PR	18-JUN-1999;	99US-0139460.
			PR	18-JUN-1999;	99US-0139461.
			PR	18-JUN-1999;	99US-0139462.
			PR	18-JUN-1999;	99US-0139463.
			PR	18-JUN-1999;	99US-0139750.
			PR	18-JUN-1999;	99US-0139763.
			PR	21-JUN-1999;	99US-0139817.
			PR	22-JUN-1999;	99US-0139899.
			PR	23-JUN-1999;	99US-0140353.
			PR	23-JUN-1999;	99US-0140354.
			PR	24-JUN-1999;	99US-0140695.
			PR	28-JUN-1999;	99US-0140823.
			PR	29-JUN-1999;	99US-0140991.
			PR	30-JUN-1999;	99US-0141287.
			PR	01-JUL-1999;	99US-0141842.
			PR	01-JUL-1999;	99US-0142154.
			PR	02-JUL-1999;	99US-0142055.
			PR	06-JUL-1999;	99US-0142390.
			PR	08-JUL-1999;	99US-0142803.
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			PR	12-JUL-1999;	99US-0142977.
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			PR	14-JUL-1999;	99US-0143624.
			PR	15-JUL-1999;	99US-0144005.
			PR	16-JUL-1999;	99US-0144085.
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			PR	19-JUL-1999;	99US-0144325.
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			PR	19-JUL-1999;	99US-0144333.
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			PR	20-JUL-1999;	99US-0144632.
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			PR	22-JUL-1999;	99US-0145192.
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Query Match

88.6%; Score 39; DB 21; Length 304;

Best local Similarity 87.5%; Pred. No. 28;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 MLLGKPPF 8

163 MLLGKPPF 170

Db

163 MLLGKPPF 170

RESULT 18

AAG37267

ID AAG37267 standard; Protein; 304 AA.

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AC AAG37267;

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CT 18-OCT-2000 (first entry)

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DE Arabidopsis thaliana protein fragment SEQ ID NO: 45796.

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KW Protein identification; signal transduction pathway; metabolic pathway;

KW Hybridisation assay; genetic mapping; gene expression control; promoter;

KW Termination sequence.

XX

CS Arabidopsis thaliana.

XX

FN EP1033405-A2.

XX

LC 06-SEP-2000.

XX

PF 25-FEB-2000; 200CEP-0301439.

XX

PR 25-FEB-1999; 99US-0121825.

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05-MAR-1999; 99US-0123180.

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09-MAR-1999; 99US-0123548.

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06-APR-1999; 99US-0128234.

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16-APR-1999; 99US-0129845.

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Query Match 88.6%; Score 39; DB 21; Length 304;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 3; Gaps 0;

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Db 163 MLTGKPPF 170

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AC AAG38660;

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DT 18-OCT-2000 (first entry)

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DE Arabidopsis thaliana protein fragment SEQ ID NO: 47727.

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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

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PF 25-FEB-2000; 2000EP-03C1439.

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PR 09-MAR-1999; 99US-0123548.

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Query Match: 88.6%; Score 39; DB 21; Length 105;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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AC AAG36346;
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
CS Arabidopsis thaliana.
XX
FN EF1033405 A2.
XX
EC 26-SEP-2000.
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FF 25-FEB-2000; 2000EP-0301439.
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KW	hybridisation assay; genetic mapping; gene expression control; promoter;					
KW	termination sequence.					
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PR 30-AUG-1999; 99JS-0151303.
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PD 06-SEP-2000.
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PR	18-OCT-1999;	99US-0159584.	PR	07-MAY-1999; 99US-0132863.
PR	21-OCT-1999;	99US-0160742.	PR	11-MAY-1999; 99US-0134256.
PR	21-OCT-1999;	99US-0160767.	PR	14-MAY-1999; 99US-0134218.
PR	21-OCT-1999;	99US-0160768.	PR	14-MAY-1999; 99US-0134219.
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PR	22-OCT-1999;	99US-0160989.	PR	21-MAY-1999; 99US-0135353.
PR	25-OCT-1999;	99US-0161404.	PR	24-MAY-1999; 99US-0135629.
PR	25-OCT-1999;	99US-0161405.	PR	25-MAY-1999; 99US-0136021.
PR	25-OCT-1999;	99US-0161406.	PR	27-MAY-1999; 99US-0136392.
PR	26-OCT-1999;	99US-0161359.	PR	28-MAY-1999; 99US-0136782.
PR	26-OCT-1999;	99US-0161360.	PR	01-JUN-1999; 99US-0137222.
PR	26-OCT-1999;	99US-0161361.	PR	03-JUN-1999; 99US-0137528.
PR	28-OCT-1999;	99US-0161920.	PR	04-JUN-1999; 99US-0137502.
PR	28-OCT-1999;	99US-0161992.	PR	07-JUN-1999; 99US-0137724.
PR	28-OCT-1999;	99US-0161993.	PR	08-JUN-1999; 99US-0138094.
PR	29-OCT-1999;	99US-0162142.	PR	10-JUN-1999; 99US-0138540.
PR	29-OCT-1999;	99US-0162142.	PR	10-JUN-1999; 99US-0138847.
PR	29-OCT-1999;	99US-0162142.	PR	14-JUN-1999; 99US-0139119.
PR	29-OCT-1999;	99US-0162142.	PR	16-JUN-1999; 99US-0139452.
PR	29-OCT-1999;	99US-0162142.	PR	16-JUN-1999; 99US-0139453.
PR	29-OCT-1999;	99US-0162142.	PR	17-JUN-1999; 99US-0139454.
PR	29-OCT-1999;	99US-0162142.	PR	17-JUN-1999; 99US-0139454.
PR	29-OCT-1999;	99US-0162142.	PR	18-JUN-1999; 99US-0139455.
PR	29-OCT-1999;	99US-0162142.	PR	18-JUN-1999; 99US-0139456.
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PR	29-OCT-1999;	99US-0162142.	PR	18-JUN-1999; 99US-0139459.
PR	29-OCT-1999;	99US-0162142.	PR	18-JUN-1999; 99US-0139460.
PR	29-OCT-1999;	99US-0162142.	PR	18-JUN-1999; 99US-0139461.
PR	29-OCT-1999;	99US-0162142.	PR	18-JUN-1999; 99US-0139462.
PR	29-OCT-1999;	99US-0162142.	PR	18-JUN-1999; 99US-0139463.
PR	29-OCT-1999;	99US-0162142.	PR	18-JUN-1999; 99US-0139750.
PR	29-OCT-1999;	99US-0162142.	PR	18-JUN-1999; 99US-0139763.
PR	29-OCT-1999;	99US-0162142.	PR	21-JUN-1999; 99US-0139817.

Query Match 88.6%; Score 39; DB 21; Length 330;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY : MLLGKPPF 8
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DB 188 MLLGKPPF 195

RESULT 23
AAG36345
ID AAG36345 standard; Protein; 465 AA.
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AC AAG36345;
XX
DT 18-OCT-2000 (first entry)
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PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
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PR 24-JUN-1999; 99US-0140695.
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PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141942.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 19-JUL-1999; 99US-0144333.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147263.
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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 12-AUG-1999; 99US-0148341.
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PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 27-AUG-1999;

PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153370.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 14-OCT-1999; 99US-0159329.
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PR 21-OCT-1999; 99US-0160815.
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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 88.6%; Score 39; DB 21; Length 465;

Best Local Similarity 87.5%; Pred. No. 43;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8

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Db 324 MLTGKPPF 331

RESULT 24

AAG37265

ID AAG37265 standard; Protein; 465 AA.

XX AAG37265;

XX

DT 18-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 45794.

XX

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX

OS Arabidopsis thaliana.

XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
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PR 03-JUN-1999; 99US-0137528.
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PR 01-JUL-1999; 99US-0141842.
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PR 26-AUG-1999; 99US-0150884.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 15-SEP-1999; 99US-0154018.

PR 16 SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05 OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07 OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 22-OCT-1999; 99US-0160980.
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PR 22-OCT-1999; 99US-0160989.
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PR 29 OCT-1999; 99US-0162142.

Query Match 88.6%; Score 39; DB 21; Length 465;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 MLLGKPPF 8
L I I I I
DE 324 MLTGKPPF 331

RESULT 25
AAG38658
ID AAG38658 standard; Protein; 466 AA.
XX
AC AAG38658;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47725.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
CS Arabidopsis thaliana.
XX
PN EP:033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB 2000; 200SEP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
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PR 06-APR-1999; 99US-0128234.
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PR 07-JUN-1999; 99US-0137724.
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PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0148684.
PR 17-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 21-AUG-1999; 99US-0149902.
PR 21-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.

PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 88.6%; Score 39; DB 21; Length 466;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLGKPPF 8
|||
Db 324 MLTGKPPF 331

RESULT 26

AA935C0
ID AA935C0 standard; Protein; 592 AA.

XX AC AA935C0;

XX DT 25-SEP-2000 (first entry)

XX DE Amino acid sequence of the protein kinase KSG1 polypeptide.

XX KW protein kinase; Pkh1; Pkh2; Ypk1; Yrk2; protein kinase B-alpha;
XX KW human serum and glucocorticoid induced protein kinase; SGK; PKBalpha;
XX KW 3-phosphoinositide-dependent protein kinase-1; PDK1; fungal infection;
XX KW thrush; cancer; diabetes; obesity; antifungal; Candida infection.

XX OS Schizosaccharomyces pombe.

XX PN WO200036135-A2.

XX PD 22-JUN-2000.

XX PF 14-DEC-1999; 99WO-GB04228.

XX PR 14-DEC-1998; 98US-0112114.

XX PA (MEDI-) MEDICAL RES COUNCIL.
XX PA (REGC) UNIV CALIFORNIA.

PI Thorner JW, Alessi DR, Torrance PD, Casamayor A;

XX WPI; 2000-442391/38.
DR N-PSDB; AAA46568.
XX
PT Screening method identifying compounds which modulate protein kinase
PT activity for use in treating fungal infections and cancer -
XX
PS Disclosure; Page 21; 155pp; English.
XX
CC The present sequence represents a protein kinase KSG1. The specification
CC describes a screening method to identify a compound which modulates the
CC activity of protein kinases from different sources, using host yeast
CC cells. The method is used to identify a compound which modulates
CC (inhibits) the activity of a protein kinase Pkh1 or Pkh2 phosphorylate
CC and activate Ypk1, Yrk2, human serum and glucocorticoid induced protein
CC kinase (SGK) or protein kinase B-alpha (PKBalpha). 3-phosphoinositide-
CC dependent protein kinase-1 (PDK1) is used to phosphorylate and activate
CC Ypk1 and Yrk2 or SGK but not PKBalpha or p70S6 kinase. Compounds
CC identified by the methods are used to treat fungal infections e.g.
CC thrush, and to treat cancer. To treat cancer, the compounds inhibit PKB,
CC PDK1 or the activation of PKB by PDK1. Compounds which activate PKB or
CC PDK1 can be used in the treatment of diabetes or obesity, and compounds
CC which inhibit a fungal functional homologue of PDK1 (Pkh1 or Pkh2) or
CC SGK (Ypk1 or Yrk2) can be used as an antifungal agent to treat Candida
CC infections, e.g. thrush.
XX
SQ Sequence 592 AA;

Query Match 88.6%; Score 39; DB 21; Length 592;
Best Local Similarity 87.5%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
||| |||
Db 305 MLGKPPF 312

RESULT 27
AAU74657
ID AAU74657 standard; Protein; 604 AA.
XX
AC AAU74657;
XX
DT 09 APR-2002 (first entry)
XX
DE Yeast cyclin dependent kinase 5 (cdc5).
XX
KW Polo-like kinase; PLK; polo-box; cytochrome neoplasia;
KW hyperproliferative disorder; cytokinesis; solid tumour;
KW carcinoma; sarcoma; cancer; small cell carcinoma; adenocarcinoma;
KW Mullerian tumour; squamous cell carcinoma; proteinase yeast;
KW cyclin dependent kinase; cdc5.
XX
OS Saccharomyces cerevisiae.
XX
PH Key Location/Qualifiers
PT Region 513..542
PT /label= Polo-box
PT /note= "Core polo-box consensus sequence"
XX
PN WO200190401-A2.
XX
XX 29-NOV-2001.
XX
XX 23-MAY-2001; 2001WO-US16903.
XX
XX 23-MAY-2000; 2000US-206588P.
XX
XX (HARD) HARVARD COLLEGE.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH) US NAT INST OF HEALTH.
XX
PI Lee KS, Song S, Erikson R;

XX WPI; 2002-106210/14.
DR
XX
PT Identifying polo-like kinase modulators by contacting eukaryotic cells
PT expressing polo-box peptides with test compounds and evaluating changes
PT in dominant negative cytokinesis-defective growth patterns -
XX
PS Example 2; Fig 5; 57pp; English.
XX
CC The invention describes a novel method of detecting compounds with
CC polo-like kinase (PLK) modulating activity. This comprises contacting
CC eukaryotic cells expressing polo-box or polo-box related peptides,
CC binding peptides comprising 25 contiguous residues from a polo-like
CC kinase C-terminal region, with a test compound. Ectopic expression of a
CC polo-box in a eukaryotic cell causes a severe cytotoxic defect in the
CC cell. These eukaryotic cells can also be tested with the test compound
CC used in the method of the invention. The polo-box related peptides and
CC polo-like kinase activity modulatory compounds can be used to inhibit or
CC enhance cellular proliferation and subsequently for treating
CC hyper-proliferative disorders including neoplasia, solid tumours,
CC carcinomas, sarcomas and cancers e.g. small cell carcinoma,
CC adenocarcinoma, Mullerian tumours and squamous cell carcinomas. This is
CC the amino acid sequence of yeast cyclin dependent kinase cdc5, identified
CC in budding yeast as encoding a polo-like kinase and used to study the
CC effects of the polo-box on cytokinesis, described in the method of the
CC invention.
XX
SQ Sequence 604 AA;

Query Match 88.6%; Score 39; DB 23; Length 604;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
||| |||
Db 204 LLGKPPF 211

RESULT 28
AAU93498
ID AAU93498 standard; Protein; 766 AA.
XX
AC AAU93498;
XX
DT 25-SEP-2000 (first entry)
XX
DE Amino acid sequence of the protein kinase Pkh1 polypeptide.
XX
KW Protein kinase; Pkh1; Pkh2; Ypk1; Yrk2; protein kinase B-alpha;
KW human serum and glucocorticoid induced protein kinase; SGK; PKBalpha;
KW 3-phosphoinositide-dependent protein kinase-1; PDK1; fungal infection;
KW thrush; cancer; diabetes; obesity; antifungal; Candida infection.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200036135-A2.
XX
PD 22-JUN-2000.
XX
PF 14-DEC-1999; 99WO-GB04228.
XX
XX 14-DEC-1998; 98US-0112114.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
PA (REGC) UNIV CALIFORNIA.
XX
XX Thorner JW, Alessi DR, Torrance PD, Casamayor A;
XX
XX WPI; 2000-442391/38.
DR N-PSDB; AAA46566.
XX
PT Screening method identifying compounds which modulate protein kinase
PT activity for use in treating fungal infections and cancer -

XX PS Disclosure; Page 15; 155pp; English.

XX CC The present sequence represents a protein kinase Pkh1. The specification describes a screening method to identify a compound which modulates the activity of protein kinases from different sources, using host yeast cells. The method is used to identify a compound which modulates (inhibits) the activity of a protein kinase Pkh1 or Pkh2 phosphorylate and activate Ypk1, Yrk2, human serum and glucocorticoid induced protein kinase (SGK) or protein kinase B-alpha (PKBalpha). 3-phosphoinositide-dependent protein kinase-1 (PDK1) is used to phosphorylate and activate Ypk1 and Yrk2 or SGK but not PKBalpha or p70S6 kinase. Compounds identified by the methods are used to treat fungal infections e.g. thrush, and to treat cancer. To treat cancer, the compounds inhibit PKB, PDK1 or the activation of PKB by PDK1. Compounds which activate PKB or PDK1 can be used in the treatment of diabetes or obesity, and compounds which inhibit a fungal functional homologue of PDK1 (Pkh1 or Pkh2) or SGK (Ypk1 or Yrk2) can be used as an antifungal agent to treat Candida infections, e.g. thrush.

XX SQ Sequence 766 AA;

Query Match 88.6%; Score 39; DB 21; Length 766;
 Best Local Similarity 87.5%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : MLLGKPPF 8
 :|||
 Db 330 MLAGKPPF 337

RESULT 29
 AAW74211

ID AAW74211 standard; peptide; 8 AA.
 XX AC AAW74211;
 XX DT 05-MAY 1999 (first entry)
 XX DE HJ loop peptide K035H001.
 XX KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy; haemorrhagic shock; cardiovascular disease; immunosuppressive disorder; inflammatory disorder; central nervous system disease; septic shock; Parkinson's disease; hypertension.
 XX OS Synthetic
 XX PH Key Location/Qualifiers
 FT Modified-site ; /note= "acetylated"
 FT Modified-site 8 /note= "amidated"
 XX WC985305G-A2.
 XX PD 26-NOV-1998.
 XX PF 20 MAY 1998; 98WO-US10319.
 XX PR 21 MAY 1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA (YISS) YISSUM RES & DEV CO.
 XX Ben-Sasson SA;
 XX WPI; 1999-070142/06.
 XX New peptides for modulating serine/threonine kinase activity - comprise a sequence corresponding to the HJ loop of a serine/threonine kinase, used for treating, e.g. cancers, inflammatory disorders or autoimmune disorders

XX PS Disclosure; Fig 6; 70pp; English.

XX CC This sequence represents a peptide of the invention, and is a derivative of the HJ loop of a serine/threonine kinase (STK). The peptides can be used for the treatment of disorders caused by overactivity or underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis, arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and hypertension), immunosuppressive and inflammatory disorders (e.g. asthma, psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression of organ transplant rejection, multiple sclerosis, inflammatory bowel disease and AIDS), central nervous system diseases (e.g. Alzheimer's disease, stroke and trauma), septic shock, Parkinson's disease or hypertension. The peptides can also be used to produce antibodies which can be used to identify cells expressing the STK and to study the intracellular distribution of the STK. In addition, the peptides can be used to identify and quantitate ligands which bind the HJ loop of the STK from which the peptide was derived.

XX SQ Sequence 8 AA;

Query Match 86.4%; Score 38; DB 20; Length 8;
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGKPPF 8
 :|||
 Db 1 LLVGKPPF 8

RESULT 30
 AAU98355

ID AAU98355 standard; Peptide; 8 AA.
 XX AC AAU98355;
 XX DT 13-AUG-2002 (first entry)
 XX DE Polo kinase Plk serine-threonine kinase HJ loop peptide K035H001.
 XX KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity; central nervous system disorder; inflammatory disorder; autoimmune disorder; cardiovascular disorder; haemorrhagic shock; lipid metabolism; cytostatic; antidiabetic; anorectic; neurological; antiinflammatory; immunosuppressive; cardiant; haemostatic; modulating STK activity; polo kinase; Plk; K035H001.
 XX OS Unidentified.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 8 /note= "C-terminal amide"
 XX US2002049301-A1.
 XX PD 25-APR-2002.
 XX PF 13-DEC-2000; 2000US-0736076.
 XX PR 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX Ben-Sasson SA;
 XX WPI; 2002-462787/49.
 XX New peptide from the HJ loop of serine-threonine kinase, useful for treating e.g. cancer and for producing diagnostic antibodies .

XX PS Disclosure; Fig 6; 4ipp; English.

XX CC The present invention relates to new peptides derived from the HJ loop

XX CC of a serine/threonine kinase (STK). The peptides of the invention are

XX CC used to modulate STK activity, especially for treating cancer, diabetes,

XX CC obesity or a wide variety of central nervous system, inflammatory,

XX CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for

XX CC regulating lipid metabolism. The peptides are also used to generate

XX CC antibodies that bind specifically to the parent STK, used e.g. for

XX CC identifying STK-expressing cells and to study intracellular distribution

XX CC of STK, and to identify or quantify ligands that bind to the HJ loop.

XX CC The present amino acid sequence represents the polo kinase Plk

XX CC serine threonine kinase HJ loop peptide K035H001. This sequence is one

XX CC of the short peptides of the invention that selectively modulate the

XX CC activity of STK.

SQ Sequence 8 AA;

Query Match 86.4%; Score 38; DB 23; Length 8;

Best Local Similarity 75.0%; Pred. No. 9; 3e+05;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 3;

QY 1 MLLGKPPF 8

Db :|||

: LLVGKPPF 8

RESULT 31

AAW74173

ID AAW74173 standard; peptide; 20 AA.

XX AC AAW74173;

XX DT 25-MAY-1999 (first entry)

XX DE HJ loop peptide POLO.

XX KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;

XX KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

XX KW inflammatory disorder; central nervous system disease; septic shock;

XX KW Parkinson's disease; hypertension.

XX OS Synthetic.

XX PN WQ9853050-A2.

XX PD 26-NOV-1998.

XX PF 20-MAY-1998; 98WQ-US10319.

XX PR 21-MAY-1997; 97US-0861338.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PA (YISS) VISSUM RES & DEV CO.

XX PI Ben-Sasson SA;

XX DR WPI; 1999-070142/C6.

XX PT New peptides for modulating serine/threonine kinase activity -

XX PT comprise a sequence corresponding to the HJ loop of a

XX PT serine/threonine kinase, used for treating, e.g. cancers,

XX PT inflammatory disorders or autoimmune disorders

XX PS Claim 41; Fig 3b; 70pp; English.

XX CC This sequence represents a peptide of the invention, and is a derivative

XX CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be

XX CC used for the treatment of disorders caused by overactivity or

XX CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic

XX CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,

XX CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and

CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,

CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression

CC of organ transplant rejection, multiple sclerosis, inflammatory bowel

CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's

CC disease, stroke and trauma), septic shock, Parkinson's disease or

CC hypertension. The peptides can also be used to produce antibodies which

CC can be used to identify cells expressing the STK and to study the

CC intracellular distribution of the STK. In addition, the peptides can be

CC used to identify and quantitate ligands which bind the HJ loop of the STK

CC from which the peptide was derived.

XX Sequence 20 AA;

SQ Query Match 86.4%; Score 38; DB 20; Length 20;

Best Local Similarity 75.0%; Pred. No. 3.1;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8

Db :|||

: LLVGKPPF 10

RESULT 32

AAU98306

ID AAU98306 standard; Peptide; 20 AA.

XX AC AAU98306;

XX DT 13-AUG-2002 (first entry)

XX DE Peptide sequence of HJ loop of serine-threonine kinase polo kinase.

XX KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;

XX KW central nervous system disorder; inflammatory disorder;

XX KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;

XX KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;

XX KW antiinflammatory; immunosuppressive; cardiant; haemostatic;

XX KW modulating STK activity; polo kinase.

XX OS Unidentified.

XX PN US2002049301-A1.

XX PD 25-APR-2002.

XX PF 13-DEC-2000; 2000US-0736076.

XX PR 21-MAY-1997; 97US-0861338.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Ben-Sasson SA;

XX DR WPI; 2002-462797/49.

XX PT New peptide from the HJ loop of serine-threonine kinase, useful for

XX PT treating e.g. cancer and for producing diagnostic antibodies -

XX PS Claim 33; Fig 3; 41pp; English.

XX CC The present invention relates to new peptides derived from the HJ loop

XX CC of a serine/threonine kinase (STK). The peptides of the invention are

XX CC used to modulate STK activity, especially for treating cancer, diabetes,

XX CC obesity or a wide variety of central nervous system, inflammatory,

XX CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for

XX CC regulating lipid metabolism. The peptides are also used to generate

XX CC antibodies that bind specifically to the parent STK, used e.g. for

XX CC identifying STK-expressing cells and to study intracellular distribution

XX CC of STK, and to identify or quantify ligands that bind to the HJ loop.

XX CC The present amino acid sequence represents the peptide sequence of the HJ

XX CC loop of serine-threonine kinase polo kinase. This sequence is one of the

XX CC short peptides of the invention that selectively modulate the activity

XX CC of STK.

XX SQ Sequence 20 AA;
Query Match 86.4%; Score 35; DB 23; Length 20;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:|
Db 3 LLVGKPPF 10

RESULT 34
AAB56690
ID AAB56690 standard; Protein: 329 AA.
XX AC AAB56690;
XX DT 13 MAR-2001 (first entry)
XX DE Human prostate cancer antigen protein sequence SEQ ID NO:1268.
XX KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW uroinary; gastrointestinal; nephrotropic; anti-infective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX CS Homo sapiens.
XX PN WP200055174-A1.
XX PD 21 SEP-2000.
XX PF 13 MAR-2000; 2000WC-US05986.
XX PR 12 MAR-1999; 99US-0124270.
XX PA (HUMAN) HUMAN GENOME SCI INC.
XX PA (ROSE/) ROSEN C A.
XX PI Rosen CA. Ruben SM;
XX WPI; 2000-587513/55.
XX N-PSDB; AAF15933.
XX PT Prostate cancer; associated gene sequences; referred to as prostate
PT cancer antigens, useful for treatment, prevention and diagnosis of
PT disorders such as prostate cancer;
XX Claim 11; Page 1691-1692; 223pp; English.
XX AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56663 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, uroinary, gastrointestinal,
CC nephrotropic, anti-infective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.
XX SQ Sequence 329 AA;

Query Match 86.4%; Score 32; DB 21; Length 20;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:|
Db 260 LLVGKPPF 267

RESULT 34
AAU83127
ID AAU83127 standard; Protein: 419 AA.
XX AC AAU83127;
XX DT 08-MAY-2002 (first entry)
XX DE Novel secreted protein Z835510GSP.
XX KW Protein secretion; mammalian secreted polypeptide; MSP.
XX OS Homo sapiens.
XX PN WO200202621-A2.
XX PD 10-JAN-2002.
XX PF 28-JUN-2001; 2001WO-US20638.
XX PR 30-JUN-2000; 2000US-215446P.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Sheppard PO, Presnell SR;
XX WPI; 2002-147999/19.
XX N-PSDB; ABK33042.
XX PT Novel isolated mammalian secreted polypeptide useful in therapeutic and
PT diagnostic methods, to direct secretion of other proteins of interest
PT from host cell, as educational tools, and as laboratory practicum kits
PT .
XX Claim 12; Page 171-173; 397pp; English.
XX CC The invention describes an isolated mammalian secreted polypeptide (MSP)
CC (I). (I) is useful to direct the secretion of other proteins of interest
CC from a host cell, to monitor secretion of proteins, to degenerate
CC sequences comprising all nucleotide sequences encoding a particular
CC polypeptide, to screen for cell metabolism effecting receptors, for
CC identifying new target receptors and drug design, for identifying, for
CC protein purification, for determining the weight of expressed MSP
CC polypeptides as a ratio to total protein expressed, for identifying
CC peptide cleavage sites, for coupling amino and carboxy terminal tags, for
CC amino acid sequence analysis, for monitoring biological activities of the
CC protein in vitro and in vivo, and to teach analytical skills and as
CC reagents for the study of cells, receptors, and other binding molecules.
CC The polynucleotide is useful for radiation hybrid mapping, and somatic
CC cell genetic technique developed for constructing high-resolution,
CC contiguous maps of mammalian chromosomes. Reagents disclosed in the
CC invention may be used to detect metabolic abnormalities characterised by
CC over or under production of the protein. This is the amino acid sequence
CC of a mammalian secreted polypeptide, described in the method of the
CC invention.
XX SQ Sequence 419 AA;

Query Match 86.4%; Score 38; DB 23; Length 419;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPP 7
:|:|:|:|
Db 170 MLLGKPP 176

RESULT 35

ABP73734
ID ABP73734 standard; Protein; 528 AA.

XX
AC ABP73734;

XX
DT 30-JAN-2003 (first entry)

XX
DE Candida albicans essential protein SEQ ID NO 7571.

XX
KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal.

XX
OS Candida albicans.

XX
PN W0200253728-A2.

XX
PD 11-JUL-2002.

XX
PF 26-DEC-2001; 2001WO-US49486.

XX
PR 29-DEC-2000; 2000US-259128P.

PR
20-FEB-2002; 2001US-0792024.

PR
22-AUG-2001; 2001US-314050P.

XX
PA (ELIT-); ELITRA PHARM INC.

XX
PI Roemer T, Jiang B, Boone C, Bussey H, Chisen KL;

XX
DR WPI; 2002-566694/60.

DR
N-PSDB; AB232284.

XX
PT Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele
PT of a gene and placing other allele of the gene under conditional
PT expression

XX
PS Claim 44; SEQ ID NO 7571; 167pp + Sequence Listing; English.

XX
CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of an
CC essential Candida albicans protein used in the method of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.

XX
SQ Sequence 528 AA;

Query Match 86.4%; Score 18; DB 23; Length 528;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8

:|:|||||

454 LLVGKPPF 461

Db

RESULT 36

AAU74656

ID AAU74656 standard; Protein; 531 AA.

XX
AC AAU74656;

XX
DT 09-APR-2002 (first entry)

XX
DE Mammalian polo-like kinase (Plk).

XX
KW Polo-like kinase; PLK; polo-box; cytostatic; neoplasm;
KW hyperproliferative disorder; cytokinesis; solid tumour;
KW carcinoma; sarcoma; cancer; small cell carcinoma; adenocarcinoma;
KW Mullerian tumour; squamous cell carcinoma; protein.

XX
OS Mammalia.

XX
FH Key Location/Qualifiers

FT Misc-difference 130

FT /label= Unknown

FT Misc-difference 131

FT /label= Unknown

FT Misc-difference 132

FT /label= Unknown

FT Misc-difference 133

FT /label= Unknown

FT Misc-difference 134

FT /label= Unknown

FT Misc-difference 135

FT /label= Unknown

FT Misc-difference 136

FT /label= Unknown

FT Misc-difference 137

FT /label= Unknown

FT Misc-difference 138

FT /label= Unknown

FT Misc-difference 139

FT /label= Unknown

FT Misc-difference 140

FT /label= Unknown

FT Misc-difference 141

FT /label= Unknown

FT Misc-difference 147

FT /label= Unknown

FT Misc-difference 148

FT /label= Unknown

FT Misc-difference 149

FT /label= Unknown

FT Misc-difference 150

FT /label= Unknown

FT Misc-difference 151

FT /label= Unknown

FT Misc-difference 152

FT /label= Unknown

FT Misc-difference 153

FT /label= Unknown

FT Misc-difference 154

FT /label= Unknown

FT Misc-difference 155

FT /label= Unknown

FT Misc-difference 156

FT /label= Unknown

FT Misc-difference 157

FT /label= Unknown

FT Misc-difference 158

FT /label= Unknown

FT Misc-difference 159

FT /label= Unknown

FT Misc-difference 160

FT /label= Unknown
FT Misc-difference 361
FT /label= Unknown
FT Misc-difference 362
FT /label= Unknown
FT Misc-difference 363
FT /label= Unknown
FT Misc-difference 364
FT /label= Unknown
FT Misc-difference 365
FT /label= Unknown
FT Region:
FT /label= Polo-box
FT /label= Polo-box
FT /note= "Core polo-box consensus sequence"
XX
PN WQ200190401-A2.
XX
PD 29-NOV-2001.
XX
XX 23-MAY 2001; 2001WO-US16903.
PF
XX 23-MAY-2000; 2000JS-206588P.
PR
XX (HARD ; HARVARD COLLEGE.
PA (USSH ; US DEPT HEALTH & HUMAN SERVICES.
PA (USSH ; US NAT INST OF HEALTH.
XX
PI Lee KS, Song S, Erikson R;
DR WPI; 2002-106210/14.
XX

Identifying polo-like kinase modulators by contacting eukaryotic cells expressing polo-box peptides with test compounds and evaluating changes in dominant negative cytokinesis-defective growth patterns

Example 2; Fig 5; 57pp; English.

The invention describes a novel method of detecting compounds with polo-like kinase (PLK) modulating activity. This comprises contacting eukaryotic cells expressing polo-box or polo-box related peptides, binding peptides comprising 25 contiguous residues from a polo-like kinase C-terminal region, with a test compound. Ectopic expression of a polo-box in a eukaryotic cell causes a severe cytokinetic defect in the cell. These eukaryotic cells can also be tested with the test compound used in the method of the invention. The polo-box related peptides and polo-like kinase activity modulatory compounds can be used to inhibit or enhance cellular proliferation and subsequently for treating hyper-proliferative disorders including neoplasia, solid tumours, carcinomas, sarcomas and cancers e.g. small cell carcinoma, adenocarcinoma, Mullerian tumours and squamous cell carcinomas. This is the amino acid sequence of a mammalian polo-like kinase (Plk), uncontrolled expression of the Plk family is implicated in the development of human cancers, discussed in the method of the invention.

Sequence 531 AA;

Query Match 86.4%; Score 38; DB 23; Length 531;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|
Db 204 LLVGKPPF 211

RESULT 37
AAR74620
ID AAR74620 standard; Protein: 603 AA.
XX
AC AAR74620;
XX
DT 25-MAR-2003 (updated)
DT 26-OCT-1995 (first entry)

XX Human lung tumour Polo-like kinase.
DE
XX Polo-like kinase; PLK; serine threonine kinase; human; lung tumour;
KW autoimmune disease; lymphocyte activity.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 60..86
FT /label= ATP-binding_motif
FT Region 174..177
FT /note= "motif that is highly conserved in protein
FT kinases"
FT Region 194..196
FT /note= "motif that is highly conserved in protein
FT kinases"
XX
PN DE4329177-A1.
XX
PD 02-MAR-1995.
XX
XX 30-AUG-1993; 93DE-4329177.
PF
XX 30-AUG-1993; 93DE-4329177.
PR
XX (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.
PA
XX Holtrich U, Rubsamen-Waigmann H, Strebhardt K;
PI Rubsamen-Waigmann H;
XX
DR WPI; 1995-099454/14.
DR N-PSDB; AAQ88155.
XX
XX A polo-like serine threonine kinase-protein - isolated from
PT proliferating human tissue, useful in the determ of lymphocyte
PT activity, eg in auto-immune diseases
XX
PS Claim 1; Page 8-10; 11pp; German.
XX
CC A human lung tumour-derived cDNA (AAQ88155) was found to have high
CC homology with sequences from members of the serine/threonine kinase
CC family. Due to the strong homology with the Drosophila polo gene,
CC the protein encoded by the new cDNA (AAR74620) was designated a polo-
CC like kinase (PLK). PLK mRNA is expressed in proliferating cells such
CC as placenta, colon and tumours of the lung, oesophagus, gut and
CC intestine. Resting lymphocytes do not express the PLK gene but after
CC stimulation with phytohaemagglutinin, PLK is expressed and can be
CC used as an indicator of lymphocyte stimulation.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 603 AA;

Query Match 86.4%; Score 38; DB 16; Length 603;
Best Local Similarity 75.0%; Pred. No. 85;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|
Db 244 LLVGKPPF 251

RESULT 38
AAU79306
ID AAU79306 standard; Peptide: 603 AA.
XX
AC AAU79306;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk).
XX
KW Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;

KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk.
XX
CS Mus musculus.
XX
PN US6358738-B1.
XX
PD 19 MAR-2002.
XX
PF 13-MAY-1999; 39US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI: 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections .
PS Example 1; Column 59-64; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of the polo-like kinase (Plk), a
CC protein from which mitotic protein polo kinase inhibitory peptides are
CC derived.
XX
SQ Sequence 603 AA;
Query Match: 86.4%; Score 38; DB 23; Length 603;
Best Local Similarity 75.0%; Pred. No. 85;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 244 LLVGKPPF 251
RESULT 39
AAU79308
ID AAU79308 standard; Peptide; 603 AA.
XX
AC AAU79308;
XX
DT 02 JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T21CD mutant.
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelmintic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
XX
CS Mus musculus.

OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Thr substituted by Asp"
FT
XX US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI: 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections .
PS Example 1; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match: 86.4%; Score 38; DB 23; Length 603;
Best Local Similarity 75.0%; Pred. No. 85;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 244 LLVGKPPF 251
RESULT 40
AAU79309
ID AAU79309 standard; Peptide; 603 AA.
XX
AC AAU79309;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T210E mutant.
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelmintic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
XX
OS Mus musculus.
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Thr substituted by Glu"
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 14-MAY-1998; 98US-085296P.
XX
PA (HARD : HARVARD COLLEGE.
XX
PI Erikson RL, Lee XS;
XX
DR WPI: 2002-314756/35
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections .
XX
PS Example 1; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAJ79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match 86.4%; Score 38; DB 23; Length 603;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGKPPF 8
DB 244 LLVOKPPF 251

Search completed: November 14, 2003, 13:59:05
Job time : 31.957. secs

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OM protein - protein search, using sw model

Run on: November 14, 2003, 13:23:00 ; Search time 10.5143 Seconds
(without alignments)
32.193 Million cell updates/sec

Title: US-09-736-076-16
Perfect score: 44
Sequence: 1 MLLGKPPF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/6C_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles.pep:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the results being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	8	3	US-08-861-338-16 Sequence 16, Appl
2	44	100.0	9	3	US-08-861-338-17 Sequence 17, Appl
3	41	93.2	9	3	US-08-861-338-19 Sequence 19, Appl
4	41	93.2	11	3	US-08-861-338-19 Sequence 19, Appl
5	41	93.2	272	1	US-08-252-995D-12 Sequence 12, Appl
6	41	93.2	272	2	US-08-834-108-12 Sequence 12, Appl
7	41	93.2	685	2	US-08-834-108-12 Sequence 12, Appl
8	41	93.2	685	3	US-08-834-108-12 Sequence 12, Appl
9	41	93.2	685	3	US-08-834-108-12 Sequence 12, Appl
10	41	93.2	685	3	US-08-834-108-12 Sequence 12, Appl
11	39	88.6	275	1	US-08-252-995D-13 Sequence 13, Appl
12	39	88.6	275	2	US-08-834-108-13 Sequence 13, Appl
13	38	86.4	20	3	US-08-861-338-6 Sequence 6, Appl
14	38	86.4	272	1	US-08-252-995D-14 Sequence 14, Appl
15	38	86.4	272	2	US-08-834-108-14 Sequence 14, Appl
16	38	86.4	603	3	US-09-135-122-2 Sequence 2, Appl
17	38	86.4	603	4	US-09-135-122-2 Sequence 2, Appl
18	37	84.1	264	2	US-07-857-224B-17 Sequence 17, Appl
19	37	84.1	459	4	US-09-509-902A-12 Sequence 12, Appl
20	37	84.1	588	4	US-09-509-902A-16 Sequence 16, Appl
21	37	84.1	668	4	US-09-135-001C-4815 Sequence 4816, Ap
22	37	84.1	962	4	US-09-442-100-6 Sequence 6, Appl
23	37	84.1	962	4	US-08-933-106-6 Sequence 6, Appl
24	37	84.1	980	4	US-09-442-100-6 Sequence 8, Appl
25	37	84.1	980	4	US-08-933-106-6 Sequence 8, Appl
26	37	84.1	1088	4	US-09-233-857-4 Sequence 4, Appl
27	37	84.1	1088	4	US-09-233-857-13 Sequence 13, Appl

28	37	84.1	1099	4	US-09-442-100-2 Sequence 2, Appl
29	37	84.1	1099	4	US-08-939-106-2 Sequence 2, Appl
30	37	84.1	1130	4	US-09-442-100-4 Sequence 4, Appl
31	37	84.1	1130	4	US-09-233-857-3 Sequence 3, Appl
32	37	84.1	1130	4	US-08-939-106-4 Sequence 4, Appl
33	36	81.8	273	1	US-08-252-995D-10 Sequence 10, Appl
34	36	81.8	273	2	US-08-834-108-10 Sequence 10, Appl
35	36	81.8	403	2	US-08-755-728-4 Sequence 4, Appl
36	36	81.8	403	2	US-08-974-655-4 Sequence 4, Appl
37	36	81.8	403	3	US-09-283-011-4 Sequence 4, Appl
38	36	81.8	416	1	US-08-252-995D-2 Sequence 2, Appl
39	36	81.8	416	2	US-08-834-108-2 Sequence 2, Appl
40	36	81.8	464	1	US-08-252-995D-6 Sequence 6, Appl
41	36	81.8	464	2	US-08-834-108-6 Sequence 6, Appl
42	36	81.8	925	1	US-08-252-995D-4 Sequence 4, Appl
43	36	81.8	925	2	US-08-834-108-4 Sequence 4, Appl
44	36	81.8	1037	4	US-09-428-711A-21 Sequence 21, Appl
45	35	79.5	20	3	US-08-861-338-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-861-338-16
; Sequence 16, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "Phenylalanine-NH2"

Query Match 100.0% Score 44; DB 3; Length 8;

```

; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 1 MLLGKPPF 8

RESULT 2
US-08-861-338-17
; Sequence 17, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; Glutamine Acid-NH2"
; US-08-861-338-17

Query Match 100.0%; Score 44; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 1 MLLGKPPF 8

RESULT 3
US-08-861-338-15
; Sequence 15, Application US/08861336
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.

```

```

; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; Glutamic Acid-NH2"
; US-08-861-338-15

Query Match 93.2%; Score 41; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 1 MLLGKPPF 8

RESULT 4
US-08-861-338-19
; Sequence 19, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Serine-NH2"
US-08-861-338-19

```

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Query Match          93.2%  Score 41; DB 3; Length 11;
Best Local Similarity 87.5%  Pred. No. 0.11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MLLGKPPF 8
      |||:|
Db      1 MLLGRPPF 8

```

```

RESULT 5
US 08 252-995D-12
; Sequence 12, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DCS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-252-995D-12

```

```

Query Match          93.2%  Score 41; DB 1; Length 272;
Best Local Similarity 87.5%  Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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QY      1 MLLGKPPF 8
      |||:|
Db      199 MLLGRPPF 206

```

```

RESULT 6
US-08-834-108-12
; Sequence 12, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-834-108-12

```

```

Query Match          93.2%  Score 41; DB 2; Length 272;
Best Local Similarity 87.5%  Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPF 8
      |||:|
Db      199 MLLGRPPF 206

```



```

RESULT 7
US-09-736-989 1
; Sequence 1, Application US/08878989
; Patent No. 5985803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lai, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: FF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415 845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENOB01
; CLONE: 39043
US 08 878-989-1

Query Match 93.2%; Score 41; DB 2; Length 685;
Best Local Similarity 87.5%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGKPPF 8
|||:|
DB 273 MLLGRPPF 280

RESULT 8
US-09-136-282-2
; Sequence 2, Application US/09136282
; Patent No. 6063609
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, KAREN
; APPLICANT: JACKSON, JEFFREY
; APPLICANT: HANSBURY, MICHAEL
; APPLICANT: NERURKAR, SANDHYA

```

```

; APPLICANT: ROSHAK, AMY
; APPLICANT: BOUZYK, MARK
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,282
; FILING DATE: 20-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/356,112
; FILING DATE: 20-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-136-282-2

Query Match 93.2%; Score 41; DB 3; Length 685;
Best Local Similarity 87.5%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGKPPF 8
|||:|
DB 273 MLLGRPPF 280

RESULT 9
US-09-272-796-1
; Sequence 1, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lai, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version: 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272.796
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/878,989
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HUVEOB01
CLONE: 39043
US-09 272-796-1

Query Match 93.2%; Score 41; DB 3; Length 685;
Best Local Similarity 87.5%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||
DB 273 MLLGRPPF 280

RESULT 10
US-09-505 744-2
Sequence 2, Application US/C9505744
Patent No. 6245544
GENERAL INFORMATION:
APPLICANT: Karen M. Anderson
APPLICANT: Mark M. Rouzyk
APPLICANT: Michael J. Hansbury
APPLICANT: Geoffrey R. Jackson
APPLICANT: Sandhya S. Nerurkar
APPLICANT: Amy K. Roshak
TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE
FILE REFERENCE: GH-70231-D1
CURRENT APPLICATION NUMBER: US/09/505.744
CURRENT FILING DATE: 2000-02-16
EARLIER APPLICATION NUMBER: 09/136,280
EARLIER FILING DATE: 1998-08-20
EARLIER APPLICATION NUMBER: 60/056,112
EARLIER FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ for Windows Version: 1.0
SEQ ID NO 2
LENGTH: 685
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-505 744-2

Query Match 93.2%; Score 41; DB 3; Length 685;
Best Local Similarity 87.5%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||
DB 273 MLLGRPPF 280

RESULT 11
US-08-252-995D-13
Sequence 13, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdzyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US-08-252-995D-13

Query Match 88.6%; Score 39; DB 1; Length 275;
Best Local Similarity 75.0%; Pred. No. 6.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||
DB 200 MLLGKPPF 207

RESULT 12
US-08-834-108-13
Sequence 13, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 362-1398
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US-08-834-108-13

Query Match: 88.4%; Score 39; DB 2; Length 275;
Best Local Similarity 75.0%; Pred. No. 67;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:|
DB 200 LLVGKPPF 207

RESULT 13
US-08-861-338-6
; Sequence 6; Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide

US-08-861-338-6
Query Match: 86.4%; Score 38; DB 3; Length 20;
Best Local Similarity 75.0%; Pred. No. 0.75;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:|
DB 3 LLVGKPPF 10

RESULT 14
US-08-252-995D-14
; Sequence 14; Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-252-995D-14

Query Match: 86.4%; Score 38; DB 1; Length 272;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:|
DB 199 LLVGKPPF 206

RESULT 15
US-08-834-108-14
; Sequence 14; Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-834-108-14

Query Match 86.4%; Score 38; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|||||
DB 199 LLVGKPPF 206

RESULT 16
US 09 198 122-2
Sequence 2, Application US/09198:22
Patent No. 6190380
GENERAL INFORMATION:
APPLICANT: Strehardt, Klaus; Rubsamen-Waigmann, Helga;
APPLICANT: Holtrich, Uwe
TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE-
TITLE OF INVENTION: THREONINE-KINASE FAMILY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HORN KRAMER & WOOES
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
MEDIUM TYPE: storage
COMPUTER: NEC Powermate SX-20
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,122
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/601,014

FILING DATE: 23-FEB-1996
APPLICATION NUMBER: PCT/EP94/02863
FILING DATE: 30-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4329177
FILING DATE: 30-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9516-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-09-198-122-2

Query Match 86.4%; Score 38; DB 3; Length 603;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|||||
DB 244 LLVGKPPF 251

RESULT 17
US-09-311-311C-26
Sequence 26, Application US/09311311C
Patent No. 6358738
GENERAL INFORMATION:
APPLICANT: Erikson, et al.
TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS,
TITLE OF INVENTION: METHODS, AND USES THEREFOR
FILE REFERENCE: 1874/117
CURRENT APPLICATION NUMBER: US/09/311,311C
CURRENT FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,296
PRIOR FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 603
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)...(603)
OTHER INFORMATION: Plk protein
US-09-311-311C-26

Query Match 86.4%; Score 38; DB 4; Length 603;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|||||
DB 244 LLVGKPPF 251

RESULT 18
US-07-857-224B-17
Sequence 17, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Steven A. Benner
;; STREET: Hadlaubstrasse 151
;; CITY: Zurich
;; STATE: none
;; COUNTRY: Switzerland
;; ZIP: (note: this is an international post code) CH-8092
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh 7.0
;; SOFTWARE: Microsoft Word
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/857,224B
;; FILING DATE: 03/25/92
;; CLASSIFICATION: 436
;; PRIOR APPLICATION DATA: none
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (International) 41 1 632 2830
;; TELEFAX: (International) 41 1 262 2437
;; TELEX: none
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 264
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; DESCRIPTION: protein
;; ORIGINAL SOURCE:
;; ORGANISM: Drosophila melanogaster
;; FEATURE: Protein kinase; Table 8 Column 18
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; AUTHORS: Hanks, S. K.
;; AUTHORS: Quinn, A. M.
;; AUTHORS: Hunter, T.
;; TITLE: The protein kinase family
;; JOURNAL: Science
;; VOLUME: 241
;; PAGES: 42-52
;; DATE: 1988
US-07-857-224B-17

Query Match 84.1%; Score 37; DB 2; Length 264;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 195 MLVGQPPF 202

RESULT 19
US-09-509-902A-12
; Sequence 12, Application US/09509902A
; Patent No. 6387676
; GENERAL INFORMATION:
; APPLICANT: Virca, Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Marken, John S.
; TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase Functions
; FILE REFERENCE: 2877-US
; CURRENT APPLICATION NUMBER: US/09/509,902A
; CURRENT FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-509-902A-12

Query Match 84.1%; Score 37; DB 4; Length 499;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 407 MLVGQPPF 414

RESULT 20
US-09-509-902A-16
; Sequence 16, Application US/09509902A
; Patent No. 6387676
; GENERAL INFORMATION:
; APPLICANT: Virca, Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Marken, John S.
; TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase Functions
; FILE REFERENCE: 2877-US
; CURRENT APPLICATION NUMBER: US/09/509,902A
; CURRENT FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-509-902A-16

Query Match 84.1%; Score 37; DB 4; Length 588;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 406 MLVGQPPF 413

RESULT 21
US-09-134-001C-4816
; Sequence 4816, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4816
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4816

Query Match 84.1%; Score 37; DB 4; Length 668;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 203 MLVGQPPF 210

RESULT 22
US-09-442-100-6
; Sequence 6, Application US/09442100


```
; Patent No. 6359193
; GENERAL INFORMATION:
; APPLICANT: Xu, Tian
; APPLICANT: Tao, Wufan
; APPLICANT: Wang, Weiyl
; APPLICANT: Zhang, Sheng
; APPLICANT: Yu, Wan
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
; TITLE OF INVENTION: GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/442,100
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/411,111
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-003
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 962 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-442-100-6

Query Match 84.1%; Score 37; DB 4; Length 962;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 775 MLVGQPPF 782

RESULT 23
US-08-939 106-6
; Sequence 6, Application US/08939106
; Patent No. 6559285
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/442,100
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/411,111
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-003
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 962 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-442-100-6

Query Match 84.1%; Score 37; DB 4; Length 962;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 775 MLVGQPPF 782
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,106
; FILING DATE: 26-No. 6559285-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-007-228
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 962 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-939-106-6

Query Match 84.1%; Score 37; DB 4; Length 962;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 775 MLVGQPPF 782

RESULT 24
US-09-442-100-8
; Sequence 8, Application US/09442100
; Patent No. 6359193
; GENERAL INFORMATION:
; APPLICANT: Xu, Tian
; APPLICANT: Tao, Wufan
; APPLICANT: Wang, Weiyl
; APPLICANT: Zhang, Sheng
; APPLICANT: Yu, Wan
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
; TITLE OF INVENTION: GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/442,100
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/411,111
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-003
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
```

```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 980 amino acids
;   TYPE: amino acid
;   TOPOLOGY: unknown
;   MOLECULE TYPE: protein
US-09-442-100-8

Query Match      84.1%; Score 37; DB 4; Length 980;
Best Local Similarity 75.0%; Pred. No. 56;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

QY      1 MLLGKPPF 8
      |||:|
DB      802 MLVGQPPF 809

RESULT 25
US-08-939-106-8
; Sequence 8, Application US/08939:06
; Patent No. 6559285
; GENERAL INFORMATION:
;   APPLICANT: Yale University
;   TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
;   GENES AND METHODS BASED THEREON
;   NUMBER OF SEQUENCES: 16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/939:06
;     FILING DATE: 26-NOV-1997
;     CLASSIFICATION: <Unknown>
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Misrock, S. Leslie
;       REGISTRATION NUMBER: 18,872
;       REFERENCE/DOCKET NUMBER: 6523 007-228
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212) 790 9240
;       TELEFAX: (212) 969-9741/8664
;       TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 980 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-08-939-106-8

Query Match      84.1%; Score 37; DB 4; Length 980;
Best Local Similarity 75.0%; Pred. No. 56;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

QY      1 MLLGKPPF 8
      |||:|
DB      802 MLVGQPPF 809

RESULT 26
US-09-233-857-4
; Sequence 4, Application US/09233857
; Patent No. 6495353
; GENERAL INFORMATION:
;   APPLICANT: Plowman, Gregory

```

```

;   APPLICANT: Planagan, Peter
;   TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
;   FILE REFERENCE: 239/251
;   CURRENT APPLICATION NUMBER: US/09/233.857
;   CURRENT FILING DATE: 1999-01-20
;   EARLIER APPLICATION NUMBER: USSN 60/072,023
;   EARLIER FILING DATE: 1998-01-21
;   NUMBER OF SEQ ID NOS: 18
;   SOFTWARE: FastSeq for Windows Version 3.0
;   SEQ ID NO 4
;   LENGTH: 1088
;   TYPE: PRT
;   ORGANISM: HUMAN
US-09-233-857-4

Query Match      84.1%; Score 37; DB 4; Length 1088;
Best Local Similarity 75.0%; Pred. No. 62;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

QY      1 MLLGKPPF 8
      |||:|
DB      906 MLVGQPPF 913

RESULT 27
US-09-233-857-13
; Sequence 13, Application US/09233857
; Patent No. 6495353
; GENERAL INFORMATION:
;   APPLICANT: Plowman, Gregory
;   APPLICANT: Planagan, Peter
;   TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
;   FILE REFERENCE: 239/251
;   CURRENT APPLICATION NUMBER: US/09/233.857
;   CURRENT FILING DATE: 1999-01-20
;   EARLIER APPLICATION NUMBER: USSN 60/072,023
;   EARLIER FILING DATE: 1998-01-21
;   NUMBER OF SEQ ID NOS: 18
;   SOFTWARE: FastSeq for Windows Version 3.0
;   SEQ ID NO 13
;   LENGTH: 1088
;   TYPE: PRT
;   ORGANISM: HUMAN
US-09-233-857-13

Query Match      84.1%; Score 37; DB 4; Length 1088;
Best Local Similarity 75.0%; Pred. No. 62;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

QY      1 MLLGKPPF 8
      |||:|
DB      952 MLVGQPPF 958

RESULT 28
US-09-442-100-2
; Sequence 2, Application US/09442100
; Patent No. 6359193
; GENERAL INFORMATION:
;   APPLICANT: Xu, Tian
;   APPLICANT: Tao, Wufan
;   APPLICANT: Wang, Weiyl
;   APPLICANT: Zhang, Sheng
;   APPLICANT: Yu, Wan
;   TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
;   TITLE OF INVENTION: GENES AND METHODS BASED THEREON
;   NUMBER OF SEQUENCES: 16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA

```

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,100
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/411,111
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1099 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US 09 442 100-2

Query Match 84.1%; Score 37; DB 4; Length 1099;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
Db 948 MLVGQPPF 955

RESULT 29

US-08-939-106-2
Sequence 2, Application US/08939106
Patent No. 6559285
GENERAL INFORMATION:
APPLICANT: Yale University
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,106
FILING DATE: 26-Nov-6559285-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-007-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 1099 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-939-106-2

Query Match 84.1%; Score 37; DB 4; Length 1099;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
Db 948 MLVGQPPF 955

RESULT 30

US-09-442-100-4
Sequence 4, Application US/09442100
Patent No. 6359193
GENERAL INFORMATION:
APPLICANT: Xu, Tian
APPLICANT: Tao, Wufan
APPLICANT: Wang, Weiye
APPLICANT: Zhang, Sheng
APPLICANT: Yu, Wan
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,100
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/411,111
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1130 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-442-100-4

Query Match 84.1%; Score 37; DB 4; Length 1130;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
Db 943 MLVGQPPF 950

RESULT 31
US-09-233-857-3
; Sequence 3, Application US/09233857
; Patent No. 6495353
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Flanagan, Peter
; TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
; FILE REFERENCE: 239/251
; CURRENT APPLICATION NUMBER: US/09/233-857
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: USSN 60/072,023
; EARLIER FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1130
; TYPE: PRT
; ORGANISM: HUMAN
US-09-233-857-3

Query Match 84.1%; Score 37; DB 4; Length 1130;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|:|:|:
Db 943 MLVGQPPF 950

RESULT 32
US-08-939-106-4
; Sequence 4, Application US/08939106
; Patent No. 6559285
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939-106
; FILING DATE: 26-Nov-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mastrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-007-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8804
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-939-106-4

Query Match 84.1%; Score 37; DB 4; Length 1130;

Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
|:|:|:
Db 943 MLVGQPPF 950
RESULT 33
US-08-252-995D-10
; Sequence 10, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Hefernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-252-995D-10

Query Match 81.8%; Score 36; DB 1; Length 273;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|:|:|:
Db 200 LLIGRPPF 207

RESULT 34
US-08-834-108-10
; Sequence 10, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Hefernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR

STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-834-108-10

Query Match 81.8% Score 36; DB 2; Length 273;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLGKPPF 8
DB 200 LLGKPPF 207

RESULT 35
US-08-755-728-4
Sequence 4, Application US/08/755728
Patent No. 5962312
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR 1
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,728
FILING DATE: No. 5962312ember 25, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
APPLICATION NUMBER: 60/023,943

FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-755-728-4

Query Match 81.8% Score 36; DB 2; Length 403;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
DB 323 LVGKPPF 329

RESULT 36
US-08-974-655-4
Sequence 4, Application US/08/974655
Patent No. 5972676
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,655
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/755,728
FILING DATE: No. 5972676ember 25, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-974-655-4

Query Match      81.8%; Score 36; DB 2; Length 403;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLGKPPF 8
Db      323 LVGKPPF 329

RESULT 37
US-09-283-011-4
; Sequence 4, Application US/09283011
; Patent No. 6207401
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE:
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/283,011
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/012,133
; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 6207401,ember 24, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEtical: NO
; ANTI-SENSE: NO

US-09-283-011-4
Query Match      81.8%; Score 36; DB 3; Length 403;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLGKPPF 8
Db      323 LVGKPPF 329

RESULT 38
US-08-252-995D-2
; Sequence 2, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3:53-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-252-995D-2

Query Match      81.8%; Score 36; DB 1; Length 416;
Best Local Similarity 62.5%; Pred. No. 37;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPPF 8
Db      204 LLIGRPPF 211

RESULT 39
US-08-834-108-2
; Sequence 2, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR

```

STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08 834-108-2

Query Match 81.8% Score 36; DB 2; Length 416;
Best Local Similarity 62.5%; Pred. No. 37;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|
DB 204 LLIGRPPF 21;

RESULT 40
US-08-252-995D-6
Sequence 6, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRESKIN & FARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-995D-6
Query Match 81.8% Score 36; DB 1; Length 464;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
:|:|:|
DB 204 LLIGRPPF 21;

Search completed: November 14, 2003, 13:29:50
Job time : 11.5143 secs

GenCore version 5.1.6
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QM protein: protein search, using sw model

Run on: November 14, 2003, 13:28:05 ; Search time 19.6867 Seconds
without alignments:
73.443 Million cell updates/sec

Title: US 09-736-076-16
Perfect score: 44
Sequence: 1 MLLGKPPF 8

Scoring table: BLASTUM62
Gapop 10.0, Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0
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Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA:
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pept.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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2	44	100.0	9	9	US-09-736-076-17
3	41	93.2	9	9	US-09-736-076-15
4	41	93.2	10	9	US-09-736-076-57
5	41	93.2	11	9	US-09-736-076-19
6	41	93.2	400	15	US-10-026-021-5
7	41	93.2	469	15	US-10-059-585-14
8	41	93.2	685	10	US-09-771-161A-249
9	41	93.2	685	10	US-09-771-161A-250
10	41	93.2	685	10	US-09-771-161A-251
11	41	93.2	685	12	US-10-024-299A-101
12	41	93.2	685	12	US-09-769-970-1
13	41	93.2	685	12	US-10-042-211A-101
14	39	86.6	40	10	US-09-842-582-9
15	39	86.6	122	10	US-09-515-806-24

16	39	88.6	183	15	US-10-172-088-12	Sequence 12, Appl
17	39	88.6	256	11	US-09-898-837A-32	Sequence 32, Appl
18	38	86.4	8	9	US-09-736-076-55	Sequence 55, Appl
19	38	86.4	20	9	US-09-736-076-6	Sequence 6, Appl
20	38	86.4	329	10	US-09-925-300-1268	Sequence 1268, Ap
21	38	86.4	367	15	US-10-026-021-6	Sequence 6, Appl
22	38	86.4	419	10	US-09-893-737-106	Sequence 106, App
23	38	86.4	516	10	US-09-771-161A-123	Sequence 123, App
24	38	86.4	528	12	US-10-032-585-7571	Sequence 7571, Ap
25	38	86.4	603	10	US-09-771-161A-214	Sequence 214, App
26	38	86.4	603	15	US-10-171-311-186	Sequence 186, App
27	37	84.1	445	10	US-09-836-392-15	Sequence 15, Appl
28	37	84.1	499	15	US-10-024-828-12	Sequence 12, Appl
29	37	84.1	588	15	US-10-024-828-16	Sequence 16, Appl
30	37	84.1	660	9	US-09-815-242-5470	Sequence 5470, Ap
31	37	84.1	664	9	US-09-815-242-12179	Sequence 12179, A
32	37	84.1	1089	12	US-10-390-303-3	Sequence 3, Appl
33	37	84.1	1088	12	US-10-390-303-4	Sequence 4, Appl
34	36	81.8	48	9	US-09-922-138-19	Sequence 19, Appl
35	36	81.8	133	9	US-09-916-790-26	Sequence 26, Appl
36	36	81.8	180	9	US-09-910-150-29	Sequence 29, Appl
37	36	81.8	194	9	US-09-910-150-28	Sequence 28, Appl
38	36	81.8	230	9	US-09-797-039-11	Sequence 11, Appl
39	36	81.8	230	12	US-10-170-789-11	Sequence 11, Appl
40	36	81.8	231	10	US-09-515-806-13	Sequence 13, Appl
41	36	81.8	231	10	US-09-515-806-14	Sequence 14, Appl
42	36	81.8	231	10	US-09-882-166-5	Sequence 5, Appl
43	36	81.8	231	10	US-09-934-406-6	Sequence 6, Appl
44	36	81.8	231	12	US-10-170-789-18	Sequence 18, Appl
45	36	81.8	231	12	US-10-170-789-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-736-076-16
; Sequence 16, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1C15-039
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(0)
; NAME/KEY: AMIDATION
; LOCATION: (0)...(8)
; OTHER INFORMATION: J43
US-09-736-076-16

Query Match 100.0%; Score 44; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLLGKPPF 8
| | | | |
Db 1 MLLGKPPF 8

RESULT 2

US-09-736-076-17

; Sequence 17, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (9)...(9)
; OTHER INFORMATION: J43.1
US 09-736-076 17

Query Match 100.0%; Score 44; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
Db 2 MLLGKPPF 8

RESULT 3

US-09-736-076-15
; Sequence 15, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (9)...(9)
; OTHER INFORMATION: J42
US-09-736-076-15

Query Match 93.2%; Score 41; DB 9; Length 9;
Best Local Similarity 87.5%; Pred. No. 5.9e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
Db 1 MLLGKPPF 8

RESULT 4

US-09-736-076-57
; Sequence 57, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MYRISTATE
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 10 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (9)...(10)
; OTHER INFORMATION: SNK
US-09-736-076-57

Query Match 93.2%; Score 41; DB 9; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.52;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
Db 2 MLLGKPPF 9

RESULT 5

US-09-736-076-19
; Sequence 19, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (9)...(11)
; OTHER INFORMATION: J46
US-09-736-076-19

Query Match 93.2%; Score 41; DB 9; Length 11;
Best Local Similarity 87.5%; Pred. No. 0.57;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
Db 1 MLLGKPPF 8

```

RESULT 6
US-10-026 021-5
; Sequence 5, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demco, Susan
; APPLICANT: Genkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation Of Cellular Proliferation for
; TITLE OF INVENTION: Treatment Of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: 11..(400)
; OTHER INFORMATION: human SNK mitotic kinase kinase domain
US 10 026-021-5

```

```

Query Match      93.2%   Score 41; DB 15; Length 400;
Best Local Similarity 87.5%   Pred. No. 19;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPF 8
      |||||
DB      273 MLLGRPPF 280

```

```

RESULT 7
US 10-059-585-14
; Sequence 14, Application US/10059585
; Publication No. US20030382776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29

```

```

; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-14

Query Match      93.2%   Score 41; DB 15; Length 469;
Best Local Similarity 87.5%   Pred. No. 23;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPF 8
      |||||
DB      57 MLLGRPPF 64

```

```

RESULT 8
US-09-771-161A-249
; Sequence 249, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 249
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-249

```

```

Query Match      93.2%   Score 41; DB 10; Length 685;
Best Local Similarity 87.5%   Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPF 8
      |||||
DB      273 MLLGRPPF 280

```

```

RESULT 9
US-09-771-161A-250
; Sequence 250, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 250
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-250

```


Query Match 93.2%; Score 41; DB 10; Length 685;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 273 MLLGRPPF 280

RESULT 10
US-09-771-161A-251
; Sequence 251, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 822620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 251
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-251

Query Match 93.2%; Score 41; DB 10; Length 685;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 273 MLLGRPPF 280

RESULT 11
US-10-024-298A-101
; Sequence 101, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 685

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-101

Query Match 93.2%; Score 41; DB 12; Length 685;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 273 MLLGRPPF 280

RESULT 12
US-09-769-970-1
; Sequence 1, Application US/09769970
; Publication No. US20030170219A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Corley, Neil C.
; Guegler, Karl G.
; Lai, Preeti
; Goli, Surya K.
; Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/769,970
; FILING DATE: 24-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/272,796
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVEOB01
; CLONE: 39043
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-769-970-1

Query Match 93.2%; Score 41; DB 12; Length 685;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 273 MLLGRPPF 280

Db 273 MLLGKPPF 280

```
RESULT 13
US-10-042-211A-101
; Sequence 101, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NPKB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: JP 2001-089912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/279,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-101
```

Query Match 93.2%; Score 41; DB 10; Length 685;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||
Db 273 MLLGKPPF 280

```
RESULT 14
US-09-842-582-9
; Sequence 9, Application US/09842582
; Patent No. US20020155570A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 2246, NOVEL PROTEIN KINASE VECTORS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 38155-20054.00
; CURRENT APPLICATION NUMBER: US/09/842,582
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,391
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-842-582-9
```

Query Match 89.6%; Score 39; DB 10; Length 40;
Best Local Similarity 87.5%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||
Db 33 MLLGKPPF 40

```
RESULT 15
US-09-515-806-24
; Sequence 24, Application US/09515806
; Patent No. US20020132321A1
; GENERAL INFORMATION:
; APPLICANT: COOK, WILLIAM J.
; APPLICANT: KAPPELLER-LIBERMANN, ROSANA
; TITLE OF INVENTION: 14790, NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR
; FILE REFERENCE: 38155-20002.C0
; CURRENT APPLICATION NUMBER: US/09/515,806
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: Kinase sequence
US-09-515-806-24
```

Query Match 88.6%; Score 39; DB 10; Length 122;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||
Db 30 MLLGKPPF 37

```
RESULT 16
US-10-172-089-12
; Sequence 12, Application US/10172088
; Publication No. US20030008370A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 13295 NOVEL PROTEIN KINASE MOLECULES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 38155-20010.01
; CURRENT APPLICATION NUMBER: US/10/172,088
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US/09/596,071
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/199,391
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-10-172-089-12
```

Query Match 88.6%; Score 39; DB 15; Length 183;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||
Db 176 MLLGKPPF 183

```
RESULT 17
US-09-898-837A-32
; Sequence 32, Application US/09898837A
; Publication No. US20030077697A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Quinn, Kerry E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Herrmann, John L.
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Rastelli, Luca
; APPLICANT: Curagen Corporation
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: MacDougall, John R.
; TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: 15966-598 CIP
; CURRENT APPLICATION NUMBER: US/09/898,837A
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-898-837A-32

```

```

Query Match: 88.6%; Score 39; DB 11; Length 256;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGKPPF 8
Db 193 MLLGKPPF 200

RESULT 18
US-09-736-076-55
; Sequence 55, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLTATION

```

```

; LOCATION: (1)...(0)
; NAME/KEY: AMIDATION
; LOCATION: (0)...(8)
; OTHER INFORMATION: Plk
; US-09-736-076-55

Query Match: 86.4%; Score 38; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 5.9e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 1 MLLGKPPF 8

RESULT 19
US-09-736-076-6
; Sequence 6, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: POLG
; US-09-736-076-6

```

```

Query Match: 86.4%; Score 38; DB 9; Length 20;
Best Local Similarity 75.0%; Pred. No. 3.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGKPPF 8
Db 3 MLLGKPPF 10

RESULT 20
US-09-925-300-1268
; Sequence 1268, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen.
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE

```

```

; LOCATION: (59)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (307)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (308)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (314)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (317)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (323)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (327)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (329)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-300-1268

```

```

Query Match      86.4%; Score 38; DB 10; Length 329;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPF 8
      :|:|:|:|
Db      260 LLVGKPPF 267

```

```

RESULT 21
US-10-026-021-6
; Sequence 6, Application US/1002602;
; Publication No. US2003002756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi;
; APPLICANT: Demo, Susan;
; APPLICANT: Jenkins, Yonchu;
; APPLICANT: Rigel Pharmaceuticals, Inc.;
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026-021
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,612
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)-(367)
; OTHER INFORMATION: human PLK1 mitotic kinase kinase domain
; US-10-026-021-6

```

```

Query Match      86.4%; Score 38; DB 10; Length 367;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPF 8
      :|:|:|:|
Db      244 LLVGKPPF 251

```

```

RESULT 22
US-09-893-737-106
; Sequence 106, Application US/09893737
; Patent No. US20020110855A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.;
; APPLICANT: Presnell, Scott R.;
; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
; FILE REFERENCE: 00-41
; CURRENT APPLICATION NUMBER: US/09/893,737
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-893-737-106

```

```

Query Match      86.4%; Score 38; DB 10; Length 419;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPP 7
      :|:|:|:|
Db      170 MLLGKPP 176

```

```

RESULT 23
US-09-771-161A-123
; Sequence 123, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.;
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 123
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-771-161A-123

```

```

Query Match      86.4%; Score 38; DB 10; Length 516;
Best Local Similarity 75.0%; Pred. No. 85;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPF 8
      :|:|:|:|
Db      157 LLVGKPPF 164

```

```

RESULT 24
US-10-032-585-7571
; Sequence 7571, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.;
; APPLICANT: Bo, Jiang;
; APPLICANT: Charles, Boone;
; APPLICANT: Howard, Bussey

```

; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
 ; FILE REFERENCE: 10182-005-999
 ; CURRENT APPLICATION NUMBER: US/10/032,585
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 8000
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7571
 ; LENGTH: 528
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-10-032-585-757:

Query Match 86.4%; Score 38; DB 12; Length 528;
 Best Local Similarity 75.0%; Pred. No. 97;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 DB 454 LLVGKPPF 461

RESULT 25
 US-09-771-161A-214
 ; Sequence 214, Application US/09/771:161A
 ; Patent No. US2002011081:1A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09/771:161A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 214
 ; LENGTH: 603
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-771-161A-214

Query Match 86.4%; Score 38; DB 10; Length 603;
 Best Local Similarity 75.0%; Pred. No. 99;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 DB 244 LLVGKPPF 251

RESULT 26
 US-10-171-311-186
 ; Sequence 186, Application US/10/171:311
 ; Publication No. US20030087270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schiegel, Robert
 ; APPLICANT: Chen, Yan
 ; APPLICANT: Zhao, Xumei
 ; APPLICANT: Morahan, John
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Glatt, Karen
 ; APPLICANT: Gannavarapu, Manjula
 ; APPLICANT: Hoersht, Sebastian
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
 ; TITLE OF INVENTION: OF CERVICAL CANCER
 ; FILE REFERENCE: MRI-035
 ; CURRENT APPLICATION NUMBER: US/10/171:311
 ; CURRENT FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: US 60/298,159
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/298,155
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/335,936
 ; PRIOR FILING DATE: 2001-11-14
 ; NUMBER OF SEQ ID NOS: 238
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 186
 ; LENGTH: 603
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-171-311-186

Query Match 86.4%; Score 38; DB 15; Length 603;
 Best Local Similarity 75.0%; Pred. No. 99;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 DB 244 LLVGKPPF 251

RESULT 27
 US-09-836-392-15
 ; Sequence 15, Application US/09836392
 ; Patent No. US20020173458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptide
 ; TITLE OF INVENTION: Antibodies
 ; FILE REFERENCE: PT020P1
 ; CURRENT APPLICATION NUMBER: US/09/836,392
 ; CURRENT FILING DATE: 2001-04-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/28066
 ; PRIOR FILING DATE: 2000-10-11
 ; PRIOR APPLICATION NUMBER: 60/159,542
 ; PRIOR FILING DATE: 1999-10-15
 ; PRIOR APPLICATION NUMBER: 60/165,914
 ; PRIOR FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: 60/189,027
 ; PRIOR FILING DATE: 2000-03-14
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-836-392-15

Query Match 84.1%; Score 37; DB 10; Length 445;
 Best Local Similarity 75.0%; Pred. No. 11e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 DB 263 MLVGQPPF 270

RESULT 28
 US-10-024-828-12
 ; Sequence 12, Application US/10024828
 ; Publication No. US20030036051A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Virca, Duke
 ; APPLICANT: Bird, Timothy A.
 ; APPLICANT: Anderson, Dirk M.
 ; APPLICANT: Marken, John S.
 ; TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase
 ; TITLE OF INVENTION: Functions
 ; FILE REFERENCE: 2877-US
 ; CURRENT APPLICATION NUMBER: US/10/024,828
 ; CURRENT FILING DATE: 2001-12-18

; PRIOR APPLICATION NUMBER: US/09/509,902A
 ; PRIOR FILING DATE: 1999-08-03
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 499
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-024 828 12

Query Match 84.1% Score 37; DB 15; Length 499;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 | : : : :
 DB 407 MLVGQPPF 414

RESULT 29
 US-10-024-828-16
 ; Sequence 16, Application US/10024828
 ; Publication No. US2003036051A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Virga, Duke
 ; APPLICANT: Bird, Timothy A.
 ; APPLICANT: Anderson, Dirk M.
 ; APPLICANT: Marken, John S.
 ; TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase
 ; FILE REFERENCE: 2877-US
 ; CURRENT APPLICATION NUMBER: US/10/024,828
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: US/09/509,902A
 ; PRIOR FILING DATE: 1999-08-03
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 16
 ; LENGTH: 588
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-024 828-16

Query Match 84.1% Score 37; DB 15; Length 588;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 | : : : :
 DB 406 MLVGQPPF 413

RESULT 30
 US-09-815-242-547C
 ; Sequence 547C, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 547C
 ; LENGTH: 660
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-815-242-547C

Query Match 84.1% Score 37; DB 9; Length 660;
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 | : : : :
 DB 201 MLVGEPF 208

RESULT 31
 US-09-815-242-12179
 ; Sequence 12179, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12179
 ; LENGTH: 664
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-815-242-12179

Query Match 84.1% Score 37; DB 9; Length 664;
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPF 8

```
Db          202 MLVGKPPF 209
||:||||
Query Match      84.1%; Score 36; DB 12; Length 1088;
Best Local Similarity 75.0%; Pred. No. 2,7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          1 MLGKPPF 8
||:||||
Db          906 MLVGKPPF 913

RESULT 33
US-10-390-303-4
; Sequence 4, Application US/10390303
; Publication No. US20030171569A1
; GENERAL INFORMATION:
; APPLICANT: JCR Pharmaceuticals Co., Ltd.
; TITLE OF INVENTION: Human Tumor Suppressing Gene
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/390,303
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 3
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-390-303-3
Query Match      84.1%; Score 37; DB 12; Length 1088;
Best Local Similarity 75.0%; Pred. No. 2,7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          1 MLGKPPF 8
||:||||
Db          906 MLVGKPPF 913

RESULT 34
US-10-390-303-4
; Sequence 4, Application US/10390303
; Publication No. US20030171569A1
; GENERAL INFORMATION:
; APPLICANT: JCR Pharmaceuticals Co., Ltd.
; TITLE OF INVENTION: Human Tumor Suppressing Gene
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/390,303
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 4
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-390-303-4
Query Match      84.1%; Score 37; DB 12; Length 1088;
Best Local Similarity 75.0%; Pred. No. 2,7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          1 MLGKPPF 8
||:||||
Db          906 MLVGKPPF 913

RESULT 34
US-09-922-138-19
; Sequence 19, Application US/09922138
; Patent No. US20020061574A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 16658, 14223, AND 16002, NOVEL HUMAN
; TITLE OF INVENTION: KINASES AND USES THEREFOR
; FILE REFERENCE: 38155-20030.00
; CURRENT APPLICATION NUMBER: US/09/922,138
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/229,295
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; TYPE: PRT
```

```
; SEQ ID NO 19
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-09-922-138-19
Query Match      81.8%; Score 36; DB 9; Length 48;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          1 MLGKPPF 8
||:||||
Db          35 LLTGKPPF 42

RESULT 35
US-09-916-790-26
; Sequence 26, Application US/09916790
; Patent No. US20020061573A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachael
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 18431 AND 32374, NOVEL HUMAN PROTEIN
; TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
; FILE REFERENCE: 381552002700
; CURRENT APPLICATION NUMBER: US/09/916,790
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 6C/221,543
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-09-916-790-26
Query Match      81.8%; Score 36; DB 9; Length 133;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          1 MLGKPPF 8
||:||||
Db          44 LLTGKPPF 51

RESULT 36
US-09-910-150-29
; Sequence 29, Application US/09910150
; Patent No. US20020068698A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Tsai, Fong Ying
; TITLE OF INVENTION: 13237, 18480, 2245 OR 16228 NOVEL HUMAN
; FILE REFERENCE: 38155-20020.00
; CURRENT APPLICATION NUMBER: US/09/910,150
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 180
; TYPE: PRT
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-09-910-150-29

Query Match      81.8%; Score 36; DB 9; Length 194;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLLGKPPF 8
Db      105 LDTGKPPF 112

RESULT 37
US-09-910-150-28
; Sequence 28, Application US/099797039
; Patent No. US20020042099A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Tsai, Fong Ying
; TITLE OF INVENTION: 13237, 18490, 2245 OR 16228 NOVEL HUMAN
; TITLE OF INVENTION: PROTEIN KINASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 39155-20020000
; CURRENT APPLICATION NUMBER: US/09/910,150
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-09-910-150-28

Query Match      81.8%; Score 36; DB 9; Length 194;
Best Local Similarity 75.0%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLLGKPPF 8
Db      122 LDTGKPPF 129

RESULT 38
US-09-797-039-11
; Sequence 11, Application US/099797039
; Patent No. US20020042099A1
; GENERAL INFORMATION:
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
; TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
; FILE REFERENCE: 10448-017001
; CURRENT APPLICATION NUMBER: US/09/797,039
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-797-039-11
```

```

Query Match      81.8%; Score 36; DB 9; Length 230;
Best Local Similarity 75.0%; Pred. No. 87;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLLGKPPF 8
Db      175 LDTGKPPF 182

RESULT 39
US-10-170-789-11
; Sequence 11, Application US/10170789
; Publication No. US20030160930A1
; GENERAL INFORMATION:
; APPLICANT: Rachel E. Meyers
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Williamson, Mark
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE, PHOSPHATASE,
; TITLE OF INVENTION: AND PROTEASE FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-191001
; CURRENT APPLICATION NUMBER: US/10/170,789
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06525
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/882,166
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19269
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/212,078
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/934,406
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26052
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,740
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16549
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/801,267
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: PCT/US01/07138
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/187,454
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/829,671
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: PCT/US01/40483
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,508
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/961,721
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/29904
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/235,023
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 10/045,367
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/246,561
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/801,275
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/ PRIOR FILING DATE: 2001-03-06
 / PRIOR APPLICATION NUMBER: PCT/US01/07074
 / PRIOR FILING DATE: 2001-03-05
 / PRIOR APPLICATION NUMBER: US 60/187,420
 / PRIOR FILING DATE: 2000-03-07
 / NUMBER OF SEQ ID NOS: 63
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 1:
 / LENGTH: 230
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: consensus sequence
 US-10 170-789-11

Query Match 81.8% Score 26; DB 12; Length 230;
 Best Local Similarity 75.0%; Pred. No. 87;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 DB 175 LLTGKPPF 182

RESULT 40
 US-09-515-806 13
 / Sequence 13, Application US/09515806
 / Patent No. US20020132321A1
 / GENERAL INFORMATION:
 / APPLICANT: COOK, WILLIAM J.
 / APPLICANT: KAPPELER-LIBERMANN, ROSANA
 / TITLE OF INVENTION: 14790, NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR
 / FILE REFERENCE: 38155-20002.00
 / CURRENT APPLICATION NUMBER: US/99/515,806
 / CURRENT FILING DATE: 2000-02-29
 / NUMBER OF SEQ ID NOS: 32
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 13
 / LENGTH: 231
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: Consensus
 / OTHER INFORMATION: Kinase sequence
 Us-09 515-806 13

Query Match 81.8% Score 26; DB 12; Length 231;
 Best Local Similarity 75.0%; Pred. No. 87;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 DB 176 LLTGKPPF 183

Search completed: November 14, 2003, 13:43:27
 Job time : 20.8857 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 13:20:05 ; Search time 9.6 Seconds
(without alignments)
80.141 Million cell updates/sec

Title: US-09-736-076-16

Perfect score: 44

Sequence: 1 MLLGKPPF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 3.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	93.2	682	2 A44493	serum-inducible ki
2	39	98.6	371	2 T16391	hypothetical prote
3	39	98.6	465	2 S68462	protein kinase ATP
4	39	98.6	471	2 S68463	protein kinase ATP
5	39	98.6	480	2 S56639	ribosomal protein
6	39	98.6	592	2 T43402	probable protein k
7	39	98.6	683	2 T38254	serine/threonine-s
8	39	98.6	705	2 A48144	protein kinase CDC
9	39	98.6	766	2 S69657	hypothetical prote
10	38	86.4	525	2 S45884	probable serine/th
11	38	86.4	603	2 S34130	serine/threonine-s
12	38	86.4	603	2 A47545	protein kinase (EC
13	38	86.4	603	2 A54596	protein kinase - m
14	37	84.1	639	2 A32545	protein kinase C (
15	37	84.1	664	2 G89894	protein kinase (im
16	37	94.1	1018	2 T22318	hypothetical prote
17	37	84.1	1081	2 S51899	probable protein k
18	37	84.1	1099	2 A56155	tumor suppressor p
19	36	81.8	217	2 S28754	NADH2 dehydrogenas
20	36	81.8	305	2 T43221	serine/threonine-s
21	36	81.8	329	2 B87790	protein B0207.4 (i
22	36	81.8	389	2 S52242	protein kinase (EC
23	36	81.8	403	2 JC5974	aurora-related kin
24	36	81.8	407	2 S52243	p46Eg265 protein -
25	36	81.8	465	2 B55748	protein kinase (EC
26	36	81.8	521	2 D88640	protein F55A8.2 (i
27	36	81.8	830	2 T41509	serine/threonine-p
28	36	81.8	925	2 A55748	protein kinase (EC
29	35	79.5	294	2 S32947	hupK protein - Rho

30	35	79.5	465	2 I38133	protein kinase (EC
31	35	79.5	484	2 F82190	sigma-54 dependent
32	35	79.5	511	2 T17298	hypothetical prote
33	35	79.5	672	1 KIHUCA	protein kinase C (
34	35	79.5	672	1 KIRTC	protein kinase C (
35	35	79.5	672	1 KIMSCA	protein kinase C (
36	35	79.5	672	1 KIRBC	protein kinase C (
37	35	79.5	672	1 KIBOC	protein kinase C (
38	35	79.5	676	2 A37237	protein kinase C (
39	35	79.5	682	1 KIBOGC	protein kinase C (
40	35	79.5	697	1 KIRTC	protein kinase C (
41	35	79.5	697	1 KIRBGC	protein kinase C (
42	35	79.5	697	2 JN0548	protein kinase C (
43	35	79.5	697	2 D24664	protein kinase C (
44	35	79.5	767	2 AD3221	dehydrogenase Atu5
45	35	79.5	861	2 T15903	protein kinase C h

ALIGNMENTS

RESULT 1

A44493
serum-inducible kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 10-Sep-1997
C;Accession: A44493
R;Simmons, D.L.; Neel, B.G.; Stevens, R.; Evett, G.; Erikson, R.L.
Mol. Cell. Biol. 12, 4164-4169, 1992
A;Title: Identification of an early-growth-response gene encoding a novel putative pr
A;Reference number: A44493; MUID:92375085; PMID:1508211
A;Accession: A44493
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-682 <SIM>
A;Experimental source: F-2 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:111721, NCBIP:111722)
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C;Keywords: ATP
F;77-331/Domain: protein kinase homology <KIN>

Query Match 93.2%; Score 41; DB 2; Length 682;
Best Local Similarity 87.5%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
Db 270 MLLGRPPF 277

RESULT 2

T16391
hypothetical protein F47F2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C;Accession: T16391
R;Bentley, D.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F47F2.
A;Reference number: Z18506
A;Accession: T16391
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-371 <BEN>
A;Cross-references: EMBL:U40943; NID:g1072202; PID:g1072204; PIDN:AAA81716.1; CESP:F4
C;Genetics:
A;Gene: CESP:F47F2.1
A;Introns: 39/3; 70/1; 126/2; 156/2; 182/3; 214/2; 286/2; 331/3
C;Superfamily: kinase-related transforming protein; protein kinase homology
F;61-317/Domain: protein kinase homology <KIN>

Query Match 88.6%; Score 39; DB 2; Length 371;
Best Local Similarity 75.0%; Pred. No. 6.1;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGKPPF 8
|||

Db 251 MWVGKPPF 258

RESULT 3
S68462
protein kinase ATPK6/ATPK1 (EC 2.7.1.1) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cress)
C>Date: 05-Dec-1996 #sequence_revision 13 Mar-1997 #text_change 24-Sep-1999
C:Accession: S68462; A5414;
R/Mizoguchi, T.; Hayashida, N.; Yamaguchi Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 358, 199-204, 1995
A:Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold
A:Reference number: S68462; MUID:95129712; PMID:7828736
A:Accession: S68462
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-465 <M12>
A:Cross-references: EMBL:D42056; NID:q867996; PIDN:BAA07656.1; PID:di008238; PID:g867997
R/Zhang, S.H.; Lawton, M.A.; Hunter, T.; Lamb, C.J.
J. Biol. Chem. 269, 17586-17592, 1994
A:Title: atpk1, a novel ribosomal protein kinase gene from Arabidopsis. I. Isolation, characterization and expression
A:Reference number: A54141; MUID:94292519; PMID:7912697
A:Contents: ecotype Landsberg erecta
A:Accession: A54141
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-465 <ZHA>
A:Cross-references: GB:L29030; NID:q508307; PIDN:AAA21142.1; PID:g508308
A:Note: sequence extracted from NCBI: backbone (NCBIN:149344, NCBI:P:149415)
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:132-389/Domain: protein kinase homology <KIN>
F:140-148/Region: protein kinase ATP-binding motif

Query Match 88.6%; Score 39; DB 2; Length 465;
Best Local Similarity 87.5%; Pred. No. 7.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : MLLGKPPF 8
|||

Db 324 MLTGKPPF 331

RESULT 4
S68463
protein kinase ATPK19 (EC 2.7.1.1) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cress)
C>Date: 05-Dec-1996 #sequence_revision 27 Feb-1997 #text_change 24-Sep-1999
C:Accession: S68463
R/Mizoguchi, T.; Hayashida, N.; Yamaguchi Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 358, 199-204, 1995
A:Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold
A:Reference number: S68462; MUID:95129712; PMID:7828736
A:Accession: S68463
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-471 <M12>
A:Cross-references: EMBL:D42061; NID:gl526412; PIDN:BAA0766.1; PID:di008243; PID:g867999
C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase; serine/threonine specific protein kinase
F:138-395/Domain: protein kinase homology <KIN>
F:146-154/Region: protein kinase ATP-binding motif

Query Match 88.6%; Score 39; DB 2; Length 471;
Best Local Similarity 87.5%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : MLLGKPPF 8
|||

Db 330 MLTGKPPF 337

RESULT 5
S56639
ribosomal protein S6 kinase homolog (clone Aspkl1) - oat
N:Alternate names: mitogen-activated protein kinase pp70 homolog
C:Species: Avena sativa (oat)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
C:Accession: S56639
R/Huttly, A.K.; Phillips, A.L.
Plant Mol. Biol. 27, 1043-1052, 1995
A:Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that
A:Reference number: S56638; MUID:95284341; PMID:7766874
A:Accession: S56639
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-480 <HUT>
A:Cross-references: EMBL:X79992; NID:g871985; PIDN:CAA56313.1; PID:g871986
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase; protein kinase
F:149-407/Domain: protein kinase homology <KIN>
F:157-165/Region: protein kinase ATP-binding motif

Query Match 88.6%; Score 39; DB 2; Length 480;
Best Local Similarity 87.5%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||

Db 341 MLTGKPPF 348

RESULT 6
T43402
probable protein kinase (EC 2.7.1.1) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T43402; T41425
R/Niederberger, C.
submitted to the EMBL Data Library, July 1998
A:Reference number: 222486
A:Accession: T43402
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-592 <NIE>
A:Cross-references: EMBL:X99280; PIDN:CAA67672.1
A:Experimental source: strain h90
R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A:Reference number: 221954
A:Accession: T41425
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-592 <WOO>
A:Cross-references: EMBL:AL031798; PIDN:CAA21194.1; GSPDB:GN00068; SPDB:SPCCS76.15c
A:Experimental source: strain 972h-; cosmid c576
C:Genetics:
A:Gene: KSG1; SPCCS76.15c
A:Map position: 3
A:Introns: 191/3
C:Keywords: phosphotransferase

Query Match 88.6%; Score 39; DB 2; Length 592;
Best Local Similarity 87.5%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||

Db 305 MLAGKPPF 312

RESULT 7

T38254
 serine/threonine-specific protein kinase plot (EC 2.7.1.1) - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
 C:Accession: T38254; T45128
 R:Brown, D.; Churcher, C.M.; Bartell, B.G.; Rajandream, N.A.; Wood, V.
 submitted to the EMBL Data Library, August 1995
 A:Reference number: Z21781
 A:Accession: T38254

A:Status: preliminary; translated from GB/EMBL/CDR

A:Molecule type: DNA

A:Residues: 1-683 <BRO>

A:Cross-references: EMBL:Z98559; PIDN:CA811167.1; GSPOR:GN30066; SPDB:SPAC23C11.16

A:Experimental source: strain 972h; cosmid C23C11

R:Okura, H.; Hagan, L.M.; Glover, D.M.

Genes Dev. 9, 1039-1073, 1995

A:Title: The conserved Schizosaccharomyces pombe kinase p.c1, required to form a bipolar

A:Reference number: Z22921; MUID:95262899; PMID:7744248

A:Accession: T45128

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-683 <CHK>

A:Cross-references: EMBL:X85758; NID:9887640; PIDN:CAA59766.1; PID:9887641

A:Experimental source: strain 972 derivative

C:Genetics:

A:Gene: plot; SPAC23C11.16

A:Map position: 1

C:Function:

A:Description: required to form a bipolar spindle and early in the regulatory cascade th

C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolo

C:Keywords: phosphotransferase; protein kinase

Query Match 88.6%; Score 39; DB 2; Length 683;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 3;

QY : MLLGKPPF 3

||| |||

Db 233 LLAGKPPF 240

RESULT 8

S45144

protein kinase CDC5 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein kinase PKX2; protein Y8270.090; protein YMR001C

C:Species: Saccharomyces cerevisiae

C:Date: 30-Jun-1999 #sequence_revision 30-Jun-1999 #text_change 24-Sep-1999

C:Accession: A48144; S53030; S27445

R:Kitada, K.; Johnson, A.L.; Johnston, L.B.; Sugino, A

Yol. Cell. Biol. 13, 4445-4457, 1993

A:Title: A multicopy suppressor gene of the Saccharomyces cerevisiae G-1 cell cycle muta

A:Reference number: A48144; MUID:93309479; PMID:8321244

A:Accession: A48144

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-705 <KIT>

A:Cross-references: EMBL:M84220; NID:g172187; PIDN:AA60576.1; PID:g172187

R:Devlin, K.; Churcher, C.M.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53028

A:Accession: S53030

A:Molecule type: DNA

A:Residues: 1-705 <DEV>

A:Cross-references: EMBL:Z48613; NID:g729645; PIDN:CA785516.1; PID:g728648; MIPS:YMR001C

A:Experimental source: strain AB972

C:Genetics:

A:Gene: SGD: CDC5; PKX2

A:Cross-references: SGD:S0004603; MIPS:YMR001C

A:Map position: 13R

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C:Keywords: ATP; cell cycle control; phosphotransferase; protein kinase

F:80-337/Domain: protein kinase homology <KIN>

Query Match 88.6%; Score 39; DB 2; Length 705;

Best Local Similarity 75.0%; Pred. No. 12;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8

||| |||

Db 274 LLAGKPPF 281

RESULT 9

S69657

hypothetical protein YDR490C - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002

C:Accession: S69657

R:Dietrich, F.S.

submitted to the EMBL Data Library, August 1995

A:Description: The sequence of S. cerevisiae cosmid 9410, 8035, 8166, and 9787.

A:Reference number: S69554

A:Accession: S69657

A:Molecule type: DNA

A:Residues: 1-766 <DIE>

A:Cross-references: EMBL:U33C50; NID:g927726; PIDN:AA864917.1; PID:g927745; MIPS:YDR4

C:Genetics:

A:Gene: SGD: PKH1

A:Cross-references: SGD:S0002898

A:Map position: 4R

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho

C:Keywords: ATP

F:123-391/Domain: protein kinase homology <KIN>

F:131-139/Region: protein kinase ATP-binding motif

Query Match 88.6%; Score 39; DB 2; Length 766;
 Best Local Similarity 87.5%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8

||| |||

Db 330 MLAGKPPF 337

RESULT 10

S45894

probable serine/threonine-specific protein kinase (EC 2.7.1.1) - yeast (Sacc

N:Alternate names: protein YBR0312

C:Species: Saccharomyces cerevisiae

C:Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002

C:Accession: S45884; S46558

R:Grivelli, L.A.; de Haan, M.; Maat, M.J.; Smits, P.H.M.

submitted to the Protein Sequence Database, August 1994

A:Reference number: S45875

A:Accession: S45884

A:Molecule type: DNA

A:Residues: 1-525 <GRI>

A:Cross-references: EMBL:Z35897; NID:g536370; PIDN:CAA84970.1; PID:g536371; MIPS:YBR1

A:Experimental source: strain S288C

R:Smits, P.H.M.; de Haan, M.; Maat, C.; Grivelli, L.A.

Yeast 10(Suppl.A), S75-S80, 1994

A:Title: The complete sequence of a 33 kb fragment on the right arm of chromosome II

ly identified genes and a homologue of the SCO1 gene.

A:Reference number: S46551; MUID:94378725; PMID:8091864

A:Accession: S46558

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-525 <SMI>

A:Cross-references: EMBL:X76078; NID:g498748; PIDN:CAA53684.1; PID:g498756

A:Experimental source: strain S288C

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 199

C:Genetics:

A:Cross-references: SGD:S0000232

A:Map position: 2R

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:126-423/Domain: protein kinase homology <KIN>
F:134-142/Region: protein kinase ATP-binding motif
F:177/Active site: Asp #status predicted

Query Match 86.4% Score 38; DB 2; Length 525;
Best Local Similarity 75.0% Pred. No. 14;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:
DB 355 LLVGKPPY 362

RESULT 11

S34130
serine/threonine-specific protein kinase Plk (EC 2.7.1.1) - human
N:Alternate names: polo-like protein kinase; protein kinase plk-1
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C:Accession: S34130; J38123; S61543
R:Golsteyn, R.M.; Schultz, S.C.; Bartek, J.; Ziemiecki, A.; Ried, T.; Nigg, E.A.
submitted to the EMBL Data Library, June 1993
A:Description: Cloning and characterization of a novel human protein kinase plk-1 a pote
through mitosis.
A:Reference number: S34130
A:Accession: S34130
A:Molecule type: mRNA
A:Residues: 1-603 <COL>
A:Cross-references: EMBL:X73458; NID:g312997; PIDN:CAA51817.1; PID:g312998
A:Experimental source: nasopharyngeal carcinoma
R:Hoelrich, U.; Wolf, G.; Brauningner, A.; Karr, T.; Bohme, H.; Rubsamen-Waigmann, H.; S
Proc. Natl. Acad. Sci. U.S.A. 91, 1736-1740, 1994
A:Title: Induction and down-regulation of Plk, a human serine/threonine kinase expressed
A:Reference number: A53134; MUID:94173904; PMID:8127874
A:Accession: J38123
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-140, P', 142-226, E', 228-603 <RES>
A:Cross-references: EMBL:X75932; NID:g460768; PIDN:CAA53538.1; PID:g460769
A:Experimental source: lung tumor
R:Braeuningner, A.; Strebhardt, K.; Rubsamen-Waigmann, H.
Oncogene 11, 1793-1800, 1995
A:Title: Identification and functional characterization of the human and murine polo-like
A:Reference number: S61543; MUID:96068906; PMID:7478607
A:Accession: S61543
A:Molecule type: DNA
A:Residues: 1-122, T', 124-136 <BRA>
A:Cross-references: EMBL:X90725; NID:g1361143; PIDN:CAA60560.1; PID:g1361144
A:Experimental source: placenta
A:Note: the authors translated the codon ATG for position 124 as Val
C:Genetics:
A:Gene: CDB:PLK
A:Cross references: GDB:331003
A:Map position: 17pter-17p12
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
C:Keywords: ATP; phosphotransferase; serine/threonine specific protein kinase
F:51-305/Domain: protein kinase homology <KIN>

Query Match 86.4% Score 38; DB 2; Length 603;
Best Local Similarity 75.0% Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:
DB 244 LLVGKPPF 251

RESULT 12

A47545
protein kinase (EC 2.7.1.37) Plk - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Accession: A47545

R:Clay, F.J.; McEwen, S.J.; Bertoncello, I.; Wilks, A.F.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4882-4886, 1993
A:Title: Identification and cloning of a protein kinase-encoding mouse gene, Plk, re
A:Reference number: A47545; MUID:93281660; PMID:8099445
A:Accession: A47545
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-603 <CJA>
A:Cross-references: GB:L06144; NID:g309461; PIDN:AAA39948.1; PID:g309462
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hc
C:Keywords: ATP; phosphotransferase
F:51-305/Domain: protein kinase homology <KIN>

Query Match 86.4% Score 38; DB 2; Length 603;
Best Local Similarity 75.0% Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:
DB 244 LLVGKPPF 251

RESULT 13

A54596
protein kinase - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: A54596
R:Lake, R.J.; Jelinek, W.R.
Mol. Cell. Biol. 13, 7793-7801, 1993
A:Title: Cell cycle- and terminal differentiation-associated regulation of the mouse
A:Reference number: A54596; MUID:94067140; PMID:7902533
A:Accession: A54596
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-603 <RES>
A:Cross-references: GB:L19558; NID:g403473; PIDN:AAA16071.1; PID:g403474
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hc
F:51-305/Domain: protein kinase homology <KIN>

Query Match 86.4% Score 38; DB 2; Length 603;
Best Local Similarity 75.0% Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:
DB 244 LLVGKPPF 251

RESULT 14

A32545
protein kinase C (EC 2.7.11.1) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1999
C:Accession: A32545
R:Rosenthal, A.; Rhee, L.; Yadegari, R.; Paro, R.; Ullrich, A.; Goeddel, D.V.
EMBO J. 6, 433-441, 1987
A:Title: Structure and nucleotide sequence of a Drosophila melanogaster protein kin-
A:Reference number: A32545; MUID:87218499; PMID:3107983
A:Accession: A32545
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-639 <ROS>
A:Cross-references: GB:X05076; NID:g8352; PIDN:CAA28736.1; PID:g8353; GB:Y00042
C:Genetics:
A:Gene: FlyBase:PKC53B
A:Cross-references: FlyBase:FBgr0003091
C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:46-95/Domain: protein kinase C zinc-binding repeat homology <K21>
F:111-160/Domain: protein kinase C zinc-binding repeat homology <K22>
F:161-273/Domain: protein kinase C C2 region homology <KC2>
F:339-599/Domain: protein kinase homology <KIN>

Query Match 86.4% Score 38; DB 2; Length 603;
Best Local Similarity 75.0% Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:
DB 244 LLVGKPPF 251

F:347-355/Region: protein kinase ATP-binding motif

Query Match: 84.1%; Score 37; DB 2; Length 639;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGKPPF 8
 ||:||||
 Db 533 MLVGQPPF 540

RESULT 15

G89894
 protein kinase [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10 May 2001 #text_change 22-Oct-2001
 C:Accession: G89894
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.: Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418148
 A:Accession: G89894
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-664 <KUR>
 A:Cross-references: GB:SA000018; FID:G1301020; PIDN:BAF42315.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SA1063

Query Match: 84.1%; Score 37; DB 2; Length 664;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGKPPF 8
 ||:||||
 Db 202 MLVGEPFF 209

RESULT 16

T22318
 hypothetical protein F46F6.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15 Oct-1999 #text_change 16-Feb 2000
 C:Accession: T22318; T27624
 R:Cottage, A.
 submitted to the EMBL Data Library, July 1999
 A:Reference number: Z19547
 A:Accession: T22318
 A:Status: preliminary; translated from GP EMBL:U0041
 A:Molecule type: DNA
 A:Residues: 1-1018 <WIL>
 A:Cross references: EMBL:Z50028; PIDN:CAA90345.1; GSPDB:GN00028; CESP:F46F6.2
 A:Experimental source: clone F46F6
 R:Kershaw, J.
 submitted to the EMBL Data Library, July 1995
 A:Reference number: Z20394
 A:Accession: T27624
 A:Status: preliminary; translated from GB/EMBL/CDR3
 A:Molecule type: DNA
 A:Residues: 1-1018 <W12>
 A:Cross-references: EMBL:Z50029; PIDN:CAA90345.1; GSPDB:GN00028; CESP:F46F6.2
 A:Experimental source: clone ZC504
 C:Genetics:
 A:Gene: CESP:F46F6.2
 A:Map position: X
 A:Introns: 41/2; 139/1; 446/3; 520/1; 554/1; 601/3; 859/1; 923/3; 972/3; 1017/2
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match: 84.1%; Score 37; DB 2; Length 1019;
 Best Local Similarity 75.0%; Pred. No. 43;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGKPPF 8
 ||:||||
 Db 883 MLVGEPFF 890

RESULT 17

S51899
 probable protein kinase HRC108; (EC 2.7.1.1.-) - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein C0784; protein YOL100w
 C:Species: Saccharomyces cerevisiae
 C:Date: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 19-Apr-2002
 C:Accession: S51899; S59175; S66796
 R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
 submitted to the EMBL Data Library, January 1995
 A:Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV including a delta element.
 A:Reference number: S51848
 A:Accession: S51899
 A:Molecule type: DNA
 A:Residues: 1-1081 <VAN>
 A:Cross-references: EMBL:Z48149; NID:G663234; PIDN:CAA88162.1; PID:G663254
 R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
 Yeast 11, 1069-1075, 1995
 A:Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including a delta element.
 A:Reference number: S59156; MUID:96076631; PMID:7502582
 A:Accession: S59175
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1081 <VAW>
 A:Cross-references: EMBL:Z48149; NID:G663234; PIDN:CAA88162.1; PID:G663254
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
 R:Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S66791
 A:Accession: S66796
 A:Molecule type: DNA
 A:Residues: 1-1081 <DJR>
 A:Cross-references: EMBL:Z74842; NID:G1419951; PIDN:CAA99113.1; PID:e251892; PID:G14

Query Match: 84.1%; Score 37; DB 2; Length 1081;
 Best Local Similarity 75.0%; Pred. No. 46;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY : MLLGKPPF 8
 ||:||||
 Db 382 MZAGKPPF 389

RESULT 18

A56155
 tumor suppressor protein warts (EC 2.7.1.1.-) - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 24-Sep-1999
 C:Accession: A56155
 R:Justice, R.W.; Zilian, O.; Woods, D.F.; Noll, M.; Bryant, P.J.
 Genes Dev. 9, 534-546, 1995
 A:Title: The Drosophila tumor suppressor gene warts encodes a homolog of human myoD.
 A:Reference number: A56155; MUID:95212904; PMID:7698644
 A:Accession: A56155
 A:Status: preliminary
 A:Molecule type: mRNA

A;Residues: 1-1099 <JUS>
A;Cross-references: GB:L39837; NID:G755007; PIDN:AAA73959.1; PID:G755008
C;Genetics:
A;Gene: wts
A;Cross-references: FlyBase:FBgn0017739
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP; phosphotransferase
F;711-1014/Domain: protein kinase ATP-binding motif
F;719-727/Region: protein kinase ATP-binding motif

Query Match: 84.1%; Score 37; DB 2; Length 1039;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLGKPPF 8
|:|||||
DB 948 MLVGQPPF 955

RESULT 19
S28754
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 blue mussel mitochondrion (fragm
C;Species: Mitochondrion Mytilus edulis (blue mussel)
C;Date: 12-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Jun-2002
C;Accession: S28754; S28755
R;Hofmann, R.J.; Boore, J.L.; Brown, W.M.
Genetics 131, 397-412, 1992
A;Title: A novel mitochondrial genome organization for the blue mussel, Mytilus edulis.
A;Reference number: S28743; MUID:92354892; PMID:1386586
A;Accession: S28754
A;Molecule type: DNA
A;Residues: 1-131;132-217 <BRC>
A;Cross-references: EMBL:M83760; EMBL:M83761
C;Genetics:
A;Gene: ND2
A;Genome: Mitochondrion
A;Genetic code: SGC4
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match: 81.8%; Score 36; DB 2; Length 217;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
|:|||||
DB 135 MLVGKPPF 142

RESULT 20
T4322;
serine/threonine-specific protein kinase (EC 2.7.1.1) Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Accession: T4322;
R;Schumacher, C.M.; Golden, A.; Donovan, P.A.
J. Cell Biol. 143, 1635-1646, 1998
A;Title: AIR-2; An aurora/tp11-related protein kinase associated with chromosomes and mi
A;Reference number: Z22347; MUID:99069487; PMID:9852157
A;Accession: T43221
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-305 <SCH>
A;Cross-references: EMBL:AF071207; PIDN:AAU70945.1
C;Genetics:
A;Gene: AIR-2
A;Map position: 1
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: phosphotransferase

Query Match: 81.8%; Score 36; DB 2; Length 305;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
|:|||||
DB 220 LVGKPPF 226

RESULT 21

B87790
protein B0207.4 (imported) - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: B87790
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating b1
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999.
A;Accession: B87790
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-329 <STO>
A;Cross-references: GB:chr_1; PIDN:AAB52459.1; PID:G1943805; GSPDB:GN00019; CESP:B02
C;Genetics:
A;Gene: B0207.4
A;Map position: 1
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match: 81.8%; Score 36; DB 2; Length 329;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
|:|||||
DB 244 LVGKPPF 250

RESULT 22

S52242
protein kinase (EC 2.7.1.1) p46XIEg22 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 18-Jun-1999
C;Accession: S52242
R;Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A;Description: Eg2, selected by differential screening encodes a new xenopus protein
A;Reference number: S52242
A;Accession: S52242
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-389 <POG>
A;Cross-references: EMBL:Z17206; NID:G609279; PIDN:CAA78914.1; PID:G609280
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;119-371/Domain: protein kinase homology <KIN>
F;127-135/Region: protein kinase ATP-binding motif

Query Match: 81.8%; Score 36; DB 2; Length 389;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
|:|||||
DB 311 LVGKPPF 317

RESULT 23

JC5974
aurora-related kinase 1 (EC 2.7.1.1) - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jan-2000
C;Accession: JC5974
R;Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara, M.; Gilbert, D.J.,

Biochem. Biophys. Res. Commun. 244, 285-292, 1998
A;Title: cDNA cloning, expression, subcellular localization, and chromosomal assignment
A;Reference number: JC5974; MUID:98183439; PMID:9514916
A;Accession: JC5974
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-403 <SH1>
A;Cross-references: GB:AF008551
C;Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolog
C;Keywords: phosphotransferase
F;131-383/Domain: protein kinase homology <KIN>

Query Match 81.8%; Score 36; DB 2; Length 403;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLGKPPF 8
:|:|:|
Db 323 LVGKPPF 329

RESULT 24
S52243
p46Eg265 protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1999
C;Accession: S52243; S34642; I51695
R;Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A;Description: Eg2, selected by differential screening encodes a new Xenopus protein kinase
A;Reference number: S52242
A;Accession: S52243
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-407 <ROG>
A;Cross-references: EMBL:Z17207; NID:g60281; PIDN:CAA78915.1; PID:g603282
R;Bouvet, P.; Omilli, F.; Ariot-Bonnemain, Y.; Legagneux, V.; Roghi, C.; Basset, T.; Ogb
submitted to the EMBL Data Library, June 1993
A;Description: Targetted deadenylation of specific mRNAs in Xenopus embryos by a mechanism
A;Reference number: S34642
A;Accession: S34642
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 328-407 <BOU>
A;Cross-references: EMBL:Z24453; NID:g394756; PIDN:CAA80826.1; PID:g394757
R;Bouvet, P.; Omilli, F.; Ariot-Bonnemain, Y.; Legagneux, V.; Roghi, C.; Bassez, T.; Ogb
Cell. Biol. 14, 1893-1900, 1994
A;Title: The deadenylation conferred by the 3' untranslated region of a developmentally
A;Reference number: I51695; MUID:94158861; PMID:811472;
A;Accession: I51695
A;Status: preliminary; translated from GB/EMBL/CCD
A;Molecule type: mRNA
A;Residues: 328-407 <BO2>
A;Cross-references: EMBL:Z24453; NID:g394756; PIDN:CAA80826.1; PID:g394757
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP; phosphotransferase; protein kinase
F;138-390/Domain: protein kinase homology <KIN>
F;146-154/Region: protein kinase ATP-binding motif

Query Match 81.8%; Score 36; DB 2; Length 407;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLGKPPF 8
:|:|:|
Db 330 LVGKPPF 336

RESULT 25
B55748
protein kinase (EC 2.7.1.37) Sak-b - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Dec-1997

C;Accession: B55748
R;Fode, C.; Motro, B.; Yousefi, S.; Heffernan, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
A;Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosoph
A;Reference number: A55748; MUID:94294387; PMID:8022793
A;Accession: B55748
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-465 <FOO>
A;Cross-references: GB:L29480
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C;Keywords: ATP; phosphotransferase
F;10-265/Domain: protein kinase homology <KIN>
F;18-26/Region: protein kinase ATP-binding motif

Query Match 81.8%; Score 36; DB 2; Length 465;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|
Db 204 LLIGRPPF 211

RESULT 26
D88640
protein F55A8.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
C;Accession: D88640
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bic
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A;Accession: D88640
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-521 <STO>
A;Cross-references: GB:chr_IV; PIDN:AAC19186.1; PID:g3193148; GSPDB:GN00022; CESP:F55
C;Genetics:
A;Gene: F55A8.2
A;Map position: 4
C;Superfamily: cGMP-dependent protein kinase; cAMP receptor protein cyclic nucleotide

Query Match 81.8%; Score 36; DB 2; Length 521;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|
Db 401 LMLGRPPF 408

RESULT 27
T41509
serine/threonine-protein kinase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C;Accession: T41509
R;Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21999
A;Accession: T41509
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-830 <MUR>
A;Cross-references: EMBL:AL049522; PIDN:CAB40012.1; GSPDB:GN00068; SPDB:SPCC63.08c
A;Experimental source: strain 972h-; cosmid c63
C;Genetics:
A;Gene: SPDB:SPCC63.08c
A;Map position: 3

```
A:Introns: 34/3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match      81.8%; Score 36; DB 2; Length 830;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLLGKPPF 8
Db      242 MAVGKPPF 249

RESULT 28
A55748
protein kinase (EC 2.7.1.37) Sak-a - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Sep-1999
C:Accession: A55748
R:Fode, C.; Motro, B.; Yousefi, S.; Hafterman, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosophila
A:Reference number: A55748; MUID:94294387; PMID:8022793
A:Accession: A55748
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-925 <FOD>
A:Cross-references: GB:L29479; NID:G497869; PIDN:AA037648.1; PID:G497870
C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolo
C:Keywords: ATP; phosphotransferase
F:10-265/Domain: protein kinase homology <KIN>
F:18-26/Region: protein kinase ATP-binding motif

Query Match      81.8%; Score 36; DB 2; Length 925;
Best Local Similarity 62.5%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPPF 8
Db      204 MLLGRPPF 211

RESULT 29
S32947
hupK protein - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C:Accession: S32947; B38532; S25691
R:Colbeau, A.; Richard, P.; Toussaint, B.; Caballero, F.; Elster, C.; Delphin, C.; Smi
Mol. Microbiol. 8, 15-29, 1993
A:Title: Organization of the genes necessary for hydrogenase expression in Rhodobacter
A:Reference number: S32947; MUID:93268507; PMID:849479
A:Accession: S32947
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-294 <COL>
A:Cross-references: EMBL:Z15089; NID:G313868; PIDN:CAA78603.1; PID:G46048
R:Xu, H.W.; Wall, J.D.
J. Bacteriol. 173, 2401-2405, 1991
A:Title: Clustering of genes necessary for hydrogen oxidation in Rhodobacter capsulatus.
A:Reference number: A38532; MUID:91177833; PMID:2007559
A:Accession: B38532
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-69, 'A', 71-294 <XUA>
A:Cross-references: GB:M55089; NID:G151949; PIDN:AAA72024.1; PID:G151951
C:Genetics:
A:Gene: hupK

Query Match      79.5%; Score 35; DB 2; Length 294;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPP 7
```

```
Db      31 LLLGKPP 37

RESULT 30
I38133
protein kinase (EC 2.7.1.1) Ndr - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 24-Sep-1999
C:Accession: I38133
R:Millward, T.; Cron, P.; Hemmings, B.A.
Proc. Natl. Acad. Sci. U.S.A. 92, 5022-5026, 1995
A:Title: Molecular cloning and characterization of a conserved nuclear serine(threon
A:Reference number: I38133; MUID:95281588; PMID:7761441
A:Accession: I38133
A:Status: Preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-465 <RES>
A:Cross-references: EMBL:Z35102; NID:G854169; PIDN:CAA84485.1; PID:G854170
C:Genetics:
A:Gene: GDS:NDR
A:Cross-references: GDB:696269
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
C:Keywords: ATP; phosphotransferase
F:87-382/Domain: protein kinase homology <KIN>
F:95-103/Region: protein kinase ATP-binding motif

Query Match      79.5%; Score 35; DB 2; Length 465;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLLGKPPF 8
Db      315 MLLGYPPF 322

RESULT 31
F82190
sigma-S4 dependent response regulator VC1522 [imported] - Vibrio cholerae (strain N1
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Mar-2003
C:Accession: F82190
R:Heidelbergh, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: F82190
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-484 <HEI>
A:Cross-references: GB:AE004230; GB:AE003852; NID:G9656018; PIDN:AAF94676.1; GSPDB:C
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1522
A:Map position: 1
C:Superfamily: response regulator of the NtrC type; response regulator homology; RNA

Query Match      79.5%; Score 35; DB 2; Length 484;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPP 7
Db      382 LLLGKPP 388

RESULT 32
T17298
hypothetical protein DKF2p586M2123.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
```

C;Accession: T17298
R;Ansoorge, W.; Wirkner, U.; Mewes, H.W.; Gasserhuber, C.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18729
A;Accession: T17298
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-511 <ANS>
A;Cross-references: EMBL:AL117551
A;Experimental source: adult uterus; clone DKF2p586M2123
C;Genetics:
A;Note: DKF2p586M2123.1
C;Superfamily: unassigned EGF-related proteins; EGF homology

Query Match 79.5%; Score 35; DB 2; Length 511;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 7
|||
DB 410 LLLGKPPF 416

RESULT 33
KIHUCA
protein kinase C (EC 2.7.1.1) alpha - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C;Accession: S09496
R;Pinkenzeller, G.; Marne, D.; Hug, H.
Nucleic Acids Res. 18, 2183, 1990
A;Title: Sequence of human protein kinase C alpha.
A;Reference number: S09496; MUID:30245676; PMID:2336401
A;Accession: S09496
A;Molecule type: mRNA
A;Residues: 1-672 <PIN>
A;Cross-references: EMBL:X52479; NID:335482; PIDN:CAA16718.1; PID:335483
C;Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-sp
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters,
C;Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
C;Genetics:
A;Gene: GDB:PRKCA
A;Cross-references: GDB:128015; OMIM:176960
A;Map position: 17q22-17q23.2
C;Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kin
C;Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bindin
F;19-29/Region: phospholipid binding #status experimental
F;22-27/Region: pseudophosphorylation motif
F;37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
F;102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
F;152-264/Domain: protein kinase C C2 region homology <KIN>
F;337-597/Domain: protein kinase homology
F;345-353/Region: protein kinase ATP-binding motif
F;368/Active site: zinc (His, Cys, His, Cys) #status predicted
F;631,638/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match 79.5%; Score 35; DB 1; Length 672;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||
DB 531 MLAGQPPF 538

RESULT 34
KIRTC
protein kinase C (EC 2.7.1.1) alpha - rat

N;Alternate names: protein kinase C type III
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C;Accession: S02248; SC2620
R;Ono, Y.; Fujii, T.; Igarashi, K.; Kikkawa, U.; Ogita, K.; Nishizuka, Y.
Nucleic Acids Res. 16, 5199-5200, 1988
A;Title: Nucleotide sequences of cDNAs for alpha and gamma subspecies of rat brain pr
A;Reference number: S02129; MUID:88262515; PMID:3387228
A;Accession: S02248
A;Molecule type: mRNA
A;Residues: 1-672 <ONC>
A;Cross-references: EMBL:X07286; NID:956913; PIDN:CAA30266.1; PID:956914
C;Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol este
C;Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
C;Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C;Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k
C;Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin
F;19-29/Region: phospholipid binding #status experimental
F;22-27/Region: pseudophosphorylation motif
F;37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
F;102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
F;152-264/Domain: protein kinase C C2 region homology <K2>
F;337-597/Domain: protein kinase homology <KIN>
F;345-353/Region: protein kinase ATP-binding motif
F;368/Active site: Lys #status predicted
F;631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

Query Match 79.5%; Score 35; DB 1; Length 672;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||
DB 531 MLAGQPPF 538

RESULT 35
KIMSCA
protein kinase C (EC 2.7.1.1) alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C;Accession: S07104; JS0078
R;Megidish, T.; Mazurek, N.
Nature 342, 807-811, 1989
A;Title: A mutant protein kinase C that can transform fibroblasts.
A;Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bindin
A;Reference number: S07104; MUID:90098082; PMID:2601739
A;Accession: S07104
A;Molecule type: mRNA
A;Residues: 1-672 <MEG>
A;Cross-references: GB:X52685; GB:X51603; NID:949938; PIDN:CAA36908.1; PID:949939
A;Experimental source: strain Balb/c
R;Rose-John, S.; Dietrich, A.; Marks, F.
Gene 74, 465-471, 1988
A;Title: Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss 3T3 fibrob
A;Reference number: JS0078; MUID:89232737; PMID:2469625
A;Accession: JS0078
A;Molecule type: mRNA
A;Residues: 1-146, 'D', 148-217, 'N', 219-276, 'AH', 279-312, 'V', 314-466, 'N', 468-471, 'N', 47
A;Cross-references: GB:M25811
A;Note: the authors translated the codon AAC for residue 141 as Lys; the sequence sho
C;Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol este
C;Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
C;Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C;Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k
C;Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin
F;19-29/Region: phospholipid binding #status experimental
F;22-27/Region: pseudophosphorylation motif
F;37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
F;102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
F;152-264/Domain: protein kinase C C2 region homology <K2>
F;337-597/Domain: protein kinase homology <KIN>

F1345-353/Region: protein kinase ATP-binding motif
 F137-67,70,86/Binding site: zinc (His, Cys, Cys) #status predicted
 F150,53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F102,132,135,151/Binding site: zinc (His, Cys, Cys) #status predicted
 F115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F1368/Active site: Lys #status predicted
 F1631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 79.5%; Score 35; DB 1; Length 672;
 Best Local Similarity 75.0%; Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 |||
 Db 531 MLAGQPPF 538

RESULT 36
 KIBOC
 protein kinase C (EC 2.7.1.1) alpha - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C:Accession: C26037
 R:Ohno, S.; Kawasaki, H.; Imajoh, S.; Suzuki, K.; Inagaki, M.; Yokokura, H.; Sakoh, T.; Nature 325, 161-166, 1987
 A:Title: Tissue-specific expression of three distinct types of rabbit protein kinase C.
 A:Reference number: A26037; MUID:8711583; PMID:3803033
 A:Accession: C26037
 A:Molecule type: mRNA
 A:Residues: 1-672 <CHN>
 A:Cross-references: EMBL:X04796; NID:g1672; PIDN:CAA28483.1; PID:g1673
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters, f inositol phospholipids. Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding
 F19-29/Region: phospholipid binding #status experimental
 F122-27/Region: pseudophosphorylation motif
 F137-86/Domain: protein kinase C zinc-binding repeat homology <KZ1>
 F102,132,135,151/Binding site: zinc (His, Cys, Cys) #status predicted
 F115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F1368/Active site: Lys #status predicted
 F1631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 79.5%; Score 35; DB 1; Length 672;
 Best Local Similarity 75.0%; Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 |||
 Db 531 MLAGQPPF 538

RESULT 37
 KIBOC
 protein kinase C (EC 2.7.1.1) alpha - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 11-Jun-1999
 C:Accession: A00621
 R:Parker, P.J.; Coussens, L.; Totty, N.; Rhee, L.; Young, S.; Stabel, S.; Water Science 233, 853-859, 1986
 A:Title: The complete primary structure of protein kinase C - the major phorbol ester receptor
 A:Reference number: A00621; MUID:86289426; PMID:3755547
 A:Accession: A00621
 A:Molecule type: mRNA
 A:Residues: 1-672 <PAR>

A:Cross-references: GB:M13973; NID:g163529; PIDN:AAA30706.1; PID:g163530
 A:Experimental source: brain
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters, f inositol phospholipids. Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding
 F19-29/Region: phospholipid binding #status experimental
 F122-27/Region: pseudophosphorylation motif
 F137-86/Domain: protein kinase C zinc-binding repeat homology <KZ1>
 F102,132,135,151/Binding site: zinc (His, Cys, Cys) #status predicted
 F115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F1368/Active site: Lys #status predicted
 F1631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 79.5%; Score 35; DB 1; Length 672;
 Best Local Similarity 75.0%; Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 |||
 Db 531 MLAGQPPF 538

RESULT 38
 A37237
 protein kinase C (EC 2.7.1.1) I - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 28-Feb-1997
 C:Accession: A37237
 R:Chen, K.; Peng, Z.; Lavu, S.; Kung, H. Second Messengers Phosphoproteins 12, 251-260, 1989
 A:Title: Molecular cloning and sequence analysis of two distinct types of xenopus laevis protein kinase C A37237; MUID:90172230; PMID:3272298
 A:Reference number: A37237
 A:Accession: A37237
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A:Molecule type: mRNA
 A:Residues: 1-676 <CHE>
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C:Keywords: ATP; phosphotransferase
 F142-91/Domain: protein kinase C zinc-binding repeat homology <KZ1>
 F107-156/Domain: protein kinase C zinc-binding repeat homology <KZ2>
 F157-267/Domain: protein kinase C C2 region homology <K2>
 F1341-601/Domain: protein kinase homology <KIN>
 F1349-357/Region: protein kinase ATP-binding motif

Query Match 79.5%; Score 35; DB 2; Length 676;
 Best Local Similarity 75.0%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 |||
 Db 535 MLAGQPPF 542

RESULT 39
 KIBOC
 protein kinase C (EC 2.7.1.1) gamma - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C:Accession: C24664
 R:Coussens, L.; Parker, P.J.; Rhee, L.; Yang-Feng, T.L.; Chen, E.; Waterfield, M.D.; Science 233, 859-866, 1986
 A:Title: Multiple, distinct forms of bovine and human protein kinase C suggest divergent evolution
 A:Reference number: A94291; MUID:86289426; PMID:3755548
 A:Accession: C24664

A/Molecule type: tRNA
A/Residues: 1-682 <ON>
A/Cross-references: GB:M13976; NID:g163525; PIDN:AAA30784.1; PID:g163526
C/Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters, f inositol phospholipids (phosphatidylserine) in the cell membrane may
C/Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
C/Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C/Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C/Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding
F/3-13/Region: phospholipid binding #status predicted
F/6-11/Region: pseudophosphorylation motif
F/21-70/Domain: protein kinase C zinc-binding repeat homology <K21>
F/86-135/Domain: protein kinase C zinc-binding repeat homology <K22>
F/136-249/Domain: protein kinase C C2 region homology <K2>
F/334-599/Domain: protein kinase homology <KIN>
F/342-350/Region: protein kinase ATP-binding motif
F/21,51,54,70/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F/34,37,59,62/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F/86,116,119,135/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F/99,102,124,127/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F/365/Active site: Lys #status predicted
F/633,640/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 79.5%; Score 35; DB 1; Length 682;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 1 MLGKPPF 8
| :|||
Db 533 MLAGQPPF 540

RESULT 40
KIRTC
Protein kinase C (EC 2.7.1.1) gamma - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1992 #sequence_revision 30 Sep-1992 #text_change 11-Jun-1999
C/Accession: AC5105; S02129; I55317
R/Knopp, J.L.; Lee, M.H.; Sultzman, L.A.; Kriz, R.W.; Loomis, C.R.; Hewick, R.M.; Bell, Cell 46, 491-502, 1986
A/Title: Cloning and expression of multiple protein kinase C cDNAs.
A/Reference number: A90883; MUID:86272097; PMID:3755379
A/Accession: A05105
A/Molecule type: mRNA
A/Residues: 1-697 <KNO>
A/Cross-references: GB:M13707; NID:g206187; PIDN:AAA41874.1; PID:g206187
A/Note: the authors translated the codon UUU for residue 492 as Glu
R/Ono, Y.; Fujii, T.; Igarashi, K.; Kikkawa, U.; Ogita, K.; Nishizuka, Y. Nucleic Acids Res. 16, 5199-5200, 1988
A/Title: Nucleotide sequences of cDNAs for alpha and gamma subspecies of rat brain protein kinase C
A/Reference number: S02129; MUID:88262031; PMID:3187284
A/Accession: S02129
A/Molecule type: tRNA
A/Residues: 1-697 <ONO>
A/Cross-references: EMBL:X07287; NID:g56917; PIDN:CAA30267.1; PID:g56918
R/Chen, K.
C. Biol. Chem. 265, 19961-19965, 1990
A/Title: Characterization of the 5'-flanking region of the rat protein kinase C gamma gene
A/Reference number: I55317; MUID:91060619; PMID:2246272
A/Accession: I55317
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-56 <RES>
A/Cross-references: GB:M55417; NID:g206184; PIDN:AAA41873.1; PID:g554487
C/Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters, f inositol phospholipids (phosphatidylserine) in the cell membrane may
C/Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
C/Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C/Genetics:
A/Gene: PRKC-gamma
C/Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C/Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding
F/18-28/Region: phospholipid binding #status predicted

F/21-26/Region: pseudophosphorylation motif
F/36-85/Domain: protein kinase C zinc-binding repeat homology <K21>
F/101-150/Domain: protein kinase C zinc-binding repeat homology <K22>
F/151-264/Domain: protein kinase C C2 region homology <K2>
F/349-614/Domain: protein kinase homology <KIN>
F/357-365/Region: protein kinase ATP-binding motif
F/36,66,69,85/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F/49,52,74,77/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F/101,131,134,150/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F/114,117,139,142/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F/380/Active site: Lys #status predicted
F/648,655/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 79.5%; Score 35; DB 1; Length 697;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 1 MLGKPPF 8
| :|||
Db 548 MLAGQPPF 555

Search completed: November 14, 2003, 13:28:51
Job time : 10.6 secs

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QM protein - protein search, using sw model

Run on: November 14, 2003, 12:56:44 : Search time 5.94286 Seconds
(without alignments)
63,305 Million cell updates/sec

Title: US-09-736-076-16
Perfect score: 44
Sequence: 1 MLLGKPPF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	93.2	682	1	P53351 mus musculu
2	41	93.2	682	1	Q95122 rattus norv
3	41	93.2	685	1	Q9NYY3 homo sapien
4	39	88.6	465	1	P42818 arabidopsis
5	39	88.6	471	1	Q39030 arabidopsis
6	39	88.6	683	1	P33528 schizosacch
7	39	88.6	705	1	P32562 saccharomyc
8	38	86.4	282	1	Q89445 mus musculu
9	38	86.4	525	1	P38070 saccharomyc
10	38	86.4	603	1	P43350 homo sapien
11	38	86.4	603	1	Q27832 mus musculu
12	38	86.4	603	1	Q52673 rattus norv
13	37	84.1	679	1	P35130 drosophila
14	37	84.1	1081	1	Q12236 saccharomyc
15	36	81.8	217	1	Q22229 mytilus edu
16	36	81.8	403	1	Q14965 homo sapien
17	36	81.8	407	1	Q91820 xenopus lae
18	36	81.8	408	1	Q91819 xenopus lae
19	36	81.8	690	1	Q896p9 bifidobacte
20	35	79.5	294	1	P30797 rhodobacter
21	35	79.5	649	1	Q16974 aplysia cal
22	35	79.5	658	1	Q25378 lytechinus
23	35	79.5	672	1	P04409 bos taurus
24	35	79.5	672	1	P17252 homo sapien
25	35	79.5	672	1	P20444 mus musculu
26	35	79.5	672	1	P10102 oryctolagus
27	35	79.5	672	1	P35696 rattus norv
28	35	79.5	682	1	P35128 bos taurus
29	35	79.5	697	1	P35129 homo sapien
30	35	79.5	697	1	P05697 mus musculu
31	35	79.5	697	1	P10829 oryctolagus
32	34	77.3	363	1	Q42376 brachydanio
33	34	77.3	482	1	Q9ubsc h ribosomal

34	34	77.3	485	1	K6B2_MOUSE	Q9zlm4 mus musculu
35	34	77.3	502	1	KDC2_DROME	P16912 drosophila
36	34	77.3	555	1	PERF_HUMAN	P14222 homo sapien
37	34	77.3	576	1	POLO_DROME	P52304 drosophila
38	34	77.3	764	1	MPS1_YEAST	P54199 saccharomyc
39	34	77.3	1297	1	PUR4_VIBCH	Q9ktn2 vibrio chol
40	34	77.3	1320	1	PUR4_NEIMA	Q9jwc5 neisseria m
41	34	77.3	1369	1	PUR4_RALSO	Q8xyn6 ralstonia s
42	34	77.3	1374	1	M3K5_HUMAN	Q99683 homo sapien
43	34	77.3	1379	1	M3K5_MOUSE	O35099 mus musculu
44	34	77.3	1770	1	R115_YEAST	P43565 saccharomyc
45	33	75.0	156	1	STKC_PIG	Q9n0x0 sus scrofa

ALIGNMENTS

RESULT 1
SNK_MOUSE STANDARD; PRT; 682 AA.
AC P53351;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.-) (Serum inducible kinase).
DE kinase).
GN SNK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92375085; PubMed=1508211;
RA Simmons D.L., Neel B.G., Stevens R., Evett G., Erikson R.L.;
RT "Identification of an early-growth-response gene encoding a novel putative protein kinase."
RL Mol. Cell. Biol. 12:4164-4169(1992).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA.
CC -!- TISSUE SPECIFICITY: BRAIN, LUNG AND HEART.
CC -!- INDUCTION: BY SERUM AND PHORBOL ESTER.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
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CC -----
CC EMBL; M96163; -; NOT_ANNOTATED_CDS.
CC PIR; A44493; A44493.
CC MGD; MGI:1099790; Snk.
CC InterPro; IPR000959; POLO_box.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00659; POLO_box; 2.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS50078; POLO_BOX; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 54 59 POLY-HIS.
FT DOMAIN 79 331 PROTEIN KINASE.
FT NP_BIND 85 93 ATP (BY SIMILARITY).

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FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT SITE 202 202 BY SIMILARITY.
FT DOMAIN 507 570 POLC BOX 1.
FT DOMAIN 603 674 POLC BOX 2.
SQ SEQUENCE 682 AA; 77811 MW; 586DEABFD7208A9D CRC64;

Query Match 93.2%; Score 41; DB 1; Length 682;
Best Local Similarity 97.5%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGKPPF 8
DB 270 MLLGRPPF 277

RESULT 2
SNK_RAT
ID SNK_RAT STANDARD; PRT; 682 AA.
AC Q9R012;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.1) (Serum inducible kinase).
GN SNK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99452763; PubMed=12523297;
RA Kauselmann G., Weiler M., Wulff P., Gessberger S., Konietzko U.,
RA Staudt U., Staab U., Berer-Hahn J., Strebhardt K., Kuhl D.,
RT "The polo-like protein kinases Pnk and Snk associate with a Ca(2+)- and
RT integrin-binding protein and are regulated dynamically with synaptic
RT plasticity."
RL EVBO J. 18:5528-5539(1999).
CC -- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL
CC TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS,
CC WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLC SUBFAMILY.
CC -- SIMILARITY: CONTAINS 2 POLC BOX DOMAINS.
CC
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CC
CC -----
CC EMBL: AP136583; AAF08366.1;
CC InterPro: IPR000959; POLC_box.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00069; pkinase; 1.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS00078; POLC_BOX; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP binding; Repeat.
FT DOMAIN 54 59 POLY-HIS
FT DOMAIN 79 331 PROTEIN_KINASE.
FT NE BIND 85 93 ATP (BY SIMILARITY).
FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT SITE 202 202 BY SIMILARITY.
FT DOMAIN 507 570 POLC BOX 1.
FT DOMAIN 603 674 POLC BOX 2.
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SQ SEQUENCE 682 AA; 77919 MW; 58C50DEBDEB3D5F3 CRC64;

Query Match 93.2%; Score 41; DB 1; Length 682;
Best Local Similarity 87.5%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGKPPF 8
DB 270 MLLGRPPF 277

RESULT 3
SNK_HUMAN
ID SNK_HUMAN STANDARD; PRT; 685 AA.
AC Q9NYY3; O60679; Q96CV7; Q9UE61;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.1) (Serum inducible kinase).
GN SNK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ouyang B., Dai W.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Anderson K.M., Nerurkar S.S., Hansbury M.J., Fornwald J., Scott G.,
RA Bouzyk M., Mui P., Imbruglia C.S., Carlson K., Marshall L.A.,
RA Roshak A.K.;
RT "Identification and characterization of human serum-inducible kinase
RT (SNK), a novel member of the polo-kinase family of cell cycle
RT regulators: potential implication for regulation of vascular smooth
RT muscle proliferation."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Aitschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 110-408 FROM N.A.
RA Fidler C., Boulwood J., Wang Jabs E., Wainscoat J.S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL
CC TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS,
CC WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLC SUBFAMILY.
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CC CC (- SIMILARITY: Contains 2 POLO box domains. -----
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CC EMBL: AF059617; AAC14573.1; ..
CC EMBL: AF221574; AAF62897.1; ..
CC EMBL: U85755; AAC00575.1; ..
CC EMBL: BC013879; AAH13879.1; ..
CC MIM: 607023; ..
CC InterPro: IPR000959; POLO_box.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS00078; POLO_BOX; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE-ST; 1.
CC Transferase: Serine/threonine-protein kinase; ATP-binding; Repeat.
CC DOMAIN 57 64 POLY-HIS.
CC NP_BIND 82 334 PROTEIN_KINASE.
CC BINDING 88 96 ATP (BY SIMILARITY).
CC ACT_SITE 111 111 ATP (BY SIMILARITY).
CC ACT_SITE 205 205 BY SIMILARITY.
CC DOMAIN 510 573 POLO_BOX_1.
CC DOMAIN 606 677 POLO_BOX_2.
CC CONFLICT 26 28 A -> G (in Ref. 1).
CC SEQUENCE 685 AA; 78236 MW; 6429F6EFC83C5333 CRC64;
Query Match 93.2%; Score 41; DB 1; Length 685;
Best Local Similarity 87.5%; Pred. NO. 2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CY 1 MLLGKPPF 8
LE 293 MLLGPPF 280
RESULT 4
KPK1_ARATH STANDARD; PRT; 405 AA.
AC P42818;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase AtPK6/AtPK6 (EC 2.7.1.1).
GN ATPK1 OR ATPK6 OR AT3G08730 OR F17G14.20.
OS Arabidopsis thaliana (Mouse-ear cress).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eurosids 1; Brassicales; Brassicaceae; Arabidopsi.
CC NCBI_TaxId=3702;
CC [1]
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=94292519; PubMed=7912697;
RA Zhang S.-H., Lawton M.A., Hunter T., Lamb C.J.;
RT "Atpk1, a novel ribosomal protein kinase gene from Arabidopsis. I.
RT Isolation, characterization, and expression";
RL J. Biol. Chem. 269:17586-17592(1994).
RN 2
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=95129712; PubMed=7828736;
RA Yizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Katada H.,

RA Shinozaki K.;
RT "Two genes that encode ribosomal-protein S6 kinase homologs are
RT induced by cold or salinity stress in Arabidopsis thaliana.";
RL FEBS Lett. 358:199-204(1995).
RN 3
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
RA Fartmann B., Valie G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Deisner M., Boutry M., Griveil L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choinsne N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quettier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoer O., Barges M., Terol J., Clément J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Furnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schocf H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.-J., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana";
RL Nature 408:820-822(2000).
RN 4
RP CHARACTERIZATION.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=94292520; PubMed=8021267;
RA Zhang S.-H., Broome M.A., Lawton M.A., Hunter T., Lamb C.J.;
RT "Atpk1, a novel ribosomal protein kinase gene from Arabidopsis. II.
RT Functional and biochemical analysis of the encoded protein.";
RL J. Biol. Chem. 269:17593-17599(1994).
CC 1- FUNCTION: COULD BE INVOLVED IN THE CONTROL OF PLANT GROWTH AND
CC DEVELOPMENT. PHOSPHORYLATES TWO RIBOSOMAL PROTEINS, P14 AND P16.
CC 1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES.
CC 1- DEVELOPMENTAL STAGE: PREDOMINATES DURING HIGH METABOLIC ACTIVITY
CC IN GROWING BUDS, ROOT TIPS, LEAF MARGINS AND GERMINATING SEEDS.
CC 1- PTM: UNDERGOES SERINE-SPECIFIC AUTOPHOSPHORYLATION.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC S6 KINASE SUBFAMILY.
CC -----
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CC EMBL: L29030; AAA21142.1; ..
CC EMBL: D42056; BAA07656.1; ..
CC EMBL: AC012562; AAG51351.1; ..
CC PIR: S68462; S68462.
CC HSSP: Q63450; 1A06.
CC InterPro: IPR000961; Pkinase_C.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF00433; pkinase_C; 1.
CC ProDom: PD000001; Prot_kinase; 1.

DR SMART; SMO0133; S_TK_X; 1.
DR SMART; SMO0220; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 134 389 PROTEIN KINASE.
FT NP BIND 140 148 ATP (BY SIMILARITY).
FT BINDING 163 163 ATP (BY SIMILARITY).
FT ACT_SITE 257 257 BY SIMILARITY.
FT MUTAGEN 163 163 K->R; ACTIVITY SUBSTANTIALLY DIMINISHED.
SQ SEQUENCE 465 AA; 52588 MW; 407133D674CA271F CRC64;

Query Match 88.6%; Score 39; DB 1; Length 465;
Best Local Similarity 87.5%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||
DB 324 MLTGKPPF 331

RESULT 5
EP19 ARATH STANDARD; PROT; 471 AA.
AC Q19030; Q949X5; Q9C5R1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase AtPK19 (EC 2.7.1.1) [ribosomal-protein
DE S6 kinase homolog].
GN ATPK19 OR AT3G28720 OR F17014.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID:3702;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=95129712; PubMed=7828736;
RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kanada H.,
RA Shinozaki K.;
RT "Two genes that encode ribosomal protein S6 kinase homologs are
RT induced by cold or salinity stress in Arabidopsis thaliana";
RJ FEBS Lett. 358:199-204(1995);
RN 12;
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=1130719;
RA Salancubet M., Lemcke K., Rieger M., Anselme W., Besold M.,
RA Partrann B., Valle G., Bloeker H., Perez-Alonso M., Giermaier B.,
RA Delisny M., Boutry M., Grivell L.A., Maché R., Bulgakovskiy P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brothier P.,
RA Winkler F., Cattolico L., Weissenbach G., Saulin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Hones V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Bechert T.-H., Nordstok G.,
RA Reichelt J., Scharfe M., Schoen O., Sargues M., Tercl J., Clément J.,
RA Navarro P., Colliado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiriou A., Flores M., Inguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rued S., Zaccaria F., Mewes H.-W.,
RA Mayer K.F.X., Kaut S., Town C.D., Koo H.-J., Tailon L.J., Jenkins C.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Furlan G.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu C., Peterson J., Van Aken S.,
RA Pat G., Miltitscher J., Sellers P., Gili J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter G.C.,
RA Fraser G.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana";
RL Nature 408:820-822(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Theologis A., Ecker J., Davis R.W.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PGECC)";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY BE INVOLVED IN ADAPTATION OF PLANT TO COLD OR HIGH-
CC SALT CONDITIONS.
CC -!- PTM: UNDERGOES SERINE-SPECIFIC AUTOPHOSPHORYLATION (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC S6 KINASE SUBFAMILY.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to a
CC frameshift in position 391.

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CC or send an email to license@isb-sib.ch).

DR EMBL; D42061; BAA07661.1; -;
DR EMBL; AC012562; AAC51345.1; -;
DR EMBL; AF325094; AAK17162.1; -;
DR EMBL; AY050826; AAK92761.1; ALT_FRAME.
DR PIR; S68463; S68463.
DR HSP; P05132; ICTP.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0133; S_TK_X; 1.
DR SMART; SMO0220; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 140 395 PROTEIN KINASE.
FT NP BIND 146 154 ATP (BY SIMILARITY).
FT BINDING 169 169 ATP (BY SIMILARITY).
FT ACT_SITE 263 263 BY SIMILARITY.
FT CONFLICT 250 250 A -> V (IN REF. 1).
FT CONFLICT 359 360 LS -> VF (IN REF. 1).
SQ SEQUENCE 471 AA; 53037 MW; 95F007B44B58DFB5 CRC64;

Query Match 88.6%; Score 39; DB 1; Length 471;
Best Local Similarity 87.5%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||
DB 330 MLTGKPPF 333

RESULT 6
PLOC1_SCHPO STANDARD; PRT; 683 AA.
AC P50528;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase ploi (EC 2.7.1.37).
GN PLOC1 CR SPAC23C11.16.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
CX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=95262899; PubMed=7744248;
RA Okura H., Hagan I.M., Glover D.M.;
RT "The conserved Schizosaccharomyces pombe kinase ploi, required to
form a bipolar spindle, the actin ring, and septum, can drive septum
formation in G1 and G2 cells";
RL Genes Dev. 9:1059-1073(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848461; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,
Hollroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
McNeely P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Cliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Robben C., Grymonprez B.,
Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
Borzum K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Delaure V., Mottier S.,
Gallibert F., Aves S.J., Xiang Z., Hunt S., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Dominguez A., Revuelta J.L., Yereb S., Armstrong J., Forsberg S.B.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen O., Houshkin G.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.
RT "The genome sequence of Schizosaccharomyces pombe".
RL Nature 415:871-880(2002).
CC -- FUNCTION: REQUIRED TO FORM A BIPOLEAR SPINDLE, THE ACTIN RING AND
SEPTUM. FUNCTIONS UPSTREAM OF THE WHOLE SEPTUM FORMATION PATHWAY,
INCLUDING ACTIN RING FORMATION (REGULATED BY LATE SEPTATION GENES)
AND SEPTAL MATERIAL DEPOSITION (REGULATED BY EARLY SEPTATION
GENES). BEHAVES AS A "SEPTUM-PROMOTING FACTOR", AND COULD ALSO BE
INVOLVED IN INDUCING OTHER LATE EVENTS OF CELL DIVISION.
CC -- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -- SIMILARITY: Contains 2 POLO box domains.
CC
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CC
CC
CC EMBL; X85758; CAA59766.1; --

DR EMBL; Z98559; CAB11167.1; --
DR PIR; T38254; T38254.
DR HSSP; Q63450; 1A06.
DR GenedB_SPombe; SPAC23C11.16; --
DR InterPro; IPR000959; POLO box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO box; 2.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50078; POLO BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 41 296 PROTEIN KINASE.
FT NP_BIND 47 55 ATP (BY SIMILARITY).
FT BINDING 69 69 ATP (BY SIMILARITY).
FT ACT_SITE 163 163 BY SIMILARITY.
FT DOMAIN 500 567 POLO BOX 1.
FT DOMAIN 604 670 POLO BOX 2.
SQ SEQUENCE 683 AA; 77301 MW; F1ICD0EF9B913917 CRC64;

Query Match 88.6%; Score 39; DB 1; Length 683;
Best Local Similarity 75.0%; Pred.No. 5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 233 LLIGKPPF 240

RESULT 7
CDC5_YEAST
ID CDC5_YEAST STANDARD; PRT; 705 AA.
AC P32562;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cell cycle protein kinase CDC5/MSD2 (EC 2.7.1.37).
GN CDC5 OR PKX2 OR MSD2 OR YMR001C OR YM8270.03C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A364A;
RX MEDLINE=93309479; PubMed=8321244;
RA Kitada K., Sugino A., Johnston L.H., Johnson A.L.;
RT "A multicopy suppressor gene of the Saccharomyces cerevisiae G1 cell
cycle mutant gene dbf4 encodes a protein kinase and is identified as
CDC5";
RL Mol. Cell. Biol. 13:4445-4457(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
Rice P., Skellton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
XIII";
RL Nature 387:90-93(1997).
RN [3]
RP PHOSPHORYLATION OF SCC1.
RX PubMed=11371343;
RA Alexandru G., Uhlmann F., Mechtler K., Poupard M.-A., Nasmyth K.;
RT "Phosphorylation of the cohesin subunit Scc1 by Polo/Cdc5 kinase
regulates sister chromatid separation in yeast";
RL Cell 105:459-472(2001).

CC -!- FUNCTION: Protein kinase required for the cell cycle.
 CC Phosphorylates SCCL/MCD1.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLO SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 POLO box domains.
 CC -----
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 CC -----
 CC EMBL; Y84220; AAA02576.1; -
 CC EMBL; Z48613; CAA88516.1; -
 CC PIR; A48144; A48144.
 CC HSSP; Q63450; 1A06.
 CC SGD; S0004603; CDC5.
 CC GO; GO:0005634; C:nucleus; IDA.
 CC GO; GO:0006261; P:DNA dependent DNA replication; IDA.
 CC GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
 CC InterPro; IPR000959; POLO box.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR002290; Ser_thr_kinase.
 CC InterPro; IPR01245; Tyr_kinase.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00659; POLO box; 2.
 CC PRINTS; PR0109; TYRKINASE.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00220; S_TKC; 1.
 CC PROSITE; PS0078; POLO BOX; 2.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC Cell cycle; Cell division; Serine/threonine protein kinase;
 CC Transferase; ATP-binding; Repeat.
 CC DOMAIN 82 337 PROTEIN_KINASE.
 CC NP_BIND 88 96 ATP (BY SIMILARITY).
 CC BINDING 110 110 ATP (BY SIMILARITY).
 CC ACT_SITE 204 204 BY SIMILARITY.
 CC DOMAIN 520 587 POLO BOX 1.
 CC DOMAIN 619 692 POLO BOX 2.
 CC SEQUENCE 705 AA; 81030 MW; B5A25F1B8BBA3DC CRC64;
 KW TRANSFERASE; ATP-BINDING; REPEAT.
 FT DOMAIN 82 337 PROTEIN_KINASE.
 FT NP_BIND 88 96 ATP (BY SIMILARITY).
 FT BINDING 110 110 ATP (BY SIMILARITY).
 FT ACT_SITE 204 204 BY SIMILARITY.
 FT DOMAIN 520 587 POLO BOX 1.
 FT DOMAIN 619 692 POLO BOX 2.
 SQ SEQUENCE 705 AA; 81030 MW; B5A25F1B8BBA3DC CRC64;
 Query Match 88.6%; Score 39; DB 1; Length 705;
 Best Local Similarity 75.0%; Pred. No. 51;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MLLGKPPF 8
 Db 274 LLVGKPPF 281
 RESULT 8
 STKD_MOUSE
 ID STKD_MOUSE STANDARD; PRT; 252 AA.
 AC Q88445; Q9JLC2;
 DT 28-FEB-2003 (Rel. 41, Created;
 DT 28-FEB-2003 (Rel. 41, Last sequence update;
 DT 15-SEP-2003 (Rel. 42, Last annotation update;
 DE Serine/threonine protein kinase 13 (EC 2.7.1.37) (Aurora/ipli/Eg2
 DE protein 1) (Aurora-C).
 GN STK13 OR AIE1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=99025616; PubMed=9809744;

RA Tseng T.C., Chen S.H., Hsu Y.P., Tang T.K.;
 RT "Protein kinase profile of sperm and eggs: cloning and
 RT characterization of two novel testis-specific protein kinases (AIE1,
 RT AIE2) related to yeast and fly chromosome segregation regulators.";
 RL DNA Cell Biol. 17:823-833(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=20551164; PubMed=11098217;
 RA Hu H.M., Chuang C.K., Lee M.J., Tseng T.C., Tang T.K.;
 RT "Genomic organization, expression, and chromosome localization of a
 RT third aurora-related kinase gene, Aie1.";
 RL DNA Cell Biol. 19:679-688(2000).
 CC -!- FUNCTION: May play a part in organizing microtubules in relation
 CC to the function of the centrosome/spindle pole during mitosis.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Localized to spindle pole from anaphase to
 CC cytokinesis (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed only in testis.
 CC -!- DEVELOPMENTAL STAGE: Expressed on day 14 dpc in prepubertal
 CC testis, expression reached its plateau on day 21 dpc and remained
 CC at a high level in adult.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC AURORA SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AF054620; AAC25954.1; -
 CC EMBL; AF195272; AAF25838.1; -
 CC HSSP; Q63450; 1A06.
 CC MGD; MGI:1321119; Stk13.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR002290; Ser_thr_kinase.
 CC InterPro; IPR01245; Tyr_kinase.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PR0109; TYRKINASE.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00220; S_TKC; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 CC Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
 KW TRANSFERASE; ATP-BINDING; REPEAT.
 FT DOMAIN 16 266 PROTEIN_KINASE.
 FT NP_BIND 22 30 ATP (BY SIMILARITY).
 FT BINDING 45 45 ATP (BY SIMILARITY).
 FT ACT_SITE 139 139 BY SIMILARITY.
 FT CONFLICT 74 74 R -> P (IN REF. 2).
 SQ SEQUENCE 282 AA; 32907 MW; 7CB8AEC4984B7883 CRC64;
 Query Match 86.4%; Score 38; DB 1; Length 282;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPF 8
 Db 205 LLVGKPPF 212
 RESULT 9
 KBN8_YEAST
 ID KBN8_YEAST STANDARD; PRT; 525 AA.
 AC P38070;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable serine/threonine-protein kinase YBR028C (EC 2.7.1.-).
 GN YBR028C OR YBR0312.

OS Saccharomyces cerevisiae (Baker's yeast);
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
CX NCBI_TaxID=4932;
RV [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94378725; PubMed=8091864;
RA Smits P.H.M., de Haan M., Maat C., Grivell L.A.;
RT "The complete sequence of a 33 kb fragment on the right arm of
RT chromosome II from Saccharomyces cerevisiae reveals 16 open reading
RT frames, including ten new open reading frames, five previously
RT identified genes and a homologue of the SCD1 gene";
RL Yeast 10:575-580(1994).
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X76078; CAA53684.1; -
DR EMBL: Z35897; CAA84970.1; -
DR PIR: S45884; S45884.
DR HSSP: P05132; 1CTP.
DR SCOP: S0002232; YBR028C.
DR InterPro: IPR000961; pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00433; pkinase_C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; Transferase; Serine/threonine protein kinase;
KW ATP-binding.
FT DCMAIN 128 424 PROTEIN KINASE.
FT NP BIND 134 142 ATP (BY SIMILARITY);
FT BINDING 157 157 ATP (BY SIMILARITY);
FT ACT SITE 277 277 BY SIMILARITY;
SQ SEQUENCE 525 AA; 59591 MW; 58FEF61A44066672 CF 144;
Query Match 86.4%; Score 35; EB 1; Length 525.
Best Local Similarity 75.0%; Pred. NC 67
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CY : MLLGKPPF 8
DB 355 MLVGKPPY 362
RESULT 10
PLK1_HUMAN
ID PLK1_HUMAN STANDARD; PRT; 603 AA.
AC P53350;
DT 01-OCT-1996 (Rel. 34, Created;
DT 01-OCT-1996 (Rel. 34, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase pLK (EC 2.7.11.1) (PLK-1) (Serine-
DE threonine protein kinase 13) (STPK13).
GN PLK OR PJK.
CS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RV [1]
RP SEQUENCE FROM N.A.

CC
RX MEDLINE=94289293; PubMed=8018557;
RA Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.L.,
RA Ferris D.K.;
RT "Cloning and characterization of human and murine homologues of the
RT Drosophila polo serine-threonine kinase";
RL Cell Growth Differ. 5:249-257(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94067140; PubMed=7902533;
RA Lake R.J., Jelinek W.R.;
RT "Cell cycle- and terminal differentiation-associated regulation of
RT the mouse mRNA encoding a conserved mitotic protein kinase";
RL Mol. Cell. Biol. 13:7793-7801(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95051109; PubMed=7962193;
RA Golsteyn R.M., Schultz S.J., Bartek J., Ziemiecki A., Ried T.,
RA Nigg E.A.;
RT "Cell cycle analysis and chromosomal localization of human Plk1, a
RT putative homologue of the mitotic kinases Drosophila polo and
RT Saccharomyces cerevisiae Cdc5";
RL J. Cell Sci. 107:1509-1517(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94173904; PubMed=8127874;
RA Holtrich U., Wolf G., Braeuninger A., Karn T., Boehme B.,
RA Ruebsamen-Waigmann H., Strebhardt K.;
RT "Induction and down-regulation of PLK, a human serine/threonine
RT kinase expressed in proliferating cells and tumors";
RL Proc. Natl. Acad. Sci. U.S.A. 91:1736-1740(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC 1- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE.
CC 1- SUBCELLULAR LOCATION: Nuclear.
CC 1- TISSUE SPECIFICITY: PLACENTA AND COLON.
CC 1- DEVELOPMENTAL STAGE: ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
CC DURING S PHASE.
CC 1- INDUCTION: BY GROWTH-STIMULATING AGENTS.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC 1- SIMILARITY: Contains 2 POLO box domains.
CC -----
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EMBL; U01038; AAA56634.1; -
EMBL; L29559; AAA36659.1; -
EMBL; X73458; CAA51837.1; -
EMBL; X75932; CAA53536.1; -
EMBL; BC002369; AAH02369.1; -
EMBL; BC003002; AAH03002.1; -
EMBL; BC014846; AAH14846.1; -
PIR; S34130; S34130.
Genew; HGNC:9077; PLK.
GK; P53350; -
YIM; 602096; -
GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
GO; GO:0007067; P:mitosis; TAS.
GO; GO:0007048; P:oncogenesis; TAS.
GO; GO:0000074; F:regulation of cell cycle; TAS.
InterPro; IPR000959; POLO_box.
InterPro; IPR002290; Ser_thr_kinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF00659; POLO_box; 2.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS50078; POLO_BOX; 2.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP binding; Repeat;
Nuclear protein.
FT DOMAIN 53 305 PROTEIN KINASE.
FT NP BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 480 POLO_BOX_1.
FT DOMAIN 515 584 POLO_BOX_2.
FT CONFLICT 2 2 S > T (IN REF. 1).
FT CONFLICT 11 11 A -> P (IN REF. 1).
FT CONFLICT 58 58 F -> L (IN REF. 1).
FT CONFLICT 60 60 G -> S (IN REF. 1).
FT CONFLICT 73 73 A -> V (IN REF. 2).
FT CONFLICT 141 141 L -> P (IN REF. 4).
FT CONFLICT 227 227 G -> E (IN REF. 4).
FT CONFLICT 301 301 N -> G (IN REF. 2).
FT CONFLICT 495 495 A -> G (IN REF. 2).
FT CONFLICT 501 501 E -> Q (IN REF. 2).
SQ SEQUENCE 603 AA; 68254 YW. IPR000959:1-305, IPR002290:1-480.

Query Match: 86.4%; Score 101.18; Length 603;
Best Local Similarity: 75.0%; Pred. No. gaps: 0;
Matches: 6; Conservative: 2; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 MLLGKPPF 8
DB 244 LNVGKPPF 251

RESULT 11
PLK1_MOUSE
ID PLK1_MOUSE STANDARD; PRT: EC: 2.7.1.1
AC G07832;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase PLK1 (P. 2.7.1.1) (Serine-
threonine protein kinase 13) (STPK13).
GN PLK.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID:10090;

RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6; TISSUE=Bone marrow;
RC MEDLINE=93281660; PubMed=8099445;
RX Clay F.J., McEwen S.J., Bertonecello I., Wilks A.F., Dunn A.R.;
RA "Identification and cloning of a protein kinase-encoding mouse gene,
RT plk, related to the polo gene of Drosophila";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4882-4886(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=94289293; PubMed=8018557;
RA Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.L.,
RA Ferris D.K.;
RT "Cloning and characterization of human and murine homologues of the
RT Drosophila polo serine-threonine kinase";
RL Cell Growth Differ. 5:249-257(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=94067140; PubMed=7902533;
RA Lake R.J., Jelinek W.R.;
RT "Cell cycle- and terminal differentiation-associated regulation of
RT the mouse mRNA encoding a conserved mitotic protein kinase";
RL Mol. Cell. Biol. 13:7793-7801(1993).
CC -!- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: NEWBORN AND ADULT SPLEEN, FETAL AND NEWBORN
CC KIDNEY, LIVER, BRAIN, THYMUS AND ADULT BONE MARROW, THYMUS,
CC OVARY AND TESTES.
CC -!- DEVELOPMENTAL STAGE: IN THE THYMUS, LEVELS INCREASED DURING FETAL
CC DEVELOPMENT, WERE HIGHEST IN NEWBORN ANIMALS AND DECREASED IN THE
CC ADULT. IN THE TESTES, THE PLK LEVELS WERE HIGHER IN THE ADULT THAN
CC IN PREPUBESCENT MICE WHILE IN THE OVARY, THE LEVELS WERE HIGHER IN
CC THE PREPUBESCENT MICE. ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
CC DURING S PHASE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC -----
CC EMBL; L06144; AAA39948.1; -
DR EMBL; U01063; AAA56635.1; -
DR EMBL; L19558; AAA16071.1; -
DR PIR; A47545; A47545.
DR PIR; A54596; A54596.
DR MGD; MGI:97621; Plk.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Nuclear protein.
FT DOMAIN 53 305 PROTEIN KINASE.
FT NP BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.

```
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 480 POLO BOX 1.
FT DOMAIN 515 584 POLO BOX 2.
FT DOMAIN 584
FT CONFLICT 4 4 A -> V (IN REF. 1).
FT CONFLICT 15 15 A -> T (IN REF. 1).
FT CONFLICT 23 23 P -> L (IN REF. 1).
FT CONFLICT 27 27 V -> A (IN REF. 1).
FT CONFLICT 29 29 G -> S (IN REF. 1).
FT CONFLICT 41 41 F -> L (IN REF. 1).
FT CONFLICT 54 54 V -> I (IN REF. 1).
FT CONFLICT 495 495 A -> R (IN REF. 1).
FT SEQUENCE 603 AA; 68300 MW; 1B98C64626E5FALC CRC64;

Query Match 86.4%; Score 38; DB 1; Length 603;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 244 LLVGKPPF 251

RESULT 12
PK1_PAT
ID PK1_PAT STANDARD; PRT; 603 AA.
AC Q62673;
DT 16-OCT-2001 (Rel. 40; Created);
DI 16-OCT-2001 (Rel. 40; Last sequence update);
DE Serine/threonine-protein kinase PK1 (EC 2.7.1.1) (PK1-2);
GN PK1;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
OX NCBI_TaxID=10116;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Amstrup J., Hansen J.A., Hxrlis Nielsen C.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC 1- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE (BY SIMILARITY).
CC 1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC 1- SIMILARITY: Contains 2 POLO box domains.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U0188; AAA1885.1;
CC InterPro; IPR000959; POLO_box.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR022900; Ser_thr_kinase.
CC Pfam; PF00069; pk_kinase; 1.
CC Pfam; PF00659; POLO_box; 2.
CC ProDom; PDC00001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS50078; POLO_BOX; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Nuclear protein.
FT DOMAIN 53 305 PROTEIN_KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
```

```
FT DOMAIN 417 480 POLO BOX 1.
FT DOMAIN 515 584 POLO BOX 2.
FT SEQUENCE 603 AA; 68313 MW; 107AFFB3B7EDC002 CRC64;

Query Match 86.4%; Score 38; DB 1; Length 603;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 244 LLVGKPPF 251

RESULT 13
KPC1_DROME
ID KPC1_DROME STANDARD; PRT; 679 AA.
AC P05130; Q9V7V6; Q9V7V7;
DT 13-AUG-1987 (Rel. 35; Created);
DI 28-FEB-2003 (Rel. 41; Last sequence update);
DE Protein kinase C, brain isozyme (EC 2.7.1.1) (PKC) (dPKC53E(BR)).
GN PKC53E OR PKC1 OR CG6622;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1];
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=Canton-S, and Oregon-R;
RX MEDLINE=87218499; PubMed=3107983;
RA Rosenthal A., Rhee L., Yadegari R., Paro R., Ullrich A., Goeddel D.V.;
RT "Structure and nucleotide sequence of a Drosophila melanogaster
RT protein kinase C gene.";
RL EMBO J. 6:433-441(1987).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaralides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Saxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtas K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup J.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.C., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
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RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
PT "The genome sequence of Drosophila melanogaster";
RJ Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=Berkeley; TISSUE=Ovary;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Kronmiller S., Li P.W., Liao G.,
RA Miranda A., Mungall C.J., Nuccio J., Pacleb J.M., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA Celisner S.E.;
RJ Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P05130-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P05130-2; Sequence=VSP_004743;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: HEAD NEURAL TISSUE.
CC -!- MISCELLANEOUS: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-
CC DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF CREGON R.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. PKC
CC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X05276; CAA28736.1; .
CC EMBL: X05279; CAA28890.2; .
CC EXBL: X05280; CAA28890.2; JOINED.
CC EXBL: X05281; CAA28890.2; JOINED.
CC EMBL: X05282; CAA28890.2; JOINED.
CC EMBL: X05283; CAA28890.2; JOINED.
CC EMBL: AE003805; AAF57932.1; .
CC EMBL: AE003805; AAF57933.1; .
CC EMBL: AY095003; AAM11331.1; .
CC HSSP: P05697; ITBN.
CC FlyBase: FBgn003091; PKC53E.
CC GO: GO:004674; P:protein serine/threonine kinase activity; IDA.
CC GO: GO:006468; P:protein amino acid phosphorylation; IDA.
CC InterPro: IPR000008; C2.
CC InterPro: IPR002219; DAG_PE-bind.
CC InterPro: IPR000961; Pkinase_C.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC InterPro: IPR001245; Tyr_kinase.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF00168; C2; 1.
CC Pfam: PF03433; pkinase_C; 1.
CC PRINTS: PR00360; C2DOMAIN.
CC PRINTS: PR00008; DAGPEDOMAIN.
CC ProDom: P200001; Prot_kinase; 1.
CC SMART: SM00109; C1; 1.
CC SMART: SM00239; C2; 1.
CC SMART: SM00133; S_TK_X; 1.
CC SMART: SM00220; S_TKC; 1.
CC SMART: SMC0219; TyrKc; 1.

DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Multigene family; Zinc;
KW Phorbol-ester binding; Alternative splicing.
FT DOMAIN 46 104 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 120 169 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 191 278 C2 DOMAIN.
FT DOMAIN 350 608 PROTEIN KINASE.
FT NP_BIND 356 364 ATP (BY SIMILARITY).
FT BINDING 379 379 ATP (BY SIMILARITY).
FT ACT_SITE 474 474 BY SIMILARITY.
FT VARSPLIC 67 77 CGYQSGYAWMG -> WG (in isoform Short).
FT VARIANT 437 437 M -> I.
FT CONFLICT 608 608 F -> S (IN REF. 1).
FT CONFLICT 634 648 DVSNFDKQFTSEKTD -> MCPTLTSSSHQKQT (IN
FT REF. 1).
FT CONFLICT 649 679 MISSING (IN REF. 1).
SQ SEQUENCE 679 AA; 77695 MW; 3C69AD351B36B7DC CRC64;

Query Match 84.1%; Score 37; DB 1; Length 679;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLUGKPPF 8
Db 542 MLVGQPPF 549
|||:||||

RESULT 14
KOKO_YEAST STANDARD; PRT; 1081 AA.
ID KOKO_YEAST
AC Q12236;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable serine/threonine-protein kinase YOL100W (EC 2.7.1.1).
GN YOL100W OR HRC1081.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A. PubMed=7502582;
RX MEDLINE=96076631; Portetelle D., Hilger F.;
RA Vandenboi M., Durand P., Portetelle D., Hilger F.;
RT "Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV
RT including the Tyl-H3 retrotransposon, the sufl(+) frameshift
RT suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-1a and a
RT delta element";
RL Yeast 11:1069-1075(1995).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC
CC EMBL: Z48149; CAA88162.1; .
CC EMBL: Z74842; CAA99113.1; .
CC PIR: S51899; S51899.
CC HSSP: Q63450; 1AC6.
CC SGD: S000546C; PKH2.


```
DR GC: GO:0005634; C:nucleus; IDA.
DR GC: GO:000196; P:MAPKK cascade (cell wall biogenesis); IGI.
DR GC: GO:000468; P:protein amino acid phosphorylation; IDA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR02290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding.
FT DOMAIN 179 443 PROTEIN_KINASE.
FT NP_BIND 185 193 ATP (BY SIMILARITY).
FT BINDING 208 208 ATP (BY SIMILARITY).
FT ACT_SITE 303 303 BY SIMILARITY.
SQ SEQUENCE 1081 AA; 121660 MW; BE0DD3D49AC2EBC3 CR264;

Query Match 84.1%; Score 37; DB 1; Length 1081;
Best local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 3;

QY 1 MLLGKPPF 8
|:|:|
Db 382 MLAGKPPF 389

RESULT 15
NU2M_MYTED STANDARD; PRT; 217 AA.
AC QCC229;
DT 01-NOV-1995 (Rel. 32, Created);
DT 01-NOV-1995 (Rel. 32, Last sequence update);
DT 15-JUL-1993 (Rel. 38, Last annotation update);
DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3) (Fragments).
GN ND2.
OS Mytilus edulis (Blue mussel).
CG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
CX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92354892; PubMed=1386586;
RA Hoffmann R.J., Boore J.B., Brown W.M.;
RT "A novel mitochondrial genome organization for the blue mussel,
RT Mytilus edulis."
RL Genetics 131:397-412(1992).
CC 1- CATALYTIC ACTIVITY: NADH + ubiquinone -> NAD + ubiquinol.
CC 1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC 1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
-----
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-----
EMBL: M83760; AAA31908.1;
DR EMBL: M83761; AAA31909.1;
DR PIR: S28754; S28754.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
FT NON_CONS 131 132
SQ SEQUENCE 217 AA; 23553 MW; 0236172A1A3CE062 CR054;

Query Match 81.8%; Score 36; DB 1; Length 217;
Best local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 3;
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QY 1 MLLGKPPF 8
|:|:|
Db 135 MLMGMPPF 142

RESULT 16
STK6_HUMAN STANDARD; PRT; 403 AA.
ID STK6_HUMAN
AC O14965; O60445; O75873; Q9BQD6; Q9UPG5;
DT 28-FEB-2003 (Rel. 41, Created);
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Serine/threonine kinase 6 (EC 2.7.1.37) (Serine/threonine kinase 15;
DE (Aurora/IPL1-related kinase 1) (Aurora-related kinase 1) (hARK1)
DE (Aurora-A) (Breast-tumor-amplified kinase).
GN STK6 OR STK15 OR AIK OR ARK1 OR AURA OR BTAK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=97298083; PubMed=9153231;
RA Kimura M., Kotani S., Hattori T., Sumi N., Yoshioka T., Todokoro K.,
RA Okano Y.;
RT "Cell cycle-dependent expression and spindle pole localization of a
RT novel human protein kinase, Aik, related to Aurora of Drosophila and
RT yeast Ipl1."
RL J. Biol. Chem. 272:13766-13771(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98183439; PubMed=9514916;
RA Shindo M., Nakaro H., Kuroyanagi H., Shirasawa T., Mihara M.,
RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
RT "cDNA cloning, expression, subcellular localization, and chromosomal
RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
RT 1 and 2."
RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=98442657; PubMed=9771714;
RA Zhou H., Kuang J., Zhong L., Kuo W.-L., Gray J.W., Sahin A.,
RA Brinkley B.R., Sen S.;
RT "Tumour amplified kinase STK15/BTAK induces centrosome amplification,
RT aneuploidy and transformation."
RL Nat. Genet. 20:189-193(1998).
RN [4]
RP SEQUENCE FROM N.A.
RA Wang L., Thibodeau S.N.;
RT "Mutational analysis of the STK15 gene in human tumors."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehtvaslaihio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
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RA Philadelphia B.J.C.T., Prithalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Suiston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RT "The DNA sequence and comparative analysis of human chromosome 20";
RL Nature 414:865-871(2001).
RN 16.
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix, Colon, Kidney, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huix S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.C.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 17)
RP CELL-CYCLE REGULATION.
RX MEDLINE=21895866; PubMed=11790771;
RA Tanaka M., Ueda A., Kanamori H., Ideguchi H., Yang J., Kitajima S.,
RA Ishigatsubo Y.,
RT "Cell cycle dependent regulation of human aurora A transcription is
mediated by periodic repression of E4F1";
RL J. Biol. Chem. 277:10719-10726(2002).
RN 18)
RP REVIEW.
RX MEDLINE=21306577; PubMed=11413462;
RA Nigg E.A.,
RT "Mitotic kinases as regulators of cell division and its checkpoints";
RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
CC 1)- FUNCTION: May play a role in cell cycle regulation during anaphase
and/or telophase, in relation to the function of the
centrosome/spindle pole region during chromosome segregation.
CC Maybe involved in microtubule formation and/or stabilization. May
play a key role during tumor development and progression.
CC 1)- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC 1)- SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells
and at each spindle pole in mitosis.
CC 1)- TISSUE SPECIFICITY: Highly expressed in testis and weakly in
skeletal muscle, thymus and spleen. Also highly expressed in
colon, ovarian, prostate, neuroblastoma, breast and cervical
cancer cell lines. Expression is cell-cycle regulated, low in
G1/S, accumulates during G2/M, and decreases rapidly after.
CC 1)- PTM: Phosphorylated.
CC 1)- DISEASE: Defects in STK6 are responsible for numerical centrosome
aberrations including aneuploidy.
CC 1)- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC 1)- AURORA SUBFAMILY.
CC 1)- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
in positions 105, 125, 129, 235 and 241
CC 1)- CAUTION: Although authors have considered STK6 and STK15 as two
different proteins, it is clear that they are the same protein.
CC -----
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CC -----
DR EMBL; D84212; BAA23592.1; ACT_FRAME.
DR EMBL; AF008551; AAC12708.1; -
DR EMBL; AF011467; AAC23448.1; -
DR EMBL; AF011468; AAC63902.1; -
DR EMBL; AF195947; AAF29508.1; -
DR EMBL; AF195942; AAF29508.1; JOINED.
DR EMBL; AF195943; AAF29508.1; JOINED.
DR EMBL; AF195944; AAF29508.1; JOINED.
DR EMBL; AF195945; AAF29508.1; JOINED.
DR EMBL; AF195946; AAF29508.1; JOINED.
DR EMBL; AL121914; CAC12717.1; -
DR EMBL; BC001280; AAH01280.1; -
DR EMBL; BC002499; AAH02499.1; -
DR EMBL; BC006423; AAH06423.1; -
DR EMBL; BC027464; AAH27464.1; -
DR GK; O14965; -
DR MIM; 602687; -
DR MIM; 603072; -
DR HSSP; P24941; 1BUH.
DR Genew; HGNC:11409; STK6.
DR Genew; HGNC:11393; STK15.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0005819; C:spindle; TAS.
DR GO; GO:0007067; P:mitosis; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF03069; pkinase; 1.
DR ProDom; PDC00001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 133 383 PROTEIN KINASE.
FT NP_BIND 139 147 ATP (BY SIMILARITY).
FT BINDING 162 162 ATP (BY SIMILARITY).
FT ACT_SITE 256 256 BY SIMILARITY.
FT CONFLICT 31 31 F -> I (IN REF. 3).
FT CONFLICT 57 57 V -> I (IN REF. 2).
SQ SEQUENCE 403 AA; 45809 MW; 125F3594834CD157 CRC64;

Query Match 81.8%; Score 36; DB 1; Length 403;
Best Local Similarity 85.7%; Pred No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
Db 323 LVGKPPF 329
i:|||||
-:|||||

RESULT 17
STK6_XENLA STANDARD; PRT; 407 AA.
AC Q91820;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine protein kinase Eg2 (EC 2.7.1.37) (pEg2) (p46Eg265).
GN EG2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.

to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
RA CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: Contains 4 PASTA domains.
CC -----
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CC -----
DR EMBL; AE014680; AAN24413.1;
DR InterPro; IPR005543; PASTA;
DR InterPro; IPR000719; Prot_kinase;
DR InterPro; IPR002290; Ser_thr_kinase;
DR InterPro; IPR001245; Tyr_kinase;
DR Pfam; PF03793; PASTA; 2;
DR Pfam; PF00069; pkinase; 1;
DR ProDom; PD000001; Prot_kinase; 1;
DR SMART; SM00240; PASTA; 4;
DR SMART; SM00220; S_TKc; 1;
DR SMART; SM00219; TyKc; 1;
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1;
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1;
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1;
KW Hypothetical protein; Transferase; Serine/threonine protein kinase;
KW ATP-binding; Repeat; Complete proteome;
FT DOMAIN 14 295 PROTEIN_KINASE;
FT DOMAIN 399 467 PASTA 1;
FT DOMAIN 468 536 PASTA 2;
FT DOMAIN 539 601 PASTA 3;
FT DOMAIN 602 666 PASTA 4;
FT DOMAIN 667 689 GLY_RICH;
FT NP_BIND 20 28 ATP (BY SIMILARITY);
FT BINDING 43 43 ATP (BY SIMILARITY);
FT ACT_SITE 146 146 BY SIMILARITY;
SQ SEQUENCE 690 AA; 72243 MW; 6A419EA9CED5D92D CRC64;

Query Match 91.8%; Score 36; DB 1; Length 690;
Best Local Similarity 75.0%; Pred. No 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY : MLLGKPPF 8
Db 217 MLLGRRFF 224

RESULT 20
HUPK_RHOCA
ID HUPK_RHOCA STANDARD; PRT; 294 AA.
AC E10797;
DT 01-JUL-1993 (Rel. 26, Created);
DT 01-JUL-1993 (Rel. 26, Last sequence update);
DT 14-OCT-2001 (Rel. 40, Last annotation update);
DE Hydrogenase expression/formation protein hupK.
GN HUPK.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulatus).
CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
CC Rhodobacteraceae; Rhodobacter.
CX NCBI_TaxID=10611;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91177833; PubMed=2007559;
RA Xu H.W., Wall J.D.;
RT "Clustering of genes necessary for hydrogen oxidation in Rhodobacter
capsulatus";
RL J. Bacteriol. 173:2401-2405(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 33303 / B10;

RX MEDLINE=93268090; PubMed=8497190;
RA Colbeau A., Richaud P., Toussaint B., Caballero F.J., Elster C.,
RA Delphin C., Smith R.L., Chabert J., Vignais P.M.;
RT "Organization of the genes necessary for hydrogenase expression in
RT Rhodobacter capsulatus. Sequence analysis and identification of two
RT hyp regulatory mutants";
RL Mol. Microbiol. 8:15-29(1993).
CC -!- SIMILARITY: BELONGS TO THE HUPK FAMILY.
CC -----
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CC -----
DR EMBL; M55089; AAA72924.1;
DR EMBL; Z15089; CAA78803.1;
DR PIR; S32947; S32947;
FT CONFLICT 70 70 A -> R (IN REF. 2).
SQ SEQUENCE 294 AA; 30222 MW; 2669E8B70AF35EDA CRC64;
Query Match 79.5%; Score 35; DB 1; Length 294;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY : MLLGKPP 7
Db 31 LLLGKPP 37
RESULT 21
KPC1_APLCA
ID KPC1_APLCA STANDARD; PRT; 649 AA.
AC Q16974;
DT 30-MAY-2000 (Rel. 39, Created);
DT 30-MAY-2000 (Rel. 39, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Calcium-dependent protein kinase C (EC 2.7.1.-) (APL I).
GN PRKC1.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthynura; Opisthobranchia; Anaspiidea;
OC Aplysioidae; Aplysiidae; Aplysia.
CX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91332620; PubMed=1869917;
RA Kruger K.E., Sossin W.S., Sacktor T.C., Bergold P.J., Beushausen S.,
RA Schwartz J.H.;
RT "Cloning and characterization of Ca(2+)-dependent and Ca(2+)-
RT independent PKCs expressed in Aplysia sensory cells";
RL J. Neurosci. 11:2303-2313(1991).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=93194877; PubMed=8449941;
RA Sossin W.S., Diaz-Arastia R., Schwartz J.H.;
RT "Characterization of two isoforms of protein kinase C in the nervous
RT system of Aplysia californica";
RL J. Biol. Chem. 268:5763-5768(1993).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98334636; PubMed=9668085;
RA Pepio A.M., Fan X., Sossin W.S.;
RT "The role of C2 domains in Ca2+-activated and Ca2+-independent protein
RT kinase Cs in aplysia";
RL J. Biol. Chem. 273:19040-19048(1998).
RN [4]
RP ERRATUM.
RA Pepio A.M., Fan X., Sossin W.S.;
RL J. Biol. Chem. 273:22856-22856(1998).
CC -!- FUNCTION: THIS IS CALCIUM-DEPENDENT, PHOSPHOLIPID-DEPENDENT,

CC SERINE- AND THREONINE-SPECIFIC ENZYME. ACTIVATION OF PKC BY
 CC SEROTONIN RESULTS IN PRESYNAPTIC FACILITATION OF DEPRESSED
 CC SENSORY-TO-MOTOR NEURON SYNAPSES, WHICH IS THOUGHT TO UNDERLIE
 CC BEHAVIORAL DISABILITIES.
 CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
 CC SIMILARITY).
 CC -!- ENZYME REGULATION: ACTIVATED BY PHOSPHATIDYL SERINE.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC; TRANSLOCATED TO NEURONAL
 CC MEMBRANES.
 CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol ester and DAG
 CC binding domains.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; Y94883; AAA27770.2; --
 CC HSSP; P05697; ITBN.
 CC InterPro; IPR000008; C2.
 CC InterPro; IPR002219; DAG_PE-bind.
 CC InterPro; IPR000961; Pkinase C.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00168; C2; 1.
 CC Pfam; PF00130; DAG_PE-bind; 2.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00433; pkinase C; 1.
 CC PRINTS; PR00360; C2DOMAIN.
 CC PRINTS; PR00008; DAGPEDOMAIN.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00109; C1; 2.
 CC SMART; SM00239; C2; 1.
 CC SMART; SM00133; S_TK_X; 1.
 CC SMART; SM00220; S_TKG; 1.
 CC PROSITE; PS00499; C2_DOMAIN_1; 1.
 CC PROSITE; PS00004; C2_DOMAIN_2; 1.
 CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
 CC PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC ATP-binding; Transferase; Serine/threonine-protein kinase;
 CC Phorbol-ester binding; Zinc; Repeat.
 CC DOMAIN 22 71 PHORBOL-ESTER AND DAG BINDING 1.
 CC DOMAIN 86 135 PHORBOL-ESTER AND DAG BINDING 2.
 CC DOMAIN 157 244 C2 DOMAIN.
 CC DOMAIN 320 578 PROTEIN KINASE.
 CC NP_BIND 326 334 ATP (BY SIMILARITY).
 CC BINDING 349 349 ATP (BY SIMILARITY).
 CC ACT_SITE 444 444 BY SIMILARITY.
 CC SEQUENCE 649 AA; 74079 MW; A53253399284E310 CRC64;
 Query Match 79.5%; Score 35; DB 1; Length 649;
 Best Local Similarity 75.0%; Pred. No. 29;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGKPPF 8
 Db 512 MLAGQPPF 519
 RESULT 22
 KPC1_LYTPI
 ID KPC1_LYTPI STANDARD; PRT; 658 AA.

AC Q25378;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protein kinase C (EC 2.7.1.-).
 GN PKC1.
 OS Lytechinus pictus (Painted sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinozoa; Echinacea; Temnopleuroidea; Toxopneustidae;
 OC Lytechinus.
 OX NCBI_TaxID=7653;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Rakow T.L., Shen S.S.;
 RT "Molecular cloning and characterization of protein kinase C from the
 RT sea urchin Lytechinus pictus";
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME (BY SIMILARITY).
 CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U02967; AAA03447.1; --
 CC HSSP; P05697; ITBN.
 CC InterPro; IPR000008; C2.
 CC InterPro; IPR002219; DAG_PE-bind.
 CC InterPro; IPR000961; Pkinase C.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC InterPro; IPR001245; Ty_pkinase.
 CC Pfam; PF00168; C2; 1.
 CC Pfam; PF00130; DAG_PE-bind; 2.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00433; pkinase C; 1.
 CC PRINTS; PR00360; C2DOMAIN.
 CC PRINTS; PR00008; DAGPEDOMAIN.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00109; C1; 2.
 CC SMART; SM00239; C2; 1.
 CC SMART; SM00133; S_TK_X; 1.
 CC SMART; SM00220; S_TKG; 1.
 CC PROSITE; PS00499; C2_DOMAIN_1; 1.
 CC PROSITE; PS00004; C2_DOMAIN_2; 1.
 CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
 CC PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC ATP-binding; Transferase; Serine/threonine-protein kinase;
 CC Phorbol-ester binding; Zinc; Repeat.
 CC DOMAIN 28 77 PHORBOL-ESTER AND DAG BINDING 1.
 CC DOMAIN 93 142 PHORBOL-ESTER AND DAG BINDING 2.
 CC DOMAIN 164 251 C2 DOMAIN.
 CC DOMAIN 325 583 PROTEIN KINASE.
 CC NP_BIND 331 339 ATP (BY SIMILARITY).
 CC BINDING 354 354 ATP (BY SIMILARITY).
 FT


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FT ACT_SITE 449 449 BY SIMILARITY.
SQ SEQUENCE 658 AA; 74871 MW; 74B5A27A49C835A2 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 658;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 517 MLAGQPPF 524

RESULT 23
KPCA_BOVIN STANDARD; PRT; 672 AA.
AC P04429;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP TISSUE=Brain;
RC SEQUENCE FROM N.A.
RX MEDLINE=86289425; PubMed=3755547;
RA Parker P.J., Coussens L., Tonks N., Rhee L., Young S., Chen E.,
RA Stabel S., Waterfield M.D., Ullrich A.;
RT "The complete primary structure of protein kinase C... the major
RT phorbol ester receptor.";
RL Science 233:853-859(1986).
RN [2]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
RT for cellular regulation.";
RL Nature 334:661-665(1988).
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
CC serine and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a (phosphoprotein).
CC -!- SUBUNIT: Interacts with PRKCBP (by similarity).
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.

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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBL; M13973; AAA30706.1; -
PIR; A00621; KIBOC.
HSSP; P05697; ITBN.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Kinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
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DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 672 AA; 76837 MW; 97BF46DB80FCF21A CRC64;

Query Match 79.5%; Score 35; DB 1; Length 672;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 531 MLAGQPPF 538

RESULT 24
KPCA_HUMAN STANDARD; PRT; 672 AA.
AC P17252; Q15137; Q96RE4;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA OR PKCA OR PRKACA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=90245676; PubMed=2336401;
RA Finkenzeller G., Marne D., Hug H.;
RT "Sequence of human protein kinase C alpha.";
RL Nucleic Acids Res. 18:2183-2183(1990).
RN [2]
RP SEQUENCE OF 15-445 FROM N.A.
RX MEDLINE=91332033; PubMed=1714454;
RA McSwine-Kennick R.L., McKeegan E.M., Johnson M.D., Morin M.J.;
RT "Phorbol diester-induced alterations in the expression of protein
RT kinase C isozymes and their mRNAs. Analysis in wild-type and phorbol
RT diester-resistant HL-60 cell clones.";
RL J. Biol. Chem. 266:15135-15143(1991).
RN [3]
RP SEQUENCE OF 1-57 FROM N.A.
RA Haridas V., Hackenbruck C., Glazer R.I.;
RT "Homo sapiens protein kinase C alpha 5-flanking sequence.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
```

serine- and threonine-specific enzyme.
FUNCTION: PKC is activated by diacylglycerol which in turn phosphorylates a range of cellular proteins. PKC also serves as the receptor for phorbol esters, a class of tumor promoters.
CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
SUBUNIT: Interacts with PRKCABP (By similarity).
SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.
SIMILARITY: Contains 1 C2 domain.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
PKC SUBFAMILY.

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EMBL; X52479; CAA36718.1; -
EMBL; M22199; AAA60098.1; -
EMBL; AF395829; AAK84184.1; -
PIR; SC9496; KIHJCA.
HSSP; PC4410; 1A25.
Genew; HGNC:9393; PRKCA.
MIM; 176960; -
GO; GO:0005624; Membrane fraction; TAS.
GO; GO:0004697; F:protein kinase C activity; TAS.
GO; GO:0008624; P:induction of apoptosis by extracellular sig. . . ; TAS.
GO; GO:0000074; P:regulation of cell cycle; TAS.
InterPro; IPR000008; C2.
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR00719; Prot_kinase.
InterPro; IPR002290; Ser_thr_kinase.
Pfam; PF00168; C2; 1.
Pfam; PF00130; DAG_PE-bind; 2.
Pfam; PF00369; pkinase; 1.
Pfam; PF00433; pkinase_C; 1.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00008; DAGPEDOMAIN.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00109; C1; 2.
SMART; SM00239; C2; 1.
SMART; SM00133; S_TK_X; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00499; C2_DOMAIN_1; 1.
PROSITE; PS00334; C2_DOMAIN_2; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS00381; DAG_PE_BIND_DOM_2; 2.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MCD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MCD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CONFLICT 50 50 C -> S (IN REF. 2).
SQ SEQUENCE 672 AA; 76764 MW; 8780D35C386C12DA CRC64;

Query Match 79.5%; Score 35; DB 1; Length 672;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
Db 531 MLAGQPPF 538
RESULT 25
KPCA_MOUSE
ID KPCA_MOUSE STANDARD; PRT; 672 AA.
AC P20444;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA OR PKCA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232737; PubMed=2469625;
RA Rose-John S., Dietrich A., Marks F.;
RT "Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss 3T3 fibroblasts";
RL Gene 74:465-471(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C; TISSUE=Brain;
RX MEDLINE=90098082; PubMed=2601739;
RA Megidish T., Mazurek N.;
RT "A mutant protein kinase C that can transform fibroblasts";
RL Nature 342:807-811(1989).
RN [3]
RP INTERACTION WITH PRKCABP.
RX MEDLINE=95146534; PubMed=7844141;
RA Staudinger J., Zhou J., Burgess R., Elledge S.J., Olson E.N.;
RT "PICK1: A perinuclear binding protein and substrate for protein kinase C isolated by the yeast two-hybrid system";
RL J. Cell Biol. 128:263-271(1995).
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn phosphorylates a range of cellular proteins. PKC also serves as the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with PRKCABP.
CC -!- DISEASE: Expression of the mutant form UV25 causes malignant transformation of cells.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.

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EMBL; M25811; AAA39934.1; ALT_SEQ.
EMBL; X52685; CAA36908.1; -
EMBL; X52684; CAA36907.1; -
PIR; S07104; KIMSCA.
HSSP; P04410; 1A25.
DR MGD; MGI:97595; Prkca.
DR GO; GO:0004698; F:calcium dependent protein kinase C activity; IDA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.

```

DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PRO0360; C2DOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Calcium-binding; Repeat; ATP-binding; Transferase;
DR Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
DR Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARIANT 106 106 S -> V (IN MUTANT FORM JV25).
FT VARIANT 111 111 S -> G (IN MUTANT FORM JV25).
FT VARIANT 240 240 L -> Q (IN MUTANT FORM JV25).
FT VARIANT 339 339 F -> I (IN MUTANT FORM JV25).
FT CONFLICT 147 147 D -> V (IN REF. 2).
FT CONFLICT 218 218 N -> T (IN REF. 2).
FT CONFLICT 277 278 AH -> A (IN REF. 2).
FT CONFLICT 313 313 V -> A (IN REF. 2).
FT CONFLICT 467 467 N -> D (IN REF. 2).
FT CONFLICT 472 472 N -> D (IN REF. 2).
FT CONFLICT 576 576 Q -> H (IN REF. 2).
SQ SEQUENCE 672 AA; 76852 MW; 394B48C95B56D50 CRC64.

Query Match: 79.5%; Score 35; DB 1; Length 672;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY : MLGKPPF 8
Db 531 MLGKPPF 538

RESULT 26
KPCA_RABIT
ID KPCA_RABIT STANDARD; PRT: 672 AA.
AC P10102;
DT 01-MAR-1989 (Rel. 10, Created);
DT 01-MAR-1989 (Rel. 10, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC alpha) (PKC-A).
GN PRKCA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CX NCBI_TaxID=9986;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97115883; PubMed=3838073;
RA Chuo S., Kawasaki H., Imajoh S., Suzuki K., Inagaki M., Yokokura H.,
RA Sakoh T., Hidaka H.;
RT "Tissue-specific expression of three distinct types of rabbit protein
kinase C.";
RL Nature 325:161-166(1987).
RN [2]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
for cellular regulation.";
RL Nature 334:661-665(1988).
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
serine- and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
phosphorylates a range of cellular proteins. PKC also serves as
the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with PRKCABP (By similarity).
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X04796; CAA28483.1; -.
DR PIR; C26037; KIRBC.
DR HSSP; P04410; 1A25.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PRO0360; C2DOMAIN.
DR PRINTS; PRO0008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARIANT 106 106 S -> V (IN MUTANT FORM JV25).
FT VARIANT 111 111 S -> G (IN MUTANT FORM JV25).
FT VARIANT 240 240 L -> Q (IN MUTANT FORM JV25).
FT VARIANT 339 339 F -> I (IN MUTANT FORM JV25).
FT CONFLICT 147 147 D -> V (IN REF. 2).
FT CONFLICT 218 218 N -> T (IN REF. 2).
FT CONFLICT 277 278 AH -> A (IN REF. 2).
FT CONFLICT 313 313 V -> A (IN REF. 2).
FT CONFLICT 467 467 N -> D (IN REF. 2).
FT CONFLICT 472 472 N -> D (IN REF. 2).
FT CONFLICT 576 576 Q -> H (IN REF. 2).
SQ SEQUENCE 672 AA; 76782 MW; 3D11367D3577A77 CRC64;
Query Match: 79.5%; Score 35; DB 1; Length 672;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY : MLGKPPF 8
| : |||
Db 531 MLGQPPF 538

RESULT 27
KPCA_RAT
ID KPCA_RAT STANDARD; PRT; 672 AA.
AC P05696;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PKCA OR PKCA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88262515; PubMed=3387228;
RA Ono Y., Fujii T., Igarashi K., Kikkawa U., Ogita K., Nishizuka Y.,
RT "Nucleotide sequences of cDNAs for alpha and gamma subtypes of rat
brain protein kinase C.";
RI Nucleic Acids Res. 16:5199-5200(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
EX MEDLINE=88330055; PubMed=3666147;
RA Kikkawa U., Ogita K., Ono Y., Asaoka Y., Shearman M.S., Fujii T.,
RA Ase K., Sekiguchi K., Igarashi K., Nishizuka Y.,
RT "The common structure and activities of four subtypes of rat brain
protein kinase C family.";
RI FEBS Lett. 223:212-216(1987).
RN [3]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.,
RT "The molecular heterogeneity of protein kinase C and its implications
for cellular regulation.";
RI Nature 334:661-665(1988).
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
serine- and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
phosphorylates a range of cellular proteins. PKC also serves as
the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein + H₂O -> a phosphoprotein.
CC -!- SUBUNIT: Interacts with PKCAIP1 by similarity.
CC -!- SIMILARITY: Contains 2 zinc dependent phorbol ester and DAG
binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; X07286; CAA30266.1; -
DR PIR; S02248; KIRTC.
DR PDB; IDSY; 26-CAN-00.
DR InterPro; IPR000308; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; PKinase_C.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00168; C2; 1.

DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation; 3D-structure.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 672 AA; 76792 MW; 94889E7339C17719 CRC64;
Query Match 79.5%; Score 35; DB 1; Length 672;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY : MLGKPPF 8
| : |||
Db 531 MLGQPPF 538

RESULT 28
KPCG_BOVIN
ID KPCG_BOVIN STANDARD; PRT; 682 AA.
AC P05128;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma) (Fragment).
GN PRKCG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86289426; PubMed=3755548;
RA Coussens L., Parker P.J., Rhee L., Yang-Feng T.L., Chen E.,
RA Waterfield M.D., Francke U., Ullrich A.,
RT "Multiple, distinct forms of bovine and human protein kinase C
suggest diversity in cellular signaling pathways.";
RI Science 233:859-866(1986).
RN [2]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.,
RT "The molecular heterogeneity of protein kinase C and its implications
for cellular regulation.";
RI Nature 334:661-665(1988).
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS


```
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M13976; AAA30704.1;
CC PIR: C24664; KIBGGC.
CC HSSP: P05697; ITBN.
CC InterPro: IPR000008; C2.
CC InterPro: IPR002219; DAG_PE-bind.
CC InterPro: IPR000962; Pkinase_C.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF00168; C2; 1.
CC Pfam: PF00130; DAG_PE-bind; 2.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF0433; pkinase_C; 1.
CC PRINTS: PR00360; C2DOMAIN.
CC PRINTS: PR00008; DAGPEDOMAIN.
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00109; C1; 2.
CC SMART: SM00139; C2; 1.
CC SMART: SM00133; S_TK_X; 1.
CC SMART: SM00220; S_TK; 1.
CC PROSITE: PS00499; C2_DOMAIN_1; 1.
CC PROSITE: PS00004; C2_DOMAIN_2; 1.
CC PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
CC PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
CC PROSITE: PS00011; PROTEIN_KINASE_DOM_1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST_1.
CC Calcium-binding; Repeat: ATP-binding; Transferase;
CC Serine/threonine-protein kinase; Phorbol ester binding; Kinase;
CC Phosphorylation.
CC NON_TER 1 70 PHORBOL ESTER AND DAG BINDING 1
CC DOMAIN 21 70 PHORBOL ESTER AND DAG BINDING 1
CC DOMAIN 86 135 PHORBOL ESTER AND DAG BINDING 1
CC DOMAIN 155 245 C2 DOMAIN
CC DOMAIN 336 599 PROTEIN KINASE
CC NF_BIND 342 350 ATP (BY SIMILARITY)
CC BINDING 365 365 ATP (BY SIMILARITY)
CC ACT_SITE 465 465 HY SIMILARITY
CC MOD_RES 633 633 PHOSPHORYLATION (AUTO) (POTENTIAL)
CC MOD_RES 640 640 PHOSPHORYLATION (AUTO) (POTENTIAL)
CC SEQUENCE 682 AA; 77156 MW; 20392D11B8C731C CF; 64.
CC -----
CC Query Match 79.5%; Score 150; DB 1; Length 682;
CC Best Local Similarity 75.0%; Pred. No. 11;
CC Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC : MLJGKPPF 8
CC : |||
CC 533 MLAQPPF 540
CC -----
CC RESULT 29
CC KPCG HUYN
CC ID KPCG HUYN STANDARD; P57; 447 AA.
CC P05129;
CC 13-AUG-1987 (Rel. 05, Created.
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DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma).
GN PKCG OR PKCG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cui W.C., Yu L., Chu Y.Y., Wang J., Zheng L.H., Zhou G.J., Zhao S.Y.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-318 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=86289426; PubMed=3755548;
RA Coussens L., Parker P.J., Rhee L., Yang-Feng T.L., Chen E.,
RA Waterfield M.D., Francke U., Ullrich A.;
RT "Multiple, distinct forms of bovine and human protein kinase C
RL suggest diversity in cellular signaling pathways.";
RN [3]
RP SEQUENCE OF 162-697 FROM N.A.
RC TISSUE=Hippocampus;
RX MEDLINE=93387312; PubMed=8375396;
RA Kochs G., Meyer D., Hug H., Marne D., Sarre T.F.;
RT "Activation and substrate specificity of the human protein kinase C
RL alpha and zeta isoenzymes.";
RN [4]
RP VARIANTS CYS-141; GLN-415; ASP-523 AND SER-659.
RX MEDLINE=98213587; PubMed=9545390;
RA Al-Maghteh M., Vilhena E.N., Inghearn C.F., Moore T., Bird A.C.,
RA Bhattacharya S.S.;
RT "Segregation of a PKCG mutation in two RPL1 families.";
RL Am. J. Hum. Genet. 62:1248-1252(1998).
RN [5]
RP SHOWS THAT THE VARIANTS ARE NOT A CAUSE OF RPL1.
RX MEDLINE=99375047; PubMed=10441600;
RA Dryja T.P., McEvoy J., McGee T.L., Berson E.L.;
RT "No mutations in the coding region of the PKCG gene in three families
RL with retinitis pigmentosa linked to the RPL1 locus on chromosome
RN 19q.";
RX Am. J. Hum. Genet. 65:926-928(1999).
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -!- DATABASE: NAME=Mutations of the PKCG gene;
CC NOTE=Retina International's Scientific Newsletter;
CC WWW=http://www.retina-international.com/sci-news/prkcgmut.htm.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF345987; AAK13533.1;
CC EMBL: M13977; AAA60102.1; ALT_TERM.
CC EMBL: Z15114; CAA78920.1;
CC PIR: D24664; D24664.
CC HSSP: P05697; ITBN.
CC Genew: HGNC:9402; PRKCG.
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DR MIM; 176980; -
DR GO; GO:00024697; F:protein kinase C activity; TAS.
DR GO; GO:0002468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR000208; C2.
DR InterPro; IPR002219; DAG_PE_bind.
DR InterPro; IPR000961; PKinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR032290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE_bind; 2.
DR Pfam; PF00069; pk_inase; 1.
DR Pfam; PF00433; pk_inase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPECDOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase.
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation; Polymorphism.
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT DOMAIN 351 614 PROTEIN KINASE.
FT NP_BIND 357 365 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARIANT 141 141 R -> C.
FT VARIANT 415 415 /FTID=VAR_008755.
FT VARIANT 523 523 /FTID=VAR_008756.
FT VARIANT 653 653 A -> D.
FT VARIANT 653 653 /FTID=VAR_008757.
FT SEQUENCE 697 AA; 78447 MW; 3F91E5EEF13C41 IR 1.4;
Query Match 79.5%; Score 35; DB 1; Length 697;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
Db 548 MLAGQPPF 555
RESULT 30
KPCG_MOUSE
ID KPCG_MOUSE STANDARD; PRT; 697 AA.
AC P05697;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. C9, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma)
GN PRKCG OR PKCG OR PRKCC OR PKCC.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID:10090, 10116;
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RM
RP
RC SEQUENCE FROM N.A.
RX SPECIES=Rat; TISSUE=Brain;
RX MEDLINE=88262515; PubMed=3387228;
RA Ono Y., Fujii T., Igarashi K., Kikkawa U., Ogita K., Nishizuka Y.;
RT "Nucleotide sequences of cDNAs for alpha and gamma subspecies of rat
RL brain protein kinase C.";
RL Nucleic Acids Res. 16:5199-5200(1988).
RN
RP SEQUENCE FROM N.A.
RC SPECIES=Rat;
RX MEDLINE=86272097; PubMed=3755379;
RA Knopf J.L., Lee M.-H., Sultzman L.A., Kriz R.W., Loomis C.R.,
RA Hewick R.M., Bell R.M.;
RT "Cloning and expression of multiple protein kinase C cDNAs.";
RL Cell 46:491-502(1986).
RN
RP SEQUENCE OF 1-56 FROM N.A.
RC SPECIES=Rat;
RX MEDLINE=91060619; PubMed=2246272;
RA Chen K.H., Widen S.G., Wilson S.H., Huang K.P.;
RT "Characterization of the 5'-flanking region of the rat protein kinase
RL C gamma gene.";
RL J. Biol. Chem. 265:19961-19965(1990).
RN
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; TISSUE=Brain;
RX MEDLINE=93154595; PubMed=8428669;
RA Bowers B.J., Parham C.L., Sikela J.M., Wehner J.M.;
RT "Isolation and sequence of a mouse brain cDNA coding for protein
RL kinase C-gamma isozyme.";
RL Gene 123:263-265(1993).
RN
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=BALB/c; TISSUE=Brain;
RA Tseng C.P., Verma A.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN
RP STRUCTURE BY NMR OF 91-172.
RC SPECIES=Rat;
RX MEDLINE=97419134; PubMed=9271501;
RA Xu R.X., Pawelczyk T., Xia T.-H., Brown S.C.;
RT "NMR structure of a protein kinase C-gamma phorbol-binding domain and
RL study of protein-lipid micelle interactions.";
RL Biochemistry 36:10709-10717(1997).
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
-----
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EMBL; X07287; CAA30267.1; -
EMBL; M13707; AAA41874.1; -
EMBL; M55417; AAA41873.1; -
EMBL; X67129; CAA47608.1; -
EMBL; L28035; AAA39939.1; -
PIR; A05105; K1RTGC.
PIR; JN0548; JN0548.
PDB; 1TBN; 29-APR-98.
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DR PDB; 1TBO; 29-APR-98.
DR MGD; MG1:97597; Prkcc.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00369; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00160; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00138; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation; 3D-structure.
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT DOMAIN 351 614 PROTEIN KINASE.
FT NP_BIND 357 365 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT STRAND 103 105
FT STRAND 113 113
FT STRAND 120 120
FT STRAND 123 124
FT STRAND 129 131
FT TURN 132 134
FT STRAND 137 138
FT TURN 140 145
SQ SEQUENCE 697 AA; 78357 MW; 54861A4943423F V0.14;
Query Match 79.5%; Score 35; DB 1; Length 697;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
CB 548 MLAGQPPF 555
RESULT 31
KPCG_RABBIT STANDARD; PRT; 597 AA.
AC P10829;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma) (PKC-delta).
GN PRKCC.
OS Cryptolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cryptolagus.
OX NCBI_TaxID=9986;
RN 1.
RP SEQUENCE FROM N.A.
```

```
RX MEDLINE=88241036; PubMed=2837282;
RA Ohno S., Kawasaki H., Konno Y., Inagaki M., Hidaka H., Suzuki K.;
RT "A fourth type of rabbit protein kinase C.";
RL Biochemistry 27:2083-2087(1988).
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M19338; AAA31449.1; -
DR PIR; A28708; KIRBGC.
DR HSSP; P05697; 1TBN.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00138; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT DOMAIN 351 614 PROTEIN KINASE.
FT NP_BIND 357 365 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT STRAND 103 105
FT STRAND 113 113
FT STRAND 120 120
FT STRAND 123 124
FT STRAND 129 131
FT TURN 132 134
FT STRAND 137 138
FT TURN 140 145
SQ SEQUENCE 697 AA; 78371 MW; 925D22221F78E5BF CRC64;
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Query Match 79.5%; Score 35; DB 1; Length 697;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
CB 548 MLAGQPPF 555
```

```
RESULT 32
MK12 BRARE STANDARD; PRT; 363 AA.
AC 042376;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Mitogen-activated protein kinase 12 (EC 2.7.1.37) -Stress activated
DE protein kinase-3).
DE MAPK12 OR SAPK3.
GN Brachydanio rerio (Zebrafish) (Danio rerio).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Somatic embryo;
RA Goedert M.;
RU Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
CC -! FUNCTION: Responds to activation by environmental stress and pro-
CC inflammatory cytokines by phosphorylating downstream targets (By
CC similarity).
CC -! CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -! COFACTOR: Magnesium (By similarity).
CC -! ENZYME REGULATION: Activated by threonine and tyrosine
CC phosphorylation (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC
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CC or send an email to license@sb-slb.ch).
CC
CC EMBL; Y15075; CAA75355.1;
CC HSSP; Q16539; 1WFC.
CC
CC ZFIN; ZDB-GENE-990415-257; sapk3.
CC GO; GO:0005737; Cytoplasm; ISS.
CC GO; GO:0016910; F:SAP kinase 3; ISS.
CC GO; GO:0000169; P:MAPKKK cascade; ISS.
CC InterPro; IPR003527; MAP_kin.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKC_1.
CC PROSITE; PS01351; MAPK; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
CC ATP-binding; Transferase; Serine/threonine-protein kinase;
KW Phosphorylation.
KW DOMAIN 25 309 PROTEIN KINASE.
FT NP_BIND 31 39 ATP (BY SIMILARITY).
FT BINDING 54 54 ATP (BY SIMILARITY).
FT ACT_SITE 151 151 BY SIMILARITY.
FT MOD_RES 181 181 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT (BY SIMILARITY).
FT MOD_RES 183 183 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT (BY SIMILARITY).
CC SEQUENCE 363 AA; 41970 MW; 81B06D414254EFBF CRC64;
Query Match: 77.3%; Score 34; DB 1; Length 363;
Best Local Similarity 87.5%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 MLLGKPPF 8
Db 217 MLLGKPLF 224

RESULT 33
K6B2 HUMAN STANDARD; PRT; 482 AA.
AC Q9UBS0; O94809; Q9UEC1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribosomal protein S6 kinase beta 2 (EC 2.7.1.-) (S6K-beta 2) (70 kDa
DE ribosomal protein S6 kinase 2) (p70-S6KB) (p70 ribosomal S6 kinase
DE beta) (p70 S6Kbeta) (S6K2) (S6 kinase-related kinase) (SRK)
DE (Serine/threonine-protein kinase 14 beta).
GN RPS6KB2 OR STK14B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99023916; PubMed=9804755;
RA Gout I., Minami T., Hara K., Tsujishita Y., Filonenko V.,
RA Waterfield M.D., Yonezawa K.;
RT "Molecular cloning and characterization of a novel p70 S6 kinase, p70
RT S6 kinase beta containing a proline-rich region.";
RL Biochem. Biophys. Res. Commun. 253:470-476(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99097259; PubMed=9878560;
RA Saitoh M., ten Dijke P., Miyazono K., Ichijo H.;
RT "Cloning and characterization of p70 S6Kbeta defines a novel family of
RT p70 S6 kinases.";
RL Biochem. Biophys. Res. Commun. 253:470-476(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99422045; PubMed=10490847;
RA Lee-Fruman K.K., Kuo C.J., Lippincott J., Terada N., Bienen J.;
RT "Characterization of S6K2, a novel kinase homologous to S6K1.";
RN [4]
RP SEQUENCE FROM N.A.
RA Koh H.J., Lee B.N., Choi H.S., Chung J.;
RT "Cloning and characterization of a novel S6 kinase-related kinase,
RT SRK.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.C., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -! FUNCTION: PHOSPHORYLATES SPECIFICALLY RIBOSOMAL PROTEIN S6.
```

CC : SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC S6 KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AB016869; BAA34402.1; ALT INIT;
 CC EMBL; AB019245; BAA37145.1;
 CC EMBL; AF076931; AAD46063.1;
 CC EMBL; AF099739; AAD20990.1;
 CC EMBL; BC000394; AAH00094.1;
 CC EMBL; JE0377; JE0377;
 CC HSSP; Q63450; 1A06.
 CC Genew; HGNC:10437; RPS6KB2.
 CC GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
 CC GO; GO:0006412; F:protein biosynthesis; TAS.
 CC GO; GO:000074; P:regulation of cell cycle; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR000961; Pkinase_C.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00369; pkinase; 1.
 CC Pfam; PF00433; pkinase_C; 1.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00133; S_TK_X; 1.
 CC SMART; SM00220; S_TKC; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC Transferrase; Serine/threonine protein kinase; Phosphorylation;
 CC ATP-binding.
 CC FT DOMAIN 67 328 PROTEIN KINASE.
 CC FT DOMAIN 411 482 PRO-RICH.
 CC FT NP BIND 73 81 ATP (BY SIMILARITY).
 CC FT BINDING 99 99 ATP (BY SIMILARITY).
 CC FT ACT SITE 194 194 BY SIMILARITY.
 CC FT CONFLICT 409 409 R -> C (IN REF. 2).
 CC FT CONFLICT 420 420 V -> A (IN REF. 2).
 CC SEQUENCE 482 AA; 53483 MW; 5D2C691F24A2D0A9 CRC64;
 Query Match: 77.3%; Score 34; DB 1; Length 485;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPF 8
 DB 262 MLTGSPPF 269
 RESULT 34
 K6B2 MOUSE
 ID K6B2_MOUSE STANDARD; PRT; 485 AA.
 AC Q921M4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribosomal protein S6 kinase beta 2 (p70-S6K2) (p70 ribosomal S6 kinase
 DE ribosomal protein S6 kinase 2) (p70-S6K2).
 DE beta1 (p70 S6Kbeta) (S6K2).
 GN RPS6KB2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN 1;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99043870; PubMed=9822608;

RA Shima H., Pende M., Chen Y., Fumagalli S., Thomas G., Kozma S.C.;
 RT "Disruption of the p70(s6k)/p85(s6k) gene reveals a small mouse
 RL EMBO J. 17:6649-6659(1998).
 CC -!- FUNCTION: PHOSPHORYLATES SPECIFICALLY RIBOSOMAL PROTEIN S6.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC S6 KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AJ007938; CAA07774.1;
 CC HSSP; Q63450; 1A06.
 CC MGD; MGI:1927343; Rps6kb2.
 CC InterPro; IPR000961; Pkinase_C.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00433; pkinase_C; 1.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00133; S_TK_X; 1.
 CC SMART; SM00220; S_TKC; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC Transferrase; Serine/threonine protein kinase; Phosphorylation;
 CC ATP-binding.
 CC KW DOMAIN 67 328 PROTEIN KINASE.
 CC FT DOMAIN 411 485 PRO-RICH.
 CC FT NP BIND 73 81 ATP (BY SIMILARITY).
 CC FT BINDING 99 99 ATP (BY SIMILARITY).
 CC FT ACT SITE 194 194 BY SIMILARITY.
 CC SEQUENCE 485 AA; 53538 MW; 396929ADAB0F6CB6 CRC64;
 Query Match: 77.3%; Score 34; DB 1; Length 485;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MLLGKPPF 8
 DB 262 MLTGSPPF 269
 RESULT 35
 KDC2 DROME
 ID KDC2_DROME STANDARD; PRT; 502 AA.
 AC P16912;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein kinase DC2 (EC 2.7.1.1).
 GN PKA-C3 OR DC2.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7227;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=89107990; PubMed=3215511;
 RA Kalderon D., Rubin G.M.;
 RT "Isolation and characterization of Drosophila camp-dependent protein
 RT kinase genes".
 RJ Genes Dev. 2:1539-1556(1988).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- TISSUE SPECIFICITY: MORE ABUNDANT IN ADULT HEAD THAN ADULT BODY.
 CC -!- DEVELOPMENTAL STAGE: IN EMBRYONS, PUPAE AND ADULTS.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMP SUBFAMILY.
CC
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CC
CC EMBL: X16961; CAA34835.1; -
CC HSP; P05132; IATP.
CC FlyBase: FBgr0000499; Pka-C3.
CC GO: GO:0008602; F: CAMP-dependent protein kinase, catalyst act. ; IDA.
CC GO: GO:0006468; P: protein amino acid phosphorylation; IDA.
CC InterPro: IPR000961; Pkinase_C.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002293; Ser_thr_kinase.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF00433; Pkinase_C; 1.
CC PRINTS: PR00129; TYRKINASE.
CC PRODOM: PD000001; Prot_kinase; 1.
CC SMART: SM00133; S_TK_X; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
CC Transferrase: Serine/threonine-protein kinase; ATP-binding.
CC DOMAIN 193 447 PROTEIN_KINASE.
CC NP_BIND 193 207 ATP (BY SIMILARITY).
CC BINDING 222 222 ATP (BY SIMILARITY).
CC ACT_SITE 316 316 BY SIMILARITY.
CC SEQUENCE 502 AA: 56960 MW: 646440.910 CR064;

CC Query Match 77.3% Score 147 DB 17 Length 502;
CC Best Local Similarity 75.0% Pred. No. 35;
CC Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CC QY : MLVGKPPF 8
CC 38: MLVGYPFF 388

CC RESULT 16
CC PERF HUMAN STANDARD; PRT: 100 AA.
CC AC P14227
CC DT 01-JAN-1990 (Rel. 13, Created)
CC DT 01-APR-1990 (Rel. 14, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Perforin 1 precursor (P1) (Lymphocyte pore forming protein) (PFP)
CC DE (Cytolysin).
CC GN PFP.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumecostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CC CX NCBI_TaxID=9606;
CC RN [1]
CC SEQUENCE FROM N.A.
CC RX MEDLINE=90079042; PubMed=2480391;
CC RA Lichtenheld M.G., Podack E.R.;
CC RT "Structure of the human perforin gene. A simple gene organization
CC with interesting potential regulatory sequences."
CC J. Immunol. 143:4267-4274(1989).
CC
CC SEQUENCE FROM N.A.
CC RX MEDLINE=88334728; PubMed=3419519;
CC RA Lichtenheld M.G., Olsen K.J., Lu P., Lowry D.M., Hargrett A.,
CC RA Hargreth-Neale M., Podack E.R.;
CC RT "Structure and function of human perforin."
CC Nature 335:448-451(1988).

RN
RX SEQUENCE FROM N.A.
RX MEDLINE=90077533; PubMed=2592021;
RA Shinkai Y., Yoshida C.M., Maeda K., Kobata T., Maruyama K.,
RA Yodoi J., Yagita H., Okumura K.;
RT "Molecular cloning and chromosomal assignment of a human perforin
RT (PFP) gene."
RL Immunogenetics 30:452-457(1989).
RN [4]
RN SEQUENCE OF 520-555 FROM N.A., AND INDUCTION.
RC TISSUE=Natural killer cells;
RX MEDLINE=96265183; PubMed=8676885;
RA Goebel W.S., Schleimer R.H., Brahma Z.;
RT "Target cell-induced perforin mRNA turnover in NK3.3 cells is mediated
RT by multiple elements within the mRNA coding region."
RL Mol. Immunol. 33:341-349(1996).
RN [5]
RN 3D-STRUCTURE MODELING OF MEMBRANE-SPANNING DOMAIN (MSD).
RX MEDLINE=90370039; PubMed=2395434;
RA Peitsch M.C., Amiguet P., Guy R., Brunner J., Maizel J.V. Jr.,
RA Tschoopp J.;
RT "Localization and molecular modelling of the membrane-inserted domain
RT of the ninth component of human complement and perforin."
RL Mol. Immunol. 27:589-602(1990).
RN [6]
RN VARIANTS HPLH2 GLY-183; TRP-225; SER-252; TYR-279; LEU-345 AND
RX GLU-429.
RX MEDLINE=20050957; PubMed=10583959;
RA Stepp S.E., Dufourcq-Lageolouse R., Le Deist F., Bhawan S., Certain S.,
RA Mathew P.A., Henter J.-I., Bennett M., Fischer A., de Saint Basile G.,
RA Kumar V.;
RT "Perforin gene defects in familial hemophagocytic
RT lymphohistiocytosis."
RL Science 286:1957-1959(1999).
RN [7]
RN VARIANTS HPLH2 MET-50; ASP-224 AND LYS-285 DEL.
RX MEDLINE=21090530; PubMed=11179007;
RA Goeransdotter Ericson K., Fadeel B., Nilsson-Ardnor S.,
RA Soederhaell C., Samuelsson A., Janka G., Schneider M., Guerguey A.,
RA Yalman N., Revesz T., Egeler R., Jahnukainen K., Storm-Mathiesen I.,
RA Haraldsson A., Poole J., de Saint Basile G., Nordenskjold M.,
RA Henter J.-I.;
RT "Spectrum of perforin gene mutations in familial hemophagocytic
RT lymphohistiocytosis."
RL Am. J. Hum. Genet. 68:590-597(2001).
CC -1- FUNCTION: IN THE PRESENCE OF CALCIUM, PERFORIN POLYMERIZES INTO
CC TRANSMEMBRANE TUBULES AND IS CAPABLE OF LYSING NON-SPECIFICALLY
CC A VARIETY OF TARGET CELLS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES OF CYTOLYTIC
CC T-LYMPHOCYTES.
CC -1- INDUCTION: Repressed by contact with target cells.
CC -1- DISEASE: Defects in PFP1 are a cause of familial hemophagocytic
CC lymphohistiocytosis type 2 (HPLH2) [MIM:603553], also known as
CC FHL. HPLH2 is a rare and lethal autosomal recessive disorder of
CC early childhood characterized by excessive immune activation.
CC Patients have a nonmalignant accumulation and multivisceral
CC infiltration of activated T lymphocytes and histiocytes
CC (macrophages).
CC -1- SIMILARITY: TO COMPLEMENT FACTORS C6, C7, C8, AND C9.
CC -1- SIMILARITY: Contains 1 C2 domain.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC
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CC
CC EMBL: M31951; AAA60167.1;
CC EMBL: X3224; CAA31612.1;
CC EMBL: M28193; AAA60065.1;
CC
CC DR M31951; AAA60167.1;
CC DR X3224; CAA31612.1;
CC DR M28193; AAA60065.1;

DR EMBL: L40557; AAA63618.1; ...
 DR PIR: A45816; A37181.
 DR Genew: HGNC:9360; PRF1.
 DR MIM: 170280; ...
 DR MIM: 603553; ...
 DR GO: GO:0015469; P-channel-forming toxin activity; TAS.
 DR GO: GO:0006968; P:cellular defense response; TAS.
 DR InterPro: IPR000608; C2.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR001862; MAC_perforin.
 DR Pfam: PF0168; C2; 1.
 DR Pfam: PF01823; MACPF; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00457; MACPF; 1.
 DR PROSITE: PS00279; MAC_PERFORIN; 1.
 DR PROSITE: PS00022; EGF_1; FALSE_NEG.
 DR PROSITE: PS01186; EGF_2; FALSE_NEG.
 DR PROSITE: PS00499; C2_DOMAIN_1; 1.
 DR PROSITE: PS00094; C2_DOMAIN_2; 1.
 KW Glycoprotein; Transmembrane; Cytolysis; Calcium binding; Signal;
 KW EGF-like domain; T-cell; Disease mutation; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 555 PERFORIN 1.
 FT TRANSMEM 188 204 POTENTIAL.
 FT TRANSMEM 212 231 POTENTIAL.
 FT DOMAIN 373 408 EGF-LIKE.
 FT DOMAIN 416 498 C2 DOMAIN.
 FT DISULFID 257 279 BY SIMILARITY.
 FT CARBOHYD 235 265 N-LINKED (GLCNAC) (POTENTIAL).
 FT CARBOHYD 549 549 N-LINKED (GLCNAC) (POTENTIAL).
 FT VARIANT 50 50 V -> M (in HPLH2) /FTID=VAR_010772.
 FT VARIANT 123 123 R -> H /FTID=VAR_010773.
 FT VARIANT 183 183 V -> G (in HPLH2) /FTID=VAR_010744.
 FT VARIANT 224 224 I -> D (in HPLH2) /FTID=VAR_010774.
 FT VARIANT 225 225 R -> W (in HPLH2) /FTID=VAR_010745.
 FT VARIANT 252 252 N -> S (in HPLH2) /FTID=VAR_010746.
 FT VARIANT 279 279 C -> Y (in HPLH2) /FTID=VAR_010747.
 FT VARIANT 285 285 Missing (in HPLH2) /FTID=VAR_010748.
 FT VARIANT 345 345 P -> G (in HPLH2) /FTID=VAR_010749.
 FT VARIANT 429 429 G -> E (in HPLH2) /FTID=VAR_010749.
 FT CONFLICT 332 332 L -> V (in REF. 2)
 FT CONFLICT 426 426 G -> S (in REF. 2)
 SQ SEQUENCE 555 AA; 61377 MW; DQEDDDICAB75865 CR 64;
 Query Match 77.3% Score 34; DS 1; Length 555;
 Best Local Similarity 85.7% Pred. No. 39;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLIGKPP 7
 LIG
 LD 541 MLIGEP 547
 RESULT 37
 PCLO_DROME
 ID PCLO_DROME STANDARD; PRT: 576 AA.
 AC P52304; Q9VWB2;
 DT 21-OCT-1996 (Rel. 34, Created)
 DI 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein kinase polo (EC 2.7.1.-)
 GN PCLO OR CG12306
 OS Drosophila melanogaster (Fruit fly)

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=92084090; PubMed=1660828;
 RA Liamazares S., Moreira A., Tavares A., Girdham C., Spruce B.A.,
 RA Gonzalez C., Kares R.E., Glover D.M., Sunkei C.E.;
 RT "Polo encodes a protein kinase homolog required for mitosis in
 Drosophila";
 RL Genes Dev. 5:2153-2165(1991);
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: MAY PLAY A ROLE IN REGULATING BOTH NUCLEAR AND
 CC CYTOPLASMIC ASPECTS OF THE MITOTIC CYCLE.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: LARVAL DISCS, BRAIN AND TESTIS.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLO SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 POLO box domains.
 CC -----
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 CC -----
 DR EMBL; X63362; CAA44963.1; ...
 DR EMBL; AE003514; AAF49036.1; ...

```
DR PIR; S22127; S22127.
DR HSSP; Q63450; IAC6.
DR FlyBase; FBgn003124; polo.
CR GO; GO:0005813; Centrosome; IDA.
DR GO; GO:0005819; Cspindle; IDA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR GO; GO:0007140; P:male meiosis; IMP.
DR GO; GO:0007667; P:mitosis; IMP.
DR InterPro; IPR00959; Polo_box.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR02290; Ser_thr_kinase.
DR Pfam; PF00669; pkinase; 1.
DR Pfam; PFC0659; Polo_box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00678; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00011; PROTEIN_KINASE_DCM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 25 277 PROTEIN_KINASE.
FT NP_BIND 31 39 ATP (BY SIMILARITY).
FT BINDING 54 54 ATP (BY SIMILARITY).
FT ACT_SITE 148 148 BY SIMILARITY.
FT DOMAIN 398 461 POLO_BOX 1.
FT DOMAIN 496 564 POLO_BOX 2.
FT CONFLICT 187 187 P -> A (IN REF. 1).
SQ SEQUENCE 576 AA; 66973 MW; 5022B9ACCE886FAD CRC64;

Query Match 77.3%; Score 34; DB 1; Length 576;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 216 LNVGQPPF 223

RESULT 38
MPS1_YEAST
ID MPS1_YEAST STANDARD; PRT: 764 AA.
AC P54199;
CT 01-OCT-1996 (Rel. 34, Created);
CT 01-OCT-1996 (Rel. 34, Last sequence update);
UT 16-OCT-2001 (Rel. 40, Last annotation update);
DE Serine/threonine protein kinase MPS1 (EC 2.7.11); Regulatory cell
proliferation kinase 1.
GN MPS1 OR RPK1 OR YJL028C OR YJ2785.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FL100;
RX MEDLINE=94301294; PubMed=8028580;
RA Poch O., Schwab E., de Fraipont F., Camasses A., Hordonne R.,
RA Martin R.P.;
RT "RPK1, an essential yeast protein kinase involved in the regulation
RT of the onset of mitosis, shows homology to mammalian dual-specificity
RT kinases.";
RL Ycl. Gen. Genet. 243:641-653(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=97197972; PubMed=9046088;
RA Saren A.M., Laamaren P., Lejarcegui J.B., Paulin L.;
RT "The sequence of a 36.7 kb segment on the left arm of chromosome IV
RT from Saccharomyces cerevisiae reveals 20 non-overlapping open reading
RT frames (ORFs) including Sit4, Fd1, Naf1, Sir2, Nat1, Prp9,
RT ACT2 and MPS1 and 11 new ORFs.";
RJ Yeast 13:65-71(1997).
RN [3]

CHARACTERIZATION, AND MUTAGENESIS OF ASP-580.
MEDLINE=95255223; PubMed=7737118;
Lauze E., Stoelcker B., Luca F.C., Weiss E., Schutz A.R., Winey M.;
"Yeast spindle pole body duplication gene MPS1 encodes an essential
dual specificity protein kinase.";
EMBO J. 14:1655-1663(1995).
-!- FUNCTION: INVOLVED IN THE REGULATION OF THE ONSET OF MITOSIS.
INVOLVED IN A PATHWAY THAT COORDINATES CELL PROLIFERATION AND
DIFFERENTIATION. IMPLICATED IN SPINDLE POLE BODY (SPB)
DUPLICATION. DUAL SPECIFICITY KINASE THAT CAN PHOSPHORYLATE
SERINE, THREONINE AND TYROSINE RESIDUES.
-!- PTM: AUTOPHOSPHORYLATED.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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EMBL; L08909; AAA88731.1; -
EMBL; Z71781; CAA96461.1; -
EMBL; Z74076; CAA98587.1; -
PIR; S67561; S67561.
SGD; S0002186; MPS1.
GO; GO:0005699; C:kinetochore; IDA.
GO; GO:0005816; C:spindle pole body; IDA.
GO; GO:0004712; F:protein threonine/tyrosine kinase activity; IDA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_kinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
Phosphorylation.
FT DOMAIN 273 282 POLY-SER.
FT DOMAIN 309 315 POLY-SER.
FT DOMAIN 440 454 ATP (BY SIMILARITY).
FT NP_BIND 446 454 ATP (BY SIMILARITY).
FT BINDING 468 468 BY SIMILARITY.
FT ACT_SITE 563 563 D->A: LOSS OF ACTIVITY.
FT MUTAGEN 580 580 A -> S (IN REF. 1).
FT CONFLICT 211 213 RRE -> TKR (IN REF. 1).
SQ SEQUENCE 764 AA; 86827 MW; 26B171DFF8B8EB4D CRC64;

Query Match 77.3%; Score 34; DB 1; Length 764;
Best Local Similarity 62.5%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 647 MIYKPPY 654

RESULT 39
PUR4_VIBCH
ID PUR4_VIBCH STANDARD; PRT: 1297 AA.
AC Q9KTN2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoribosylformylglycinamide synthase (EC 6.3.5.3) (FGAM
DE synthase) (FGAMS) (Formylglycinamide ribotide amidotransferase)
DE (FGARAT) (Formylglycinamide ribotide synthetase).
GN PURL OR VCC869.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
```

```
CC Vibrionaceae; Vibrio.
CX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor N16961 / Serotype O1;
RC MEDLINE=20406833; PubMed=10952301;
KA Heidelberg J.P., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
KA Dodson R.C., Haft D.H., Hickey E.K., Peterson C.D., Mayhew D.A.,
KA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson E.,
KA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi A., Sellers P.,
KA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
KA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
KA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae";
RJ Nature 406:477-483(2000).
CC -!- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-
CC ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-
CC (formamido)-N(1)-(5-phospho-D-ribosyl)acetamide + L-glutamate.
CC -!- PATHWAY: De novo purine biosynthesis; fourth step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE FGAMS
CC FAMILY.
CC -!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
CC -----
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CC -----
CC EMBL: A5204171; AAF94031.1;
CC F18; A82272; A82272.
CC TIGR: VC0869;
CC HAVAP: MF_00419;
CC InterPro: IPR000728; AIRS_related.
CC Pfam: PF00586; AIRS; 1.
CC Pfam: PF02769; AIRS_C; 2.
KW Purine biosynthesis; Ligase; ATP-binding; Glutamine amidotransferase;
KW Complete proteome.
FT NP_BIND 307 318 ATP (POTENTIAL).
FT ACT_SITE 1137 1137 GATASE (BY SIMILARITY)
SQ SEQUENCE 1297 AA; 141420 MW; 024DA475D19269C 3-64.
Query Match 77.3%; Score 34; DB 1; Length 1297;
Best Local Similarity 85.7%; Pred. No. 93;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPP 7
DB 604 VLLGKPP 610
RESULT 40
PUR4_NEIMA STANDARD: PRI: 1320 AA.
AC Q9TWC5;
DT 16-OCT-2001 (Rel. 40, Created)
ET 16 OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoribosylformylglycinamide synthase (EC 6.3.5.3) (PGAM
DE synthase) (FGAMS) (Formylglycinamide ribotide amidotransferase)
DE (FGARAT) (Formylglycinamide ribotide synthetase).
GN PURL OR NMA0445.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN 1;
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491";
RJ Nature 404:502-506(2000).
CC -!- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-
CC ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-
CC (formamido)-N(1)-(5-phospho-D-ribosyl)acetamide + L-glutamate.
CC -!- PATHWAY: De novo purine biosynthesis; fourth step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE FGAMS
CC FAMILY.
CC -!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AL162753; CAB83743.1;
CC PIR: G81961; G81961.
CC HAMAP: MF_00419;
CC InterPro: IPR000728; AIRS_related.
CC Pfam: PF00586; AIRS; 1.
CC Pfam: PF02769; AIRS_C; 2.
KW Purine biosynthesis; Ligase; ATP-binding; Glutamine amidotransferase;
KW Complete proteome.
FT NP_BIND 311 322 ATP (POTENTIAL).
FT ACT_SITE 1162 1162 GATASE (BY SIMILARITY).
SQ SEQUENCE 1320 AA; 143790 MW; FEB32DC315CEDD50 CRC64;
Query Match 77.3%; Score 34; DB 1; Length 1320;
Best Local Similarity 85.7%; Pred. No. 95;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPP 7
DB 604 VLLGKPP 610
Search completed: November 14, 2003, 13:25:58
Job time : 6.94286 secs
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GenCore version 5.1.6
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CM protein : protein search, using sw model

Run on: November 14, 2003, 13:18:40 ; Search time 24 Seconds
(without alignments)
86,018 Million cell updates/sec

Title: US-09-736-076-16
Perfect score: 44
Sequence: 1 MLLGKPPF 8

Scoring table: BLCSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL 23.1

- 1: sp_archaea:
- 2: sp_bacteria:
- 3: sp_fungi:
- 4: sp_human:
- 5: sp_invertebrate:
- 6: sp_mammal:
- 7: sp_mhc:
- 8: sp_organelle:
- 9: sp_phage:
- 10: sp_plant:
- 11: sp_rodent:
- 12: sp_virus:
- 13: sp_vertebrate:
- 14: sp_unclassified:
- 15: sp_rvirus:
- 16: sp_bacteriap:
- 17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	93.2	316	6 Q9BDK4	Q9BDK4 sus scrofa
2	41	93.2	372	4 Q8N7M6	Q8N7M6 homo sapien
3	41	93.2	666	13 Q90XS4	Q90XS4 xenopus lae
4	41	93.2	682	11 Q8K226	Q8K226 mus musculu
5	40	90.9	456	5 Q8NYF1	Q8NYF1 dictyosteli
6	39	88.6	270	5 Q95ZT2	Q95ZT2 caenorhabdi
7	39	88.6	325	5 Q8MQ39	Q8MQ39 caenorhabdi
8	39	88.6	371	5 Q20541	Q20541 caenorhabdi
9	39	88.6	454	10 Q8M3V7	Q8M3V7 asparagus o
10	39	88.6	465	10 Q8LFC1	Q8LFC1 arabidopsis
11	39	88.6	480	10 Q43380	Q43380 avena sativ
12	39	88.6	592	3 Q12721	Q12721 schizosacch
13	39	88.6	766	3 Q03407	Q03407 saccharomyc
14	38	86.4	526	6 Q9BDP8	Q9BDP8 sus scrofa
15	38	86.4	582	5 Q9G557	Q9G557 hemiacetret
16	38	86.4	598	13 P00032	P00032 xenopus lae

17	38	86.4	623	5 Q8IU35	Q8IU35 asterina pe
18	38	86.4	673	5 C62567	C62567 suberites d
19	38	86.4	677	5 Q96997	Q96997 geodia cydo
20	38	86.4	2883	16 Q8PEX7	Q8PEX7 xanthomonas
21	37	84.1	388	2 Q9KX10	Q9KX10 staphylococ
22	37	84.1	664	16 Q99UP8	Q99UP8 staphylococ
23	37	84.1	664	16 Q8NX14	Q8NX14 staphylococ
24	37	84.1	667	16 Q8CSV9	Q8CSV9 staphylococ
25	37	84.1	962	11 Q9Z0W4	Q9Z0W4 mus musculu
26	37	84.1	1012	5 Q17874	Q17874 caenorhabdi
27	37	84.1	1042	11 Q9JMI3	Q9JMI3 mus musculu
28	37	84.1	1046	4 Q9P2X1	Q9P2X1 homo sapien
29	37	84.1	1047	11 Q8CDJ4	Q8CDJ4 mus musculu
30	37	84.1	1088	4 Q9NRM7	Q9NRM7 homo sapien
31	37	84.1	1099	5 Q24096	Q24096 drosophila
32	37	84.1	1099	5 Q24590	Q24590 drosophila
33	37	84.1	1105	5 Q9VA38	Q9VA38 drosophila
34	37	84.1	1130	4 Q95835	Q95835 homo sapien
35	37	84.1	2483	16 Q8XQB2	Q8XQB2 ralstonia s
36	37	84.1	2497	16 Q8XYB9	Q8XYB9 ralstonia s
37	36	81.8	80	13 Q91891	Q91891 xenopus lae
38	36	81.8	305	5 Q01427	Q01427 caenorhabdi
39	36	81.8	315	8 Q9TD68	Q9TD68 mytilus cal
40	36	81.8	324	11 Q9CVR6	Q9CVR6 mus musculu
41	36	81.8	568	5 Q8MXG6	Q8MXG6 caenorhabdi
42	36	81.8	690	16 Q8G6P9	Q8G6P9 bifidobacte
43	36	81.8	749	5 Q8MXG7	Q8MXG7 caenorhabdi
44	36	81.8	780	5 Q76360	Q76360 caenorhabdi
45	36	81.8	830	3 Q9Y7T4	Q9Y7T4 schizosacch

ALIGNMENTS

RESULT 1

Q9BDK4 PRELIMINARY; PRT: 316 AA.
AC Q9BDK4;
DT C1-JUN-2001 (TrEMBLrel. 17, Created)
DT C1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT C1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serum-inducible Kinase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCRI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Anger M., Kues W.A., Klimek J., Motlik J., Carnwath J.W., Niemann H.;
RT "Porcine serum-inducible kinase."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF348424; AAK27154.1;
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50078; POLO_BOX; 1.
KW ATP-binding; Kinase; PROTEIN KINASE DOM; 1.
FT NON_TER 1
FT NON_TER 316
SQ SEQUENCE 316 AA; 35330 MW; F63BBE4A2691D62F CRC64;

Query Match: 93.2%; Score 41; DB 6; Length 316;
Best Local Similarity: 87.5%; Pred. No. 3.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8

Db 25 MLLGKPPF 32

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 325 AA; 37528 MW; 21CDFB8A13FC18D7 CRC64;

Query Match 88.6%; Score 39; DB 5; Length 325;
Best Local Similarity 75.0%; Pred. NO. 8.2;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|:|:|:|:
Db 205 MMVGKPPF 212

RESULT 8
Q20541 ID Q20541 PRELIMINARY; PRT; 371 AA.
AC Q20541;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Cyclic AMP-dependent protein kinase, catalytic subunit (EC 2.7.1.37)
DE (Hypothetical protein F47F2.1b).
GN F47F2.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RX MEDLINE=99187058; PubMed=10095246;
RA Tabish M., Clegg R.A., Rees H.H., Fisher M.J.;
RT "Organization and alternative splicing of the Caenorhabditis elegans
cyclic AMP-dependent protein kinase (PK A) catalytic subunit gene
(kin-1).";
RL Biochem. J. 339:209-216(1999).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid F47F2.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN (4)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ012357; CAB41352.1; ..
DR EMBL; U40943; AAK72061.1; ..
DR HSSP; P05102; IATP.
DR WormPep; F47F2.1b; CE04603.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase C; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 371 AA; 42486 MW; 0C4873B5F3A45661 CRC64;

Query Match 88.6%; Score 39; DB 5; Length 371;
Best Local Similarity 75.0%; Pred. NO. 9.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|:|:|:|:
Db 251 MMVGKPPF 258

RESULT 9
Q9M3V7 ID Q9M3V7 PRELIMINARY; PRT; 454 AA.
AC Q9M3V7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE S6 ribosomal protein kinase.
GN PK1.
OS Asparagus officinalis (Garden asparagus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asparagaceae;
OC Asparagus.
OX NCBI_TaxID=4686;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Conovers Colossal;
RA Deacon K., Warner S.A.J., Draper J.;
RT "Characterisation of an Asparagus S6 ribosomal protein cDNA and an S6
ribosomal protein kinase homologue.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ277534; CAB89082.1; ..
DR HSSP; Q63450; IAC6.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Ribosomal protein;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 454 AA; 50467 MW; 0E4DEC52509997C5 CRC64;

Query Match 88.6%; Score 39; DB 10; Length 454;
Best Local Similarity 87.5%; Pred. NO. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|:|:|:|:
Db 315 MLTGKPPF 322

RESULT 10
Q8LFC1 ID Q8LFC1 PRELIMINARY; PRT; 465 AA.
AC Q8LFC1;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative ribosomal-protein S6 kinase ATPK6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Troupkhan M., Alexandrov N.,
RA Feldmann K.,
RT "Full-length cDNA from Arabidopsis thaliana";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY084935; AAM61496.1; -
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP binding; Kinase; Transferase.
SQ SEQUENCE 465 AA; 52587 MW; D8IEA58F1159E823 CRC64;

Query Match 88.6%; Score 39; DB 10; Length 465;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
| | | | |
DB 324 MLAGKPPF 331

RESULT 1:
Q43380 PRELIMINARY; PRT; 480 AA.
AC Q43380;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative pp70 ribosomal protein S6 kinase.
GN ASPK1.
OS Avena sativa (Oat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Aveneae; Avena.
OX NCBI_TaxID=4498;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ev. Rhannon; TISSUE=Aleurone;
RX MEDLINE=95284341; PubMed=766874;
RA Huttly A.K., Phillips A.L.;
RT "Gibberellin regulated expression in oat aleurone cells of two kinases
RT that show homology to nap kinase and a ribosomal protein kinase.";
RL Plant Mol. Biol. 27:1043-1052(1995).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; X79992; CAA56313.1; -
DR HSSP; P05132; ICTP.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Ribosomal protein;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 480 AA; 53532 MW; 33596A101DBB077D CRC64;

Query Match 88.6%; Score 39; DB 10; Length 480;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
| | | | |
DB 341 MLAGKPPF 348

RESULT 12
Q12701 PRELIMINARY; PRT; 592 AA.
ID Q12701;
AC Q12701;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein kinase (EC 2.7.1.37).
GN KSG1 OR SPCC576.15C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H90;
RA Niederberger C.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Wood V., Rajadream M.A., Barrell B.G., Murphy L., Harris D.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; X99280; CAA67672.1; -
DR EMBL; AL031798; CAA21194.1; -
DR GeneDB; SPombe; SPCC576.15C; -
DR InterPro; IPR001849; PH.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 592 AA; 65661 MW; B9A857D1989F2C61 CRC64;

Query Match 88.6%; Score 39; DB 3; Length 592;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
| | | | |
DB 305 MLAGKPPF 312

RESULT 13
Q03407 PRELIMINARY; PRT; 766 AA.
ID Q03407;
AC Q03407;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

```
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE D8035.33P.
GN PKH1 OR U8035.33 CR YDR490C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Arancio R., Aviles E., Berno A.,
RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunkeler-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oefner P., Ch C., Petel F.X.,
RA Roberts J., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Winant A., Yelton M., Botstein D., Davis R.W.
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Dietrich F.S.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Jia Y., Cherry J.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U33050; AAB64917.1; ..
DR HSSP; P28523; 1LR4.
DR SGP; SC002898; PKH1.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 766 AA; 86252 MW; 78F012E8BE89C367 CRC64;

Query Match 88.6%; Score 19; DB 3; Length 766;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:|
DB 330 MLAGKPPF 337

RESULT 14
Q9BDF8
ID Q9BDF8 PRELIMINARY; PRT: 506 AA.
AC Q9BDF8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created);
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Polo-like protein kinase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Anger M., Kues W.A., Klima J., Mielenz M., Motlik G., Carnwath J.W.,
RA Niemann H.;
RL "Expression Of Polo-like Kinase In Cell Cycle Synchronized Porcine
RT Fetal Fibroblasts.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF339021; AAK28550.1; ..
DR HSSP; Q63450; 1A06.
DR InterPro; IPR000959; Polo_box.
DR InterPro; IPR000719; Prot_kinase.

DR 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DR 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DR D8035.33P.
GN PKH1 OR U8035.33 CR YDR490C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Arancio R., Aviles E., Berno A.,
RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunkeler-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oefner P., Ch C., Petel F.X.,
RA Roberts J., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Winant A., Yelton M., Botstein D., Davis R.W.
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Dietrich F.S.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Jia Y., Cherry J.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U33050; AAB64917.1; ..
DR HSSP; P28523; 1LR4.
DR SGP; SC002898; PKH1.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 766 AA; 86252 MW; 78F012E8BE89C367 CRC64;

Query Match 88.6%; Score 19; DB 3; Length 766;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:|
DB 330 MLAGKPPF 337

RESULT 15
Q9GRB7
ID Q9GRB7 PRELIMINARY; PRT: 582 AA.
AC Q9GRB7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created);
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Polo-like kinase.
GN UPLK.
OS Hemientrotus puicherrius (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Hemientrotus.
OX NCBI_TaxID=7650;
RN [1]
RP SEQUENCE FROM N.A.
RA Yonemura I., Fujimoto H., Mabuchi I.;
RL "Cloning of sea urchin pik.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yonemura I., Fujimoto H., Mabuchi I.;
RL "Cloning of sea urchin polo-like kinase.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB043897; BAB18588.1; ..
DR InterPro; IPR001395; Aldo/ket_red.
DR InterPro; IPR000959; Polo_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00063; ALDO-KETO REDUCTASE_3; 1.
DR PROSITE; PS50078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 582 AA; 66429 MW; A3774A0CAACFDE5D CRC64;

Query Match 86.4%; Score 38; DB 5; Length 582;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
:|:|:|:|
DB 218 LLVGKPPF 225
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RESULT 16
P70032
ID P70032 PRELIMINARY; PRT; 598 AA.
AC P70032
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Plx1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
CC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN 1.
RP SEQUENCE FROM N.A.
RX MEDLINE=96355660; PubMed=8703070;
RA Kumaga, A.; Dunphy W.G.;
RT "Purification and molecular cloning of Plx1, a Cdc25-regulatory kinase
from Xenopus egg extracts."
RL Science 273:1377-1380(1996).
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U58205; AAC60017.1; --
DR HSSP; Q63450; IAC6.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DCM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 598 AA; 68211 MW; 2467195911F225E6 CRC64.

Query Match 86.4%; Score 38; DB 13; Length 598;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLLGKPPF 8
DB 235 LLVGKPPF 242

RESULT 17
Q81U35
ID Q81U35 PRELIMINARY; PRT; 623 AA.
AC Q81U35
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Polo-like kinase.
GN PLK.
OS Asterina pectinifera (Starfish).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asterozoa; Valvatacea; Valvatida; Asterinidae; Asterina.
OX NCBI_TaxID=7594;
RN 1.
RP SEQUENCE FROM N.A.
RX Uchida T.O.; Tachibana K.; Kishimoto T.;
RT "Starfish Plk."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; ABC84465; BAC22692.1; --
KW Kinase.
SQ SEQUENCE 623 AA; 70929 MW; CFCD190090C2D724A CRC64;

Query Match 86.4%; Score 38; DB 5; Length 623;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLLGKPPF 8
DB 235 LLVGKPPF 242

RESULT 18
O62567
ID O62567 PRELIMINARY; PRT; 673 AA.
AC O62567
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serine/threonine protein kinase.
OS Suberites domuncula (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Hadromerida; Suberitidae; Suberites.
OX NCBI_TaxID=55567;
RN 1.
RP SEQUENCE FROM N.A.
RA Mueller W.E.G.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; Y13099; CAA73553.1; --
DR HSSP; P28867; IPTQ.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR002219; DAG_PE_bind.
DR InterPro; IPR000961; pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE_bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DCMAIN.
DR PRINTS; PR00008; DAGPEDCMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C2; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 673 AA; 77344 MW; 86D24E554977C293 CRC64;

Query Match 86.4%; Score 38; DB 5; Length 673;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLLGKPPF 8
DB 535 MLVGRPPF 542

RESULT 19
O96997
ID O96997 PRELIMINARY; PRT; 677 AA.
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OY 1 MLLGKPPF 8
DB 220 LLVGKPPF 227

RESULT 19
O96997
ID O96997 PRELIMINARY; PRT; 677 AA.
```


Query Match 84.1%; Score 37; DB 2; Length 388;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 202 MLVGEPPF 209

RESULT 22

Q99UP8 PRELIMINARY; PRT; 664 AA.
AC Q99UP8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein kinase.
GN SAV1220 OR SA1063.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori Y., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Harakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: APC03361; BAB57382.1; -;
DR FAYL: APC03133; BAB42315.1; -;
DR HSSP: Q63450; 1A06.
DR InterPro: IPR005543; PASTA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF03793; PASTA; 3.
DR ProDom: PD00001; Prot_kinase; 1.
DR SMART: SM00740; PASTA; 3.
DR SMART: SM00220; STK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase;
KW Complete proteome.
SQ SEQUENCE 664 AA; 74377 MW; 3461386C5DB61828 CRC64;

Query Match 84.1%; Score 37; DB 16; Length 664;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 202 MLVGEPPF 209

RESULT 23

Q8NX14 PRELIMINARY; PRT; 664 AA.
AC Q8NX14;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MW1103 protein.

GN MW1103.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=120443378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
DR EMBL: AP004826; BAB94968.1; -;
DR InterPro: IPR005543; PASTA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF03793; PASTA; 3.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD00001; Prot_kinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Complete proteome.
SQ SEQUENCE 664 AA; 74363 MW; 26F1386C5DB61828 CRC64;

Query Match 84.1%; Score 37; DB 16; Length 664;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 202 MLVGEPPF 209

RESULT 24

Q8CSV9 PRELIMINARY; PRT; 667 AA.
AC Q8CSV9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein kinase.
GN SE0895.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu G., Jia J., Tu Y., Qin Z.,
RA Chen Z., Wen Y.,
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE016746; AAC04492.1; -;
KW Kinase; Complete proteome.
SQ SEQUENCE 667 AA; 75411 MW; 479877B4531CDD97 CRC64;

Query Match 84.1%; Score 37; DB 16; Length 667;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 202 MLVGEPPF 209

RESULT 25

Q9Z0W4 PRELIMINARY; PRT; 962 AA.
AC Q9Z0W4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

```
DE Large tumor suppressor 1 (Fragment).
GN LAT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95262551; PubMed=7743921;
RA Xu T., Wang W., Zhang S., Stewart R.A., Yu W.;
RT "Identifying tumor suppressors in genetic mosaics: the Drosophila lats
PT gene encodes a putative protein kinase.";
RL Development 121:1053-1063(1995);
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99140768; PubMed=9988269;
RA St John M.A., Tao W., Fei X., Fukumoto R., Carcangiu M.;
RA Brownstein D.G., Parlow A.F., McGrath J., Xu T.;
RT "Mice deficient of Lats1 develop soft-tissue sarcomas, ovarian tumours
RT and pituitary dysfunction.";
RL Nat. Genet. 21:182-186(1999);
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99140767; PubMed=9988268;
RA Tao W., Zhang S., Turenchaik G.S., Stewart R.A., St John M.A.,
RA Chen W., Xu T.;
RT "Human homologue of the Drosophila melanogaster lats tumour suppressor
RT modulates CDC2 activity.";
RL Nat. Genet. 21:177-181(1999);
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
UR EMBL; AF104414; AAD16883.1; -
UR HSSP; P05132; ICTP.
UR MGD; MGI:1333883; Lats1.
UR InterPro; IPR000961; Pkinase_C.
UR InterPro; IPR000719; Prot_kinase.
UR InterPro; IPR002965; P-rich_extensions.
UR InterPro; IPR002290; Ser_thr_pkinase.
UR Pfam; PF00069; pkinase; 1.
UR Pfam; PF00433; pkinase_C; 1.
UR PRINTS; PR01217; PRICHEXTENS.
UR ProDom; PD000001; Prot_kinase; 2.
UR SMART; SM00220; S_TKC; 1.
UR SMART; SM00133; S_TK_X; 1.
UR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
UR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON TER 1
SQ SEQUENCE 962 AA; 107312 MW; 1F6CF1C02A6C57E5 CRC64;

Query Match 84.1%; Score 37; DB 11; Length 962;
Best Local Similarity 75.0%; Pred.No. 64;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 775 MLVGQPPF 782
|:|:|:|:|

RESULT 26
Q17874 PRELIMINARY; PRT; 1012 AA.
AC Q17874; Q20475;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F46F6.2 protein.
GN F46F6.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
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OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Cottage A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998);
DR EMBL; Z50028; CAA90339.4; -
DR EMBL; Z50029; CAA90339.4; JOINED.
DR EMBL; Z50029; CAA90345.4; -
DR EMBL; Z50028; CAA90345.4; JOINED.
DR HSSP; P05132; IATP.
DR WormPep; F46F6.2; CE31703.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000861; REM_repeat.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF02185; HRI; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00074; HRI; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00636; DnaJ; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 1012 AA; 113792 MW; D2F1930254536169 CRC64;

Query Match 84.1%; Score 37; DB 5; Length 1012;
Best Local Similarity 75.0%; Pred.No. 67;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 877 MLVGQPPF 884
|:|:|:|:|

RESULT 27
Q9JMI3 PRELIMINARY; PRT; 1042 AA.
AC Q9JMI3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Warts/lats-like kinase.
GN LATS2 OR MMLATS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20139436; PubMed=10673337;
RA Yabuta N., Fujii T., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Nishiguchi H., Endo Y., Toji S., Tanaka H., Nishimune Y., Nojima H.;
RT "Structure, expression, and chromosome mapping of LATS2, a mammalian
RT homologue of the drosophila tumor suppressor gene lats/warts.";
RL Genomics 63:263-270(2000);
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB023958; BAA92380.1; -
DR HSSP; P05132; ICTP.
DR MGD; MGI:1354386; Lats2.
```

DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1042 AA; 115468 MW; 3315863485B5F4D CRC64;

Query Match 84.1%; Score 37; DB 11; Length 1042;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
DB 864 MLVGQPPF 871

RESULT 28
Q9P2X1 PRELIMINARY; PRT; 1046 AA.
AC Q9P2X1
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Large tumor suppressor 2 (Fragment).
GN HSLA7S2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=20139436; PubMed=10673337;
RA Yabuta N., Fujii T., Copeland N.G., Gilbert D.J., Jenkins N.A.,
Nishiguchi H., Endo Y., Toji S., Tanaka H., Nishimura Y., Nigima H.;
"Structure, expression, and chromosome mapping of LAT2, a mammalian
homologue of the drosophila tumor suppressor gene lats/warts.";
RL Genomics 63:263-270(2000).
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB028019; BAA32381.1; --
DR HSSP; P05132; ICTP.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON TER 1
SQ SEQUENCE 1046 AA; 115321 MW; 5908201740C3A2FA CRC64;

Query Match 84.1%; Score 37; DB 4; Length 1046;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
DB 864 MLVGQPPF 871

RESULT 29
Q8CDJ4 PRELIMINARY; PRT; 1047 AA.
AC Q8CDJ4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Large tumor suppressor 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK029966; BAC26704.1; --
SQ SEQUENCE 1047 AA; 115282 MW; E80216A3C6E478CD CRC64;

Query Match 84.1%; Score 37; DB 11; Length 1047;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
DB 864 MLVGQPPF 871

RESULT 30
Q9NRM7 PRELIMINARY; PRT; 1088 AA.
AC Q9NRM7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serine/threonine kinase KPM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Myeloid;
RX MEDLINE=20332247; PubMed=10871863;
RA Hori T., Takaori-Kondo A., Kamikubo Y., Uchiyama T.;
"Molecular cloning of a novel human protein kinase, kpm, that is
homologous to warts/lats, a Drosophila tumor suppressor.";
RL Oncogene 19:3101-3109(2000).
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF207547; AAF80561.1; --
DR HSSP; P05132; ICTP.
DR Genew; HGNC:6515; LAT2.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1088 AA; 120193 MW; 32C7580B6871FA63 CRC64;

Query Match 84.1%; Score 37; DB 4; Length 1088;

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Best Local Similarity 75.0%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 906 MLVGQPPF 913

RESULT 31:
Q24096 PRELIMINARY; PRT; 1099 AA.
AC Q24096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE LATS.
GN WTS CR LATS CR CG12072.
OS Drosophila melanogaster (Fruit fly);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1;
SEQUENCE FROM N.A.
MEDLINE=95262551; PubMed=7741921;
RA Xu T., Wang W., Zhang S., Stewart R.A., Yu W.;
RT "Identifying tumor suppressors in genetic mosaics: the Drosophila lats
gene encodes a putative protein kinase.";
RC Development 121:1053-1063(1995);
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; J29608; AAA70336.1; -.
DR HSSP; P05132; IAPM.
DR FlyBase; FBgn0011739; wts.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR022900; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1099 AA; 12719 MW; 444680461.5; P64;

Query Match 84.1%; Score 77; DB 96; Length 1099;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 906 MLVGQPPF 955

RESULT 32:
Q24590 PRELIMINARY; PRT; 1099 AA.
AC Q24590;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE tumor suppressor.
GN WTS CR CG12072.
OS Drosophila melanogaster (Fruit fly);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1;
SEQUENCE FROM N.A.
MEDLINE=95212904; PubMed=7698644;
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RA Justice R.W., Zilian O., Woods D.F., Noll M., Bryant P.J.;
RT "The Drosophila tumor suppressor gene warts encodes a homolog of human
RT myotonic dystrophy kinase and is required for the control of cell
RT shape and proliferation.";
RL Genes Dev. 9:534-546(1995);
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; L39837; AAA73959.1; -.
DR HSSP; P05132; IAPM.
DR FlyBase; FBgn0011739; wts.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR022900; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1099 AA; 121633 MW; EB35192A1C470805 CRC64;

Query Match 84.1%; Score 37; DB 5; Length 1099;
Best Local Similarity 75.0%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 948 MLVGQPPF 955

RESULT 33:
Q9VA38 PRELIMINARY; PRT; 1105 AA.
AC Q9VA38;
DT 01-MAY-2003 (TrEMBLrel. 13, Created);
DT 01-MAY-2003 (TrEMBLrel. 13, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE WTS protein.
GN WTS OR CGI2072.
OS Drosophila melanogaster (Fruit fly);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1;
SEQUENCE FROM N.A.
STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup J.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.C., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Le Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei S., McIntosh T.C., McLeod M.P., McPherson D.,
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy N., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard C., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Sider-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri A.S., Zhan X., Zhang G., Zhao Q., Zheng J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.C.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
K: "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AE003775; AAF57085.1; -.
DR HSSP: PC5132; LAPM.
DR FlyBase: FBgn001739; wts.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PDC0001; Prot_kinase; 2.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00133; S_TK_X; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATF; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1105 AA; 12248 MW; 7DC9D2AA9BA-A656 CRC64;

Query Match: 84.1%; Score 37; DB 5; Length 1105;
Best Local Similarity 75.0%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
DB 954 MLVGPFPF 96;

RESULT 34
Q95835
ID Q95835 PRELIMINARY; PRT; 103 AA.
AC Q95835;
DC 01 MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Large tumor suppressor 1.
GN LATS1 OR WATS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95262551; PubMed=7743921;
RA Xu T., Wang W., Zhang S., Stewart P.A., Yu W.;
RT "Identifying tumor suppressors in genetic mosaics: the Drosophila lats
RT gene encodes a putative protein kinase";
RL Development 121:1053-1063(1995).
RW 12;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99140767; PubMed=9985268;
RA Chen W., Zhang S., Turenchalk G.S., Stewart P.A., St John M.A.,
RA Tao W., Xu T.;
RT "Human homologue of the Drosophila melanogaster lats tumour suppressor
RT modulates CDC2 activity.";
RL Nat. Genet. 21:177-181(1999).
RW 13;

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99140768; PubMed=9988269;
RA St John M.A., Tao W., Fei X., Fukumoto R., Carcangiu M.L.,
RA Brownstein D.G., Parlow A.F., McGrath J., Xu T.;
RT "Mice deficient of Lats1 develop soft-tissue sarcomas, ovarian tumours
RT and pituitary dysfunction.";
RL Nat. Genet. 21:182-186(1999).
RW 14;
RP SEQUENCE FROM N.A.
RX MEDLINE=9947636; PubMed=10518011;
RA Nishiyama Y., Hirota T., Morisaki T., Hara T., Marumoto T., Iida S.,
RA Makino K., Yamamoto H., Hiraoka T., Kitamura N., Saya H.;
RT "A human homologue of Drosophila warts tumor suppressor, h-warts,
RT localized to mitotic apparatus and specifically phosphorylated during
RT mitosis.";
RL FEBS Lett. 459:159-165(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF104413; AAD16882.1; -.
DR EMBL: AF164041; AAD50272.1; -.
DR HSSP: P05132; ICTP.
DR Genew; HGNC:6514; LATS1.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR000449; UBA_domain.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00433; pkinase_C; 1.
DR Pfam: PF00627; UBA; 1.
DR ProDom: PDC0001; Prot_kinase; 2.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00133; S_TK_X; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1130 AA; 126869 MW; 11CFBCD8F87DCD8 CRC64;

Query Match: 84.1%; Score 37; DB 4; Length 1130;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||:|
DB 943 MLVGPFPF 950

RESULT 35
Q8XQB2
ID Q8XQB2 PRELIMINARY; PRT; 2483 AA.
AC Q8XQB2;
DC 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE SKWP protein 2.
GN RSP1374 OR RSC2084.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
CX NCBI_TaxID=305;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schliex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
RW 13;

KW Pfam; Complete proteome.
SQ SEQUENCE 2483 AA; 272286 MW; 21E5F0A4EBA93614 CRC64;
Query Match 84.1%; Score 37; DB 16; Length 2483;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|:|:|:|:
Db 1521 VLVGKPPY 1528

RESULT 36
Q8XYB9 PRELIMINARY; PRT; 2497 AA.
AC Q8XYB9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE SKWP protein 4.
GN RSC1939 OR RSC4276.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
CX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gozy G., Vandenberg S.,
RA Alier M., Billault A., Brottier P., Camus J.C., Catalicio L.,
RA Chandler M., Choisme M., Claudel-Renard C., Cunha S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RJ Nature 415:497-502(2002).
DR EMBL; AL646067; CAD15541.1; ..
KW Complete proteome.
SQ SEQUENCE 2497 AA; 270604 MW; 12BF29A75D3C5F99 CRC64;

Query Match 84.1%; Score 37; DB 16; Length 2497;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|:|:|:|:
Db 1545 VLVGKPPY 1552

RESULT 37
Q91891 PRELIMINARY; PRT; 80 AA.
AC Q91891;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 9.4 kDa protein (Fragment).
CS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Bourvet P., Omilli F., ARLOT-BONNEMA N.Y., Legagneux V., Roghi C.,
RA Bassez I., OSBORNE H.;
RT "Deadenylation conferred by the 3' untranslated region of a
RT developmentally controlled mRNA in xenopus embryos is switched to
RT polyadenylation by deletion of a short sequences element";
RI Mol. Cell. Biol. 14:1893-1900(1995).
LR EMBL; 224453; CAA80826.1; ..
DR InterPro; IPR000719; Prot_kinase.

DR Pfam; PK00069; pkinase; ..
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
KW Hypothetical protein; Atp-binding; Transferase.
FT NON_TER 1
SQ SEQUENCE 80 AA; 9388 MW; 8DFCEDBA14BE14FB CRC64;
Query Match 81.8%; Score 36; DB 13; Length 80;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
|:|:|:|:
Db 3 LVGKPPF 9

RESULT 38
O01427 PRELIMINARY; PRT; 305 AA.
AC O01427;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE C. ELEGANS AURORA/IPL1-related protein KINASE 2 (AIR-2) (GB:AF071207).
DE CONTAINS SIMILARITY to PFAM domain PF00069 (PKINASE), SCORE=295.1.
DE E-VALUE=2.8E-85, N=1 (AIR-2) (PKINASE).
GN AIR-2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Henkhaus J., Wohldmann P.;
RT "The sequence of C. elegans cosmid B0207.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=N2 BRISTOL;
RA Schumacher J.M., Golden A., Donovan P.J.;
RT "AIR-2: An aurora/Ipl1-related protein kinase associated with
RT chromosomes and midbody microtubules is required for polar body
RT extrusion and cytokinesis in C. elegans embryos.";
RL J. Cell Biol. 0:0-0(1998).

CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U97196; AAB52459.2; ...
DR EMBL: AF071207; AAC70945.1; ...
DR HSSP: P24941; 1A01.
DR InterPro: IPR000719; Prot_kinase
DR Pfam: PF00369; pkinase; 1.
DR ProDom: PDC00001; Prot_kinase; 1.
DR SMART: SMC0220; S_TKC_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00311; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 305 AA; 34749 MW; 1635EB60D2E14011 CRC64;

Query Match 81.8%; Score 36; DB 5; Length 305;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MLLGKPPF 8
220 LVGKPPF 226

RESULT 39
Q9TD68 PRELIMINARY; PRT; 315 AA.
AC Q9TD68;
DI 01-MAY-2000 (TREMBLrel. 13, Created;
DI 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update;
DE NADH dehydrogenase subunit 2.
GN ND2.
OS Mytilus californianus (California mussel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6549;
UN 1.
RP SEQUENCE FROM N.A.
RX MEDLINE=99282504; PubMed=10353906;
RA Beagley C.T., Okimoto R., Wolstenholme D.R.;
RT "Mytilus mitochondrial DNA contains a functional gene for a
RT tRNAser(UCN) with a dihydrouridine arm replacement loop and a pseudo-
RT tRNAser(UCN) gene."
RL Genetics 152:641-652(1999).
DR EMBL: AF090631; AAF02231; ...
DR InterPro: IPR001750; Oxidored_g...
DR Pfam: PF00361; oxidored_g; 1.
KW NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
SQ SEQUENCE 315 AA; 34339 MW; 819ED726373CC397 CRC64;

Query Match 81.8%; Score 36; DB 6; Length 315;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
233 MLMGNPPF 240

RESULT 40
Q9CVR6 PRELIMINARY; PRT; 324 AA.
AC Q9CVR6;
DI 01-JUN-2001 (TREMBLrel. 17, Created;
DI 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DI 01-MAR-2003 (TREMBLrel. 23, Last annotation update;
DE Serine/threonine kinase 18 (Fragment).
GN StK18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathia; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka T.,
RA Saito T., Okazaki Y., Gojebori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fietcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AKC06827; BAB24759.1; ...
DR HSSP: Q0C534; 1B18.
DR MGD; MGI:101783; Stk18.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom: PDC00001; Prot_kinase; 1.
DR SMART; SMC0220; S_TKC_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00311; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Transferase.
FT NON_TER 324 324
SQ SEQUENCE 324 AA; 36568 MW; 04247065DFB198CC CRC64;

Query Match 81.8%; Score 36; DB 11; Length 324;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
204 LLIGRPPF 211

Search completed: November 14, 2003, 13:27:57
Job time : 25 secs

GenCore version 5.2.6
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CM protein: protein search, using sw model:

Run on: November 14, 2003, 12:54 54 / Search time 34.7143 Seconds
(without alignments)
41,151 Million cell updates/sec

Title: US-09-736-076-17

Perfect score: 49

Sequence: 1 MLLGKPPFE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	AAW74161	HJ loop peptide J-
2	49	100.0	9	AAU98316	Polo kinase serine
3	46	93.9	9	AAW74150	HJ loop peptide J-
4	46	93.9	9	AAU98315	Polo kinase serine
5	46	93.9	10	AAW74219	HJ loop peptide KC
6	46	93.9	10	AAU98315	Polo kinase SNK se
7	46	93.9	11	AAW74151	HJ loop peptide J
8	46	93.9	11	AAU98315	Polo kinase serine
9	46	93.9	469	AAU94711	Human protein sequ

10	46	93.9	469	22	AAG67426	Amino acid sequenc
11	46	93.9	685	20	AAU00915	Human serum induci
12	46	93.9	685	20	AAW88432	Disease associated
13	46	93.9	685	23	ABP61474	Human NF-kB activa
14	46	93.9	753	23	ABP41992	Human ovarian anti
15	44	89.8	8	20	AAW74160	HJ loop peptide J-
16	44	89.8	8	23	AAU98316	Polo kinase serine
17	43	87.8	20	20	AAW74173	HJ loop peptide PO
18	43	87.8	20	23	AAU98306	peptide sequence o
19	329	21	329	21	AAU56690	Human prostate can
20	43	87.8	528	23	ABP73734	Candida albicans e
21	43	87.8	531	23	AAU74656	Mammalian polo-lik
22	43	87.8	603	16	AAU74620	Human lung tumour
23	43	87.8	603	23	AAU79306	Mouse polo-like ki
24	43	87.8	603	23	AAU79308	Mouse polo-like ki
25	43	87.8	603	23	AAU79309	Mouse polo-like ki
26	43	87.8	603	23	AAU79310	Mouse polo-like ki
27	43	87.8	603	23	AAU79311	Mouse polo-like ki
28	43	87.8	603	23	AAU79312	Mouse polo-like ki
29	43	87.8	603	23	AAU79313	Mouse polo-like ki
30	43	87.8	603	23	AAU79314	Mouse polo-like ki
31	43	87.8	603	23	AAU79315	Mouse polo-like ki
32	43	87.8	603	23	AAU79316	Mouse polo-like ki
33	43	87.8	603	23	AAU79317	Mouse polo-like ki
34	43	87.8	603	23	AAU79318	Mouse polo-like ki
35	43	87.8	603	23	AAU79319	Mouse polo-like ki
36	43	87.8	603	23	AAU79320	Mouse polo-like ki
37	43	87.8	603	24	ABR48196	Human bladder canc
38	41	83.7	403	18	AAW18084	Human Aurora-2, H
39	41	83.7	403	20	AAU22476	Human AUR2 protein
40	41	83.7	403	22	AAG67435	Amino acid sequenc
41	41	83.7	403	22	AAG67614	Amino acid sequenc
42	41	83.7	403	23	AAG18740	Human NOV4 protein
43	41	83.7	403	24	ABR48160	Human bladder canc
44	41	83.7	403	24	ABP97366	Human serine/threo
45	41	83.7	403	24	ABP97367	Human serine/threo

ALIGNMENTS

RESULT 1

AAW74161

ID AAW74161 standard; peptide; 9 AA.

AC AAW74161;

DT 05-MAY-1999 (first entry)

DE HJ loop peptide J-43.1.

KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "acetylated"

FT Modified-site 9 /note= "am:dated"

FT Modified-site 9 /note= "am:dated"

XX

PN WO9853050-A2.

XX

PD 26-NOV-1998.

XX

PF 20-MAY-1998; 98WO-US10319.

XX

PR 21-MAY-1997; 97US-0861335.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.

PA (YISS) YISSUM RES & DEV CO.
XX
PI Ben-Sasson SA;
XX
DR WPI: 1999-CV0142/36.
XX
PT New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Claim 14; Fig 4; 70pp; English.
XX
CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
Db 1 MLLGKPPPE 9

RESULT 2
AAU98317
ID AAU98317 standard; Peptide: 9 AA
XX
AC AAU98317;
XX
DT 11-AUG-2002 (first entry)
XX
DE Polo kinase serine-threonine kinase HJ loop peptide J-43.1.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; J-43.1.
XX
OS Unidentified.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 9 /note= "Benzyl ester of glutamic acid, C-terminal amide"
FT Modified-site 9 /note= "Benzyl ester of Glu"
XX
PN WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WG-US10319.
XX
PR 21-MAY 1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.

PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Ben-Sasson SA;
XX
DR WPI: 2002-462787/49.
XX
PT New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX
PS Disclosure; Fig 4; 41pp; English.
XX
CC The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-43.1. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
Db 1 MLLGKPPPE 9

RESULT 3
AAW74159
ID AAW74159 standard; peptide; 9 AA.
XX
AC AAW74159;
XX
DT 05-MAY-1999 (first entry)
XX
DE HJ loop peptide J-42.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 9 /note= "amidated"
FT Modified-site 9 /note= "benzyl ester of Glu"
XX
PN WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WG-US10319.
XX
PR 21-MAY 1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.

XX Ben-Sasson SA;
XX WPI; 1999-07C142/06.
XX New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX Claim 14; Fig 4; 70pp; English.
XX This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 9 AA;
Query Match 93.9%; Score 46; DB 23; Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLLGKPPFE 9
Db 1 MLLGRPPFE 9
RESULT 4
AAU98315
AAU98315 standard; Peptide: 9 AA.
XX AAU98315.
XX 13-AUG-2002 (first entry)
DE Polo kinase serine-threonine kinase HJ loop peptide J-42.
XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW anti-inflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; J-42.
XX Unidentified.
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 9 /note= "Benzyl ester of Glutamic acid"
FT /note= "C-terminal amide"
XX
PN US2002049301-A1.
XX
PD 25-APR-2002.
XX
PF 13-DEC-2000; 2000US-0736076.
XX

PR 21-MAY-1997; 97US-0861339.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX Ben-Sasson SA;
XX WPI; 2002-462787/49.
XX New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX Disclosure; Fig 4; 41pp; English.
XX The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders. The peptides are also used to generate
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-42. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.
XX Sequence 9 AA;
SQ
Query Match 93.9%; Score 46; DB 23; Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLLGKPPFE 9
Db 1 MLLGRPPFE 9
RESULT 5
AAW74213
ID AAW74213 standard; peptide: 10 AA.
XX AAW74213.
AC AAW74213.
XX 05-MAY-1999 (first entry)
DT HJ loop peptide K038H101.
DE
XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX Synthetic.
OS
XX
PH Key Location/Qualifiers
FT Modified-site 1 /note= "myristylated"
FT Modified-site 10 /note= "amidated"
FT
XX W09853050-A2.
PN
XX 26-NOV-1998.
PD
XX 20-MAY-1998; 98WO-US10319.
PF
XX 21-MAY-1997; 97US-0861339.
PR
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX Ben-Sasson SA;
PI

XX WPI; 1999-070142/06.
XX
XX
PT New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Disclosure; Fig 6; 70pp; English.
XX
CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 10 AA;

Query Match 93.9%; Score 46; DB 20; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.061;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
Db 2 MLLGRPPPE 10

RESULT 6
AAU98357
ID AAU98357 standard; Peptide; 10 AA.
XX
AC AAU98357;
XX
DT 13-AUG-2002 (first entry)
XX
DE Polo kinase SNK serine-threonine kinase HJ loop peptide K038H101.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; anti-diabetic; anorectic; neurological;
KW anti-inflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; SNK; K038H101.
XX
OS Unidentified.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal myristyl"
FT Modified-site 10 /note= "Benzyl Ester of Glutamic Acid, C-terminal amide"
XX
PN US2002049301-A1.
XX
PC 25-APR-2002.
XX
PF 13-DEC-2000; 2000US-0736076.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.

XX Ben-Sasson SA;
XX
XX WPI; 2002-462787/49.
XX
PT New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX
PS Disclosure; Fig 6; 41pp; English.
XX
CC The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase SNK
CC serine-threonine kinase HJ loop peptide K038H101. This sequence is one
CC of the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
SQ Sequence 10 AA;

Query Match 93.9%; Score 46; DB 23; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.061;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
Db 2 MLLGRPPPE 10

RESULT 7
AAW74163
ID AAW74163 standard; peptide; 11 AA.
XX
AC AAW74163;
XX
DT 05-MAY-1999 (first entry)
XX
DE HJ loop peptide J-46.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 11 /note= "amidated"
XX
PN WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US-0319.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI (YISS) YISSUM RES & DEV CO.
XX
PI Ben-Sasson SA;
XX
DR WPI; 1999-070142/06.
XX

PT New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
FT inflammatory disorders or autoimmune disorders

XX Claim 14; Fig 4; 70pp; English.

CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.

XX Sequence 11 AA;

Query Match 93.9%; Score 46; DB 20; Length 11;
Best Local Similarity 88.9%; Pred. No. 0.067;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
Db 1 MLLGRPPFE 9

RESULT 8

AAJ98319
ID AAJ98319 standard; Peptide; 11 AA.

XX
AC AAJ98319;

XX 13-AUG-2002 (first entry)

YV Polo kinase serine-threonine kinase HJ loop peptide J-46.

DE
XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disease; auto-
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; J-46.

XX Unidentified.
OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Misc-difference 9 /note= "Benzyl ester of Glutamic acid"

FT Modified-site 11 /note= "C-terminal amide"

XX US2002049301-A1.

XX 25-APR-2002.

PF 13-DEC-2000; 2000US-0736076.

XX 21-MAY-1997; 97US-0861338.

XX (CHILD-) CHILDRENS MEDICAL CENT.

XX

PI Ben-Sasson SA;

XX WPI; 2002-462787/49.

XX New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -

XX Disclosure; Fig 4; 41pp; English.

XX The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-46. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.

XX Sequence 11 AA;

Query Match 93.9%; Score 46; DB 23; Length 11;
Best Local Similarity 88.9%; Pred. No. 0.067;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
Db 1 MLLGRPPFE 9

RESULT 9

AAB94717
ID AAB94717 standard; Protein; 469 AA.

XX
AC AAB94717;

XX 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:15726.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

XX 02-MAY-2000; 2000JP-0183767.

XX 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -

XX Claim 8; SEQ ID 15726; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification; or (b) a combination
CC of an oligonucleotide comprising at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 3' end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3' end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5' end sequence/3' end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH3166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

SQ Sequence 469 AA;
Query Match 93.9%; Score 46; DB 22; Length 469;
Best Local Similarity 88.9%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLJGKPPPE 9
|||:||||
DB 57 MLJGRPPPE 65

RESULT 10

AAAG67426

ID AAG67426 standard; Protein; 469 AA.

XX
AC AAG67426;

AX
ET 26-NOV 2001 (first entry)

XX Amino acid sequence of a human protein kinase/protein phosphatase.

DE
XX Human; protein kinase; protein phosphatase; signal transduction;

KW intracellular signalling pathway.

XX
OS Homo sapiens.

XX
FN WC200109345 A1.

XX
PD 28-FEB-2001.

XX
PF 28-JUL-2000; 2000WO-JP05060.

XX
PR 29-JUL-1999; 99JP-0248036.

PR 28-OCT-1999; 99US-0159590.

PR 11-JAN-2000; 2000JP-0118776.

PR 17-FEB-2000; 2000US-0183322.

PR 02-MAY-2000; 2000JP-0183767.

XX
XX (HELI-) HELIX RES INST.

XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;

PI Senoo C, Nezu J;

XX
XX WPI; 2001-564736/63.

DR N-PSDB; AAH78069.

XX
XX New genes encoding protein kinase and protein phosphatase, useful for

PT identifying modulators which can be used to treat human or animal

PT disorders associated with the expression or function of these enzymes -
XX Claim 2; Page 136-139; 336pp; Japanese.
XX
CC The present sequence represents a human protein kinase/protein
CC phosphatase. The polypeptides are expected to participate in signal
CC transduction in cells. The kinase phosphatases are connected with
CC intracellular signalling pathways. Antisense oligonucleotides and
CC compounds identified by screening (agonists or antagonists) can be
CC used to treat human or animal disorders associated with the expression
CC or function of the protein. In addition, the polypeptides may be used
CC as target molecules for drug development.

SQ Sequence 469 AA;

Query Match 93.9%; Score 46; DB 22; Length 469;

Best Local Similarity 88.9%; Pred. No. 2.8;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLJGKPPPE 9

||||:||||

DB 57 MLJGRPPPE 65

RESULT 11

AAAY00915

ID AAAY00915 standard; Protein; 685 AA.

XX
AC AAAY00915;

XX
DT 28-MAY-1999 (first entry)

XX
DE Human serum inducible kinase.

XX
KW Serum inducible kinase; SNK protein; human; proliferative disease;

KW leukaemia; solid tumour cancer; metastasis; chronic inflammatory;

KW psoriasis; rheumatoid arthritis; proliferative cardiovascular disease;

KW restenosis; ocular disorder; diabetic retinopathy; haemangioma;

KW benign hyperproliferative disease; diagnosis.

XX
OS Homo sapiens.

XX
PN WC9909146-A1.

XX
PD 25-FEB-1999.

XX
PF 20-AUG-1998; 98WO-US17249.

XX
PR 20-AUG-1997; 97US-0056112.

XX
PA (SMIK) SMITHKLINE BEECHAM CORP.

XX
PI Anderson KM, Bouzyk M, Hansbury MJ, Jackson JR;

PI Nerurkar SS, Roshak AK;

XX
DR WPI; 1999-181027/15.

DR N-PSDB; AAX27227.

XX
PT New serum inducible kinase (Snk) polypeptides and polynucleotides -

XX useful for treating proliferative diseases

XX
PS Claim 1; Page 39-40; 4lpp; English.

XX
CC This sequence is a human serum inducible kinase (SNK) of the

CC invention. The invention relates to diagnostic assays or kits for

CC detecting diseases associated with inappropriate SNK activity or levels.

CC Disease states that can be diagnosed include proliferative diseases such

CC as leukaemia, solid tumour cancers and metastases, chronic inflammatory

CC proliferative diseases such as psoriasis and rheumatoid arthritis,

CC proliferative cardiovascular diseases such as restenosis, proliferative

CC ocular disorders such as diabetic retinopathy and benign

CC hyperproliferative diseases such as haemangiomas. The polynucleotides can

CC be used as hybridisation probes for cDNA and genomic DNA or as primers

CC for a nucleic acid amplification (PCR) reaction, to isolate full-length
CC cDNAs and genomic clones encoding polypeptides of this invention and to
CC isolate cDNA and genomic clones of other genes which have a high sequence
CC similarity to the SNK coding sequence. The differences between cDNA and
CC genomic sequences can be observed and therefore mutations detected. Any
CC mutations may then be attributed to likely causative agents of disease.
CC The nucleotide sequences are also useful for chromosome identification.
XX
SQ Sequence 685 AA;

Query Match 93.9%; Score 46; DB 20; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
Db 273 MLLGRPPFE 281

RESULT 12
AAW88432
ID AAW88432 standard; Protein; 685 AA.
XX
AC AAW88432;
XX
DT 26-APR-1999 (first entry)
XX
DE Disease associated protein kinase DAPK 1.
XX
KW DAPK 1; disease associated protein kinase; human; diagnosis;
KW therapy; adult respiratory distress syndrome; allergy; asthma;
KW arteriosclerosis; bronchitis; emphysema; hyper eosinophilia;
KW myocardial inflammation; pericardial inflammation; anaemia;
KW rheumatoid arthritis; Addison's disease; AIDS; atherosclerosis;
KW atopic dermatitis; dermatomyositis; diabetes mellitus;
KW glomerulonephritis; gout; Grave's disease; lupus erythematosus;
KW multiple sclerosis; myasthenia gravis; osteoarthritis;
KW osteoporosis; pancreatitis; polycystic kidney disease;
KW polymyositis; scleroderma; Sjorgren's syndrome;
KW autoimmune thyroiditis; cancer; infection; trauma;
KW cell proliferation.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Binding site 89..96
FT Peptide /note= "potential ATR binding site"
FT /note= 506..511
FT /note= "presumed regulatory sequence, common to
FT polo family protein kinases"
XX
PN WC9858052-A2.
XX
PD 23 DEC-1998.
XX
PF 19-JUN-1996; 98WO-US12813.
XX
PP 19-JUN-1997; 97JS-0878989.
XX
PA (INCY-1) INCYTE PHARM INC.
XX
PI Bandman C, Corley NC, Goli SK, Giegiet KJ, Hillman JL;
PI Lal P, Shah P;
XX
DR WPI; 1999-080952/07.
DR N-PSDB; AAX06831.
XX

PT New disease associated protein kinases used to stimulate cell
PT proliferation and to treat the immune response and cancer
XX
PS Claim 1; Page 54-56; 93pp; English.
XX
CC This is the amino acid sequence of human disease associated protein

CC kinase DAPK-1, as deduced from a consensus sequence (see AAX06831)
CC of overlapping cDNA clones from libraries which are immortalised
CC or cancerous and show inflammatory or immune responses. DAPK-1
CC shows 53% homology to human proliferation-related protein kinase
CC PRK (GI 1488263). The invention provides DAPK-1 to DAPK-7
CC polypeptides (see AAW88432-38) and cDNA clones encoding them (see
CC AAX06831-36 and AAX06882), as well as expression vectors, host cells,
CC agonists, antagonists and antibodies. The invention further
CC provides uses of such products in the diagnosis, prevention and
CC treatment of diseases associated with cell proliferation.
CC especially cancer or an immune response (claimed). Conditions
CC that may be treated include adult respiratory distress syndrome,
CC allergies, asthma, arteriosclerosis, bronchitis, emphysema,
CC hyper eosinophilia, myocardial or pericardial inflammation,
CC rheumatoid arthritis, Addison's disease, AIDS, anaemia,
CC atherosclerosis, various diseases of the digestive system, atopic
CC dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis,
CC gout, Grave's disease, lupus erythematosus, multiple sclerosis,
CC myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis,
CC polycystic kidney disease, polymyositis, scleroderma, Sjorgren's
CC syndrome, autoimmune thyroiditis, complications of cancer,
CC extracorporeal circulation, viral, bacterial, fungal, parasitic,
CC protozoal and helminthic infections, and trauma (disclosed).
XX
SQ Sequence 685 AA;

Query Match 93.9%; Score 46; DB 20; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
Db 273 MLLGRPPFE 281

RESULT 13
ABP61474
ID ABP61474 standard; Protein; 685 AA.
XX
AC ABP61474;
XX
DT 30-SEP-2002 (first entry)
XX
DE Human NF-kB activating protein SEQ ID NO 101.

XX
KW Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
KW immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;
KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
XX
OS Homo sapiens.
XX
PN WO200253737-A1.
XX
PD 11-JUL-2002.
XX
PF 25-DEC-2001; 2001WO-JP11389.
XX
PR 28-DEC-2000; 2000JP-C402288.
PR 26-MAR-2001; 2001JP-0088912.
PR 24-AUG-2001; 2001JP-0254018.
XX
PA (ASAH) ASahi KASEI KOGYO KK.
XX
PI Matsuda A, Honda G, Muramatsu S, Nagano Y;
XX
DR WPI; 2002-583617/62.
DR N-PSDB; ABQ91962.

XX
PT NF-approximatelykB activating gene and expressed protein, applicable in
PT diagnosis and screening inhibitors or promoters to control excessive
PT activation or inhibition for treating e.g. inflammations, autoimmune
PT diseases and cancer -

XX PS Claim 1; Page 448-453; 841pp; Japanese.

XX CC The invention relates to a purified protein (1), comprising one of 90

CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of

CC the sequences but with some amino acids deleted, substituted or added and

CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and

CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening

CC inhibitors or promoters to control excessive activation or inhibition

CC and for treating e.g. inflammations, autoimmune diseases, cancers,

CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic

CC disorders.

XX SQ Sequence 685 AA;

Query Match 93.9%; Score 46; DB 23; Length 685;

Best Local Similarity 88.9%; Pred. No. 4.5;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9

Db 273 MLLGRPPFE 281

RESULT 14

ABP41992

10 APF41992 standard; Protein; 753 AA.

XX AC ABP41992;

XX 22-AUG-2002 (first entry)

XX Human ovarian antigen HACSMC8, SEQ ID NO:3124.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;

KW ovarian cancer; breast cancer; tumour; reproductive system disorder;

KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;

KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;

KW inflammatory condition; immune disorder; blood disorder;

KW cardiovascular disorder; respiratory disorder; neurological disorder;

KW gastrointestinal disorder; urinary system disorder; drug screening;

KW gene therapy; chromosome mapping; forensic analysis;

KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;

KW anti-inflammatory; gynaecological; reproductive; chromosome 5;

XX Homo sapiens.

OS

XX WU200200677-A1.

PN

XX 01-JAN-2002.

PP 07-JUN-2001; 2001WO-US18569.

XX 07 JUN 2000; 2000US-209467P.

FR (HUNYA-1) HUMAN GENOME SCI INC.

PA Birse CE, Rosen CA;

XX WPI, 2002-147878/19.

DB N-PSDB; ABQ55069.

DR

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,

PT useful in the prevention, treatment and diagnosis of cancer (e.g.

PT ovarian cancer), immune disorders, cardiovascular disorders and

PT neurological diseases.

XX Claim 1; SEQ ID No 3124; 2922pp; English.

PS

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-

CC ABP43226) and to cDNAs encoding them (ABQ54131-ABQ56100), and also

CC encompasses polypeptides 90% identical and polynucleotides 95% identical

CC to the sequences of the invention. The invention additionally relates to

CC recombinant vectors and host cells comprising human ovarian antigen

CC polynucleotides, antibodies against human ovarian antigens, and the use

CC of ovarian antigen polynucleotides and polypeptides in diagnosing,

CC treating, prognosing or preventing various ovary and/or breast-related

CC disorders. Such conditions include ovarian cancer and breast cancer, and

CC metastatic tumours of ovarian or breast origin, reproductive system

CC disorders (e.g., infertility, disorders of pregnancy, anovulation,

CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine

CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic

CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and

CC vaginitis), immune disorders (e.g., congenital and acquired

CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),

CC blood-related disorders (e.g., anaemia), cardiovascular disorders,

CC respiratory disorders, neurological disorders, gastrointestinal disorders

CC and urinary system disorders. Ovarian antigen polypeptides and

CC polynucleotides may also be used in screening for compounds which

CC modulate ovarian antigen expression or activity. The polynucleotides may

CC further be used for gene therapy, chromosome mapping, in the

CC identification of individuals and in forensic analysis, and the

CC polypeptides may be used as food additives or to prepare antibodies

CC useful in disease diagnosis, drug targeting and phenotyping. The present

CC sequence represents a human ovarian antigen of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 753 AA;

Query Match 93.9%; Score 46; DB 23; Length 753;

Best Local Similarity 88.9%; Pred. No. 4.5;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9

Db 341 MLLGRPPFE 349

RESULT 15

AAW74160

10 AAW74160 standard; peptide; 8 AA.

XX AC AAW74160;

XX 05-MAY-1999 (first entry)

DT HJ loop peptide J-43.

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;

KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

KW inflammatory disorder; central nervous system disease; septic shock;

KW Parkinson's disease; hypertension.

XX Synthetic.

OS

XX Key Location/Qualifiers

FT Modified-site 1 /note= "acetylated"

FT Modified-site 8 /note= "amidated"

FT

XX WO9853050-A2.

PN

XX 26-NOV-1998.

PD

XX 20-MAY-1998; 98WO-US10319.

PF

XX 21-MAY-1997; 97US-0861338.

PR (CHIL-) CHILDRENS MEDICAL CENT.

XX (YISS) YISSUM RES & DEV CO.

PA Ben-Sasson SA;

XX

DR WPI; 1993-C70142/06.
XX
PT New peptides for modulating serine/threonine kinase activity -
PI comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Claim 14; Fig 4; 70pp; English.
XX
CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 8 AA;
Query Match 89.8%; Score 44; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 1 MLLGKPPF 8
RESULT 16
AAU98316
ID AAU98316 standard; Peptide; 8 AA.
AC
XX
XX AAU98316;
DT 13-AUG-2002 (first entry)
XX
DE Polo kinase serine-threonine kinase HJ loop peptide J 43.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; J 43.
XX
CS Unidentified.
CS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT
FT Modified-site 8 /note= "C-terminal amide"
FT
XX
PN US2002049301-A1.
XX
PD 25-APR-2002.
XX
PF 13-DEC-2000; 2000US-0736076.
XX
PR 21 MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX

PI Ben-Sasson SA;
XX
DR WPI; 2002-462787/49.
XX
PT New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX
PS Disclosure; Fig 4; 41pp; English.
XX
CC The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-43. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
SQ Sequence 8 AA;
Query Match 89.8%; Score 44; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 1 MLLGKPPF 8
RESULT 17
AAW74173
ID AAW74173 standard; peptide; 20 AA.
XX
AC AAW74173;
XX
DT 05-MAY-1999 (first entry)
XX
DE HJ loop peptide POLO.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
PN WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10319.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX
PI Ben-Sasson SA;
XX
DR WPI; 1999-070142/06.
XX
PT New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Claim 41; Fig 3b; 70pp; English.
XX

CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.

XX SQ Sequence 20 AA;

Query Match 87.8%; Score 43; LB 20; Length 20;
Best Local Similarity 77.8%; Pred. No. 0.43;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
:|:|:|:|:
DB 3 LLVGKPPPE 11

RESULT 19
AAU98306
ID AAU98306 standard; Peptide; 20 AA.

XX AAU98306;

DT 11-AUG-2002 (first entry)

DE Peptide sequence of HJ loop of serine-threonine kinase polo kinase.

XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase.

XX Unidentified.

XX US2002049301 A1

PD 25-APR-2002.

PF 13 DEC-2000; 2000US-0736076.

XX 21-MAY-1997; 97US-0861338.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PI Ben-Sasson SA;

XX WPI; 2002-462787/49.

XX New peptide from the HJ loop of serine threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -

PS Claim 33; Fig 3; 41pp; English.

XX The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for

CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the peptide sequence of the HJ
CC loop of serine-threonine kinase polo kinase. This sequence is one of the
CC short peptides of the invention that selectively modulate the activity
CC of STK.

XX SQ Sequence 20 AA;

Query Match 97.8%; Score 43; DB 23; Length 20;
Best Local Similarity 77.8%; Pred. No. 0.43;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
:|:|:|:|:
DB 3 LLVGKPPPE 11

RESULT 19

AAU56690

ID AAB56690 standard; Protein; 329 AA.

XX AAB56690;

DT 13-MAR-2001 (first entry)

DE Human prostate cancer antigen protein sequence SEQ ID NO:1268.

XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.

XX Homo sapiens.

XX WO200055174-A1.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000WC-US05988.

PR 12-MAR-1999; 99US-0124270.

XX (HUN-) HUMAN GENOME SC: INC.

PA (ROSE/) ROSEN C A.

PI Rosen CA, Ruben SM;

XX WPI; 2000-587513/55.

DR N-PSDB; AAF15893.

XX Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -

PS Claim 11; Page 1691-1692; 2338pp; English.

XX AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.

cg/736076

GenCore version: 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 12:54:54 ; Search time 34.7143 Seconds
(without alignments)
41.151 Million cell updates/sec

Title: US-09-736-076-15
Perfect score: 49
Sequence: 1 MJLGRPFPE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	20	AAW74159 HJ loop peptide J-
2	49	100.0	9	23	AAU98316 Polo kinase serine
3	49	100.0	10	20	AAW74213 HJ loop peptide K0
4	49	100.0	10	23	AAU98357 Polo kinase SNK se
5	49	100.0	11	20	AAW74163 HJ loop peptide J-
6	49	100.0	11	23	AAU98319 Polo kinase serine
7	49	100.0	469	22	AAU94717 Human protein sequ
8	49	100.0	469	22	AAU67426 Amino acid sequenc
9	49	100.0	685	20	AAU00915 Human serum induci

10	49	100.0	685	20	AAW88432	Disease associated
11	49	100.0	685	23	ABP61474	Human NF-kB activa
12	49	100.0	753	23	ABP41992	Human ovarian anti
13	46	93.9	9	20	AAW74161	HJ loop peptide J-
14	46	93.9	9	23	AAU98317	Polo kinase serine
15	43	87.8	626	21	AAU35805	Protein involved i
16	43	87.8	769	22	ABU63067	Drosophila melanog
17	41	83.7	8	20	AAW74160	HJ loop peptide J-
18	41	83.7	8	23	AAU98316	Polo kinase serine
19	41	83.7	416	17	AAU92176	Sak serine-threoni
20	41	83.7	464	17	AAU92214	SAK-b serine-threo
21	41	83.7	925	17	AAU92177	SAK-a serine-threo
22	41	83.7	925	23	ABU57273	Mouse ischaemic co
23	41	83.7	970	22	AAU78833	Human protein SEQ
24	41	83.7	970	22	AAU39244	Human polypeptide
25	41	83.7	980	22	AAU79817	Human protein SEQ
26	41	83.7	980	22	AAU41030	Human polypeptide
27	40	81.6	9	20	AAW74162	HJ loop peptide J-
28	40	81.6	9	23	AAU98318	Polo kinase serine
29	40	81.6	20	20	AAW74173	HJ loop peptide PO
30	40	81.6	20	23	AAU98306	Peptide sequence o
31	40	81.6	329	21	AAU56690	Human prostate can
32	40	81.6	528	23	ABP73734	Candida albicans e
33	40	81.6	531	23	AAU74656	Mammalian polo-lik
34	40	81.6	603	16	AAU74620	Human lung tumour
35	40	81.6	603	23	AAU79306	Mouse polo-like ki
36	40	81.6	603	23	AAU79308	Mouse polo-like ki
37	40	81.6	603	23	AAU79309	Mouse polo-like ki
38	40	81.6	603	23	AAU79310	Mouse polo-like ki
39	40	81.6	603	23	AAU79311	Mouse polo-like ki
40	40	81.6	603	23	AAU79312	Mouse polo-like ki
41	40	81.6	603	23	AAU79313	Mouse polo-like ki
42	40	81.6	603	23	AAU79314	Mouse polo-like ki
43	40	81.6	603	23	AAU79315	Mouse polo-like ki
44	40	81.6	603	23	AAU79316	Mouse polo-like ki
45	40	81.6	503	23	AAU79317	Mouse polo-like ki

ALIGNMENTS

RESULT 1
AAW74159
ID AAW74159 standard; peptide; 9 AA.
XX
AC AAW74159;
XX
DT 05-MAY-1999 (first entry)
XX
DE HJ loop peptide J-42.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 9 /note= "amidated"
FT Modified-site 9 /note= "benzyl ester of Glu"
FT
XX
PN WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WG US10319.
XX
PR 21-MAY-1997; 97JUS-0861338.

A

XX (CHIL-) CHILDRENS MEDICAL CENT.
FA (YISS-) YISSUM RES & DEV CO.
XX Ben-Sasson SA;
PI WPI; 1999-070142/06.
XX New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX Claim 14; Fig 4; 70pp; English.
PS This sequence represents a peptide of the invention, and is a derivative
XX of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 49; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB 1 MLLGRPPPE 9
RESULT 2
AAU98115
ID AAW74213 standard; Peptide; 10 AA.
XX AAW74213;
AC AAW74213;
XX 05 MAY-1999 (first entry)
DT 13-AUG-2000 (first entry)
XX HJ loop peptide K038H101.
DE HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiant; hemostatic;
KW modulating STK activity; polo kinase; C 42.
XX Unidentified.
CS Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl."
FT Modified-site 3 /note= "Benzyl ester of glutamic acid"
FT /note= "C-terminal amide"
XX US2002049301-A1.
XX 15-APR-2002.

XX 13-DEC-2000; 2000US-0736076.
XX 21-MAY-1997; 97US 0861338.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX Ben-Sasson SA;
PI WPI; 2002-462787/49.
XX New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX Disclosure; Fig 4; 41pp; English.
XX The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-42. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 49; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB 1 MLLGRPPPE 9
RESULT 3
AAW74213
ID AAW74213 standard; peptide; 10 AA.
XX AAW74213;
AC AAW74213;
XX 05 MAY-1999 (first entry)
DT HJ loop peptide K038H101.
DE HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "tyristylated"
FT Modified-site 10 /note= "amidated"
XX WO9853050-A2.
XX 26 NOV-1998.
PD 20-MAY-1998; 98WO-US10319.
PF 21-MAY-1997; 97US-0861338.
XX (CHIL-) CHILDRENS MEDICAL CENT.

PA (YISS) YISSUM RES & DEV CO.
 XX Ben Sasson SA;
 PI WPI; 1999-070142/06.
 XX New peptides for modulating serine/threonine kinase activity -
 XX comprise a sequence corresponding to the HJ loop of a
 XX serine/threonine kinase, used for treating, e.g. cancers,
 XX inflammatory disorders or autoimmune disorders
 XX
 PS Disclosure; Fig 6; 70pp; English.
 XX
 CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 43; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 Db 2 MLLGRPPPE 10
 RESULT 4
 AAU98157
 ID AAU98157 standard; Peptide; 10 AA.
 XX
 AC AAU98157;
 DT 11-AUG-2002 (first entry)
 DE Polo kinase SNK serine/threonine kinase HJ loop peptide K038H101.
 KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiatic; haemostatic;
 KW modulating STK activity; polo kinase; SNK; K038H101.
 XX
 CS Unidentified.
 CS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified site 1 /note= "N-terminal myristyl;"
 FT Modified-site 10
 FT /note= "Benzyl Ester; of Glutamic Acid, C-terminal amide"
 XX
 PN US2002049301-A1.
 XX
 PD 25-APR 2002.
 XX
 PF 11-DEC-2000; 2000US-0736076.
 XX

PR 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA Ben-Sasson SA;
 PI WPI; 2002-462787/49.
 XX New peptide from the HJ loop of serine-threonine kinase, useful for
 XX treating e.g. cancer and for producing diagnostic antibodies -
 XX
 PS Disclosure; Fig 6; 4pp; English.
 XX
 CC The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase SNK
 CC serine-threonine kinase HJ loop peptide K038H101. This sequence is one
 CC of the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 49; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 Db 2 MLLGRPPPE 10
 RESULT 5
 AAW74163
 ID AAW74163 standard; peptide; 11 AA.
 XX
 AC AAW74163;
 DT 05-MAY-1999 (first entry)
 DE HJ loop peptide J-46.
 XX
 KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated"
 FT Modified-site 11 /note= "amidated"
 FT
 XX
 PN WO9853050-A2.
 XX
 PD 26-NOV-1998.
 XX
 PF 20-MAY-1998; 98WO-US10319.
 XX
 PR 21-MAY-1997; 97US-0861338.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 PA (YISS) YISSUM RES & DEV CC.
 XX Ben-Sasson SA;
 PI

XX WPI; 1993-070142/06.
XX
PT New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Claim 14; Fig 4; 73pp; English.
XX
CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 49; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
Db |||||
1 MLLGRPPPE 9
RESULT 6
AAB94719
ID AAB94719 standard; Peptide; 11 AA.
XX
AC AAB94719;
XX
DT 13 AUG 2002 (first entry)
XX
DE Polo kinase serine-threonine kinase (STK) loop peptide J-46.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurologica;
KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
KW modulating STK activity; polo kinase; J-46.
XX
OS Unidentified.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Misc-difference 9 /note= "Benzyl ester of Glutamic acid"
FT Modified-site 11 /note= "C-terminal amide"
FT
XX
PN US2002049301-A1.
XX
FC 25 APR-2002.
XX
PF 13-DEC-2000; 2000US-0736076.
XX
PR 21-MAY-1997; 97US-0861338.

XX (CHIL-) CHILDRENS MEDICAL CENT.
PA Ben-Sasson SA;
XX WPI; 2002-462787/49.
XX
PT New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX
PS Disclosure; Fig 4; 41pp; English.
XX
CC The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-46. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 49; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
Db |||||
1 MLLGRPPPE 9
RESULT 7
AAB94717
ID AAB94717 standard; Protein; 469 AA.
XX
AC AAB94717;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:15726.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP:074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the

PT full-length cDNAs -
 XX Claim 8; SEQ ID 15726; 2537pp + CD ROM; English.
 PS
 XX
 CC The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 469 AA;
 Query Match 100.0%; Score 49; DB 22; Length 469;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 DE 57 MLLGRPPPE 65
 RESULT 8
 AAG67426
 ID AAG67426 standard; Protein; 469 AA.
 XX
 AC AAG67426;
 YV
 DT 26-NOV-2001 (first entry);
 XX
 DE Amino acid sequence of a human protein kinase/protein phosphatase.
 XX
 KW Human; protein kinase; protein phosphatase, signal transduction;
 KW intracellular signalling pathway.
 XX
 OS Homo sapiens.
 XX
 PN WC2001C9345-A1.
 XX
 PE 08-FEB-2001.
 XX
 PF 28-JUL-2000; 2003WO-0305060.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 18-OCT-1999; 99US-0159590.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 17-FEB-2000; 2000US-0183322.
 PR 02-MAY-2000; 2000JP-0183767.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 PI Senoo C, Nezu C;
 XX
 DR WPI; 2001-564736/63.
 DR N-PSDB; AAH78069.

XX New genes encoding protein kinase and protein phosphatase, useful for
 PT identifying modulators which can be used to treat human or animal
 PT disorders associated with the expression or function of these enzymes -
 XX
 PS Claim 2; Page 136-139; 336pp; Japanese.
 XX
 CC The present sequence represents a human protein kinase/protein
 CC phosphatase. The polypeptides are expected to participate in signal
 CC transduction in cells. The kinase phosphatases are connected with
 CC intracellular signalling pathways. Antisense oligonucleotides and
 CC compounds identified by screening (agonists or antagonists) can be
 CC used to treat human or animal disorders associated with the expression
 CC or function of the protein. In addition, the polypeptides may be used
 CC as target molecules for drug development.
 XX
 SQ Sequence 469 AA;
 Query Match 100.0%; Score 49; DB 22; Length 469;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 DE 57 MLLGRPPPE 65
 RESULT 9
 AAY00915
 ID AAY00915 standard; Protein; 685 AA.
 XX
 AC AAY00915;
 XX
 DT 28-MAY-1999 (first entry);
 XX
 DE Human serum inducible kinase.
 XX
 KW Serum inducible kinase; SNK protein; human; proliferative disease;
 KW leukaemia; solid tumour cancer; metastasis; chronic inflammatory;
 KW psoriasis; rheumatoid arthritis; proliferative cardiovascular disease;
 KW restenosis; ocular disorder; diabetic retinopathy; haemangioma;
 KW benign hyperproliferative disease; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9909146-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 20-AUG-1998; 98WO-US17248.
 XX
 PR 20-AUG-1997; 97US-0056112.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Anderson KM, Bouzyk M, Hansbury MJ, Jackson JR;
 PI Nerurkar SS, Roshak AK;
 XX
 DR WPI; 1999-181027/15.
 DR N-PSDB; AAX27227.
 XX
 PT New serum inducible kinase (Snk) polypeptides and polynucleotides -
 PT useful for treating proliferative diseases
 XX
 PS Claim 1; Page 39-40; 41pp; English.
 XX
 CC This sequence is a human serum inducible kinase (SNK) of the
 CC invention. The invention relates to diagnostic assays or kits for
 CC detecting diseases associated with inappropriate SNK activity or levels.
 CC Disease states that can be diagnosed include proliferative diseases such
 CC as leukaemia, solid tumour cancers and metastases, chronic inflammatory
 CC proliferative diseases such as psoriasis and rheumatoid arthritis,
 CC proliferative cardiovascular diseases such as restenosis, proliferative

ocular disorders such as diabetic retinopathy and benign hyperproliferative diseases such as haemangiomas. The polynucleotides can be used as hybridisation probes for cDNA and genomic DNA or as primers for a nucleic acid amplification (PCR) reaction, to isolate full-length cDNAs and genomic clones encoding polypeptides of this invention and to isolate cDNA and genomic clones of other genes which have a high sequence similarity to the SNK coding sequence. The differences between cDNA and genomic sequences can be observed and therefore mutations detected. Any mutations may then be attributed to likely causative agents of disease. The nucleotide sequences are also useful for chromosome identification.

Sequence 685 AA;
Query Match 100.0%; Score 49; DB 20; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLJGRPPPE 9
Db 273 MLJGRPPPE 281

RESULT 10
AAW88432
ID AAW88432 standard; Protein: 685 AA.
XX
AC AAW88432;
XX
DT 26 APR-1999 (first entry)
XX
DE Disease associated protein kinase DAPK-1.
XX
KW DAPK-1; disease associated protein kinase; human; diagnosis; therapy; adult respiratory distress syndrome; allergy; asthma; arteriosclerosis; bronchitis; emphysema; hyper eosinophilia; myocardial inflammation; pericardial inflammation; anaemia; rheumatoid arthritis; Addison's disease; AIDS; atherosclerosis; atopic dermatitis; dermatomyositis; diabetes mellitus; glomerulonephritis; gout; Grave's disease; lupus erythematosus; multiple sclerosis; myasthenia gravis; osteoarthritis; osteoporosis; pancreatitis; polycystic kidney disease; polymyositis; scleroderma; Sjorgren's syndrome; autoimmune thyroiditis; cancer; infection; trauma; cell proliferation.

XX Homo sapiens.
CS
FH Key Location/Qualifiers
FT Binding-site 89..96 /note= "potential ATP binding site"
FT Peptide 506..511 /note= "presumed regulatory sequence common to polo family protein kinases"
XX
PN WC9858052-A2.
XX
PD 23-DEC-1998.
XX
FF 19-JUN-1998; 98WO-US12813.
XX
PR 19-JUN-1997; 97US-0878989.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Corley NC, Goli SK, Quegler KJ, Hillman JL; Lai P, Shah P;
XX
XX WPI; 1999-080952/07.
DR N-PSDB; AAX06831.
XX
PT New disease associated protein kinases - used to stimulate cell proliferation and to treat the immune response and cancer

PS
XX This is the amino acid sequence of human disease associated protein kinase DAPK-1, as deduced from a consensus sequence (see AAX06831) of overlapping cDNA clones from libraries which are immortalised or cancerous and show inflammatory or immune responses. DAPK-1 shows 53% homology to human proliferation-related protein kinase PRK (GI 1489263). The invention provides DAPK-1 to DAPK-7 polypeptides (see AAW88432-38) and cDNA clones encoding them (see AAX06831-36 and AAX06882), as well as expression vectors, host cells, agonists, antagonists and antibodies. The invention further provides uses of such products in the diagnosis, prevention and treatment of diseases associated with cell proliferation, especially cancer or an immune response (claimed). Conditions that may be treated include adult respiratory distress syndrome, allergies, asthma, arteriosclerosis, bronchitis, emphysema, hyper eosinophilia, myocardial or pericardial inflammation, rheumatoid arthritis, Addison's disease, AIDS, anaemia, atherosclerosis, various diseases of the digestive system, atopic dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis, gout, Grave's disease, lupus erythematosus, multiple sclerosis, myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis, polycystic kidney disease, polymyositis, scleroderma, Sjorgren's syndrome, autoimmune thyroiditis, complications of cancer, extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal and helminthic infections, and trauma (disclosed).

XX
SQ Sequence 685 AA;
Query Match 100.0%; Score 49; DB 20; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLJGRPPPE 9
Db 273 MLJGRPPPE 281

RESULT 11
ABP61474
ID ABP61474 standard; Protein: 685 AA.
XX
AC ABP61474;
XX
DT 30-SEP-2002 (first entry)
XX
DE Human NF-kB activating protein. SEQ ID NO 101.
XX
KW Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory; immunomodulator; cytostatic; antiinfective; osteopathic; nootropic; neuroprotective; anti-HIV; autoimmune disease; cancer; infection; bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
XX
OS Homo sapiens.
XX
PN WO200253737-A1.
XX
PD 11-JUL-2002.
XX
PF 25-DEC-2001; 2001WO-JP11389.
XX
PR 28-DEC-2000; 2000JP-0402288.
PR 26-MAR-2001; 2001JP-0088912.
PR 24-AUG-2001; 2001JP-0254018.
XX
PA (ASAH) ASahi KASEI KOGYO KK.
XX
PI Matsuda A, Honda G, Muramatsu S, Nagano Y;
XX
DR WPI; 2002-583617/62.
DR N-PSDB; ABQ91962.
XX
PT NF-approximate,ykB activating gene and expressed protein, applicable in

PT diagnosis and screening inhibitors or promoters to control excessive
PT activation or inhibition for treating e.g. inflammations, autoimmune
PT diseases and cancer -
XX
PS Claim 1; Page 448-453; 841pp; Japanese.
XX
CC The invention relates to a purified protein (I), comprising one of 90
CC fully defined sequences (ABP61424-ASP61513) or a protein based on any of
CC the sequences but with some amino acids deleted, substituted or added and
CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
CC inhibitors or promoters to control excessive activation or inhibition
CC and for treating e.g. inflammations, autoimmune diseases, cancers,
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
CC disorders.
XX
SQ Sequence 685 AA;
Query Match 100.0%; Score 49; DB 23; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 MLLGRPPFE 9
DB 273 MLLGRPPFE 291
RESULT 12
ABP41392
ID ABP41992 standard; Protein; 753 AA.
XX
AC ASP41992;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HAOSMC8, SEQ ID NO:3124.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; chemotherapy.
XX
OS Homo sapiens.
XX
TN WO2002020277 A1.
XX
PC 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US:8569.
XX
PR 07-JUN-2000; 2000US-209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
DR N-PSDB; ABQ55069.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides.
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases -
XX
PS Claim 1; SEQ ID No 3124; 2922pp; English.
XX
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-

CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 753 AA;

Query Match 100.0%; Score 49; DB 23; Length 753;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 341 MLLGRPPFE 349
RESULT 13
AAW74161
ID AAW74161 standard; peptide; 9 AA.
XX
AC AAW74161;
XX
DT 05-MAY-1999 (first entry)
XX
DE HU loop peptide J-43.1.
XX
KW HU loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site ;
FT Modified-site 9 /note= "acetylated"
FT Modified-site 9 /note= "amidated"
XX
PN WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US:0319.
XX
PR 21-MAY-1997; 97US-C861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUX RES & DEV CO.

XX Ben-Sasson SA;
PI WPI; 1999-070142/06.
DR
XX
XX New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
XX
PS Claim 14; Fig 4; 70pp; English.
XX
XX This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
XX
SQ Sequence 9 AA;
Query Match 93.9%; Score 46; DB 20; Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB 1 MLLGKPPPE 9
RESULT 14
AAU98317
ID AAU98317 standard; Peptide; 9 AA.
XX
XX AAU98317;
AC
XX 13-AUG-2002 (first entry)
DT
XX
XX Polo kinase serine threonine kinase HJ loop peptide J-43.1.
DE
XX HJ loop; serine/threonine kinase; STK; cancer, diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; J-43.1.
XX
XX Unidentified.
CS Synthetic.
CS
XX
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Modified site 9 /note= "Benzyl ester of Glutamic acid, C-terminal amide"
FT
XX US2002049301-A1.
PN
XX 25-APR-2002.
PD
XX 11-DEC-2000; 2000US-0736076.
PF
XX 21-MAY-1997; 97US-0861338.
FR

XX (CHIL-) CHILDRENS MEDICAL CENT.
PA Ben-Sasson SA;
XX
PI WPI; 2002-462787/49.
XX
DR
XX New peptide from the HJ loop of serine-threonine kinase, useful for
XX treating e.g. cancer and for producing diagnostic antibodies -
PT
XX
XX Disclosure; Fig 4; 41pp; English.
PS
XX The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-43.1. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
XX Sequence 9 AA;
SQ
Query Match 93.9%; Score 46; DB 23; Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB 1 MLLGKPPPE 9
RESULT 15
AAB35805
ID AAB35805 standard; Protein; 626 AA.
XX
XX AAB35805;
AC
XX 23-FEB-2001 (first entry)
DT
XX Protein involved in cell cycle regulation SEQ ID 46.
DE
XX Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
KW cyclin-dependent kinase; sunflower; sorghum; canola; alfalfa;
KW cotton; rice; barley; millet.
XX
XX Zea mays.
OS
XX WO200365040-A2.
PN
XX 02-NOV-2000.
PD
XX
XX 13-APR-2000; 2000WO-US09975.
PF
XX 22-APR-1999; 99US-0130849.
PR
XX (PION-) PIONEER HI-BRED INT INC.
PA
XX Helentjaris TG, Habben JE, Sun Y;
PI
XX WPI; 2000-687333/67.
DR
XX N-PSDB; AAC83112.
DR
XX Nucleic acids useful for producing transgenic plants, preferably maize,
PT with increased cell cycle gene activity, preferably activity of cyclin
PT and/or cyclin-dependent kinase -
XX
XX Claim 16; Page 117-118; 122pp; English.
PS

XX Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
CC AAB35806 which are involved in regulating the cell cycle. The protein and
CC DNA sequences have been isolated from Zea mays (corn), and the invention
CC also includes oligonucleotides AAC83114 - AAC83119 which are related to
CC the cell cycle polynucleotides. The cell cycle polynucleotide sequences
CC are useful for producing transgenic plants such as maize, soybean,
CC sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
CC millet with increased levels of cell cycle gene activity, such as
CC activity of cyclin and cyclin-dependent kinases. The DNA sequences are
CC also useful as probes for detecting deficiencies in the level of mRNA in
CC screening for desired transgenic plants, for detecting mutations in the
CC gene, for monitoring upregulation of expression or changes in enzyme
CC activity in screening assays of compounds, for detecting any number of
CC allelic variants, orthologs or paralogues of the gene, and site-directed
CC mutagenesis in eukaryotic cells. The DNA sequences are also useful for
CC recombinant expression of the encoded polypeptides and as immunogens for
CC preparing and screening antibodies. A transgenic plant comprising an
CC expression cassette including a cell cycle regulatory gene is useful for
CC assaying enzyme agonists and antagonists, and as immunogens or antigens
CC to obtain antibodies. The antibodies are useful in assaying expression
CC levels of cell cycle regulatory proteins, for identifying and isolating
CC nucleic acids from expression libraries, for identifying homologues of
CC polypeptides from other species, and for purification of the proteins.
XX
SQ Sequence 626 AA;

Query Match 97.8%; Score 43; DB 21; Length 626;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
:|:|:|
DB 228 LLVGRPPFE 236

RESULT 16
A5563067
ID A5563067 standard; Protein; 769 AA.
XX
AC A5563067;
XX
DT 26-MAR-2002 (first entry)
YV
DE Drosophila melanogaster polypeptide SEQ ID NO 15993
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
CS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
FR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL07170.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
PS Disclosure; SEQ ID NO 15993; 21pp + Sequence Listing; English.
XX

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (AAB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 769 AA;

Query Match 87.8%; Score 43; DB 22; Length 769;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
:|:|:|:|
DB 206 LLVGRPPFE 214

RESULT 17
AAW74160
ID AAW74160 standard; peptide; 8 AA.
XX
AC AAW74160;
XX
DT 05-MAY-1999 (first entry)
XX
DE HJ loop peptide J-43.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 8 /note= "amidated"
FT
XX
FN WO9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WC-US:0319.
XX
PR 21-MAY-1997; 97US-0861338.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) VISSUM RES & DEV CO.
XX
XX Ben-Sasson SA;
PI
XX
DR WPI; 1999-070142/06.
XX
XX New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Claim 14; Fig 4; 70pp; English.
XX
XX This sequence represents a peptide of the invention, and is a derivative
XX of the HJ loop of a serine/threonine kinase (STK). The peptides can be
XX used for the treatment of disorders caused by overactivity or
XX underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
XX shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
XX

arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and hypertension), immunosuppressive and inflammatory disorders (e.g. asthma, psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression of organ transplant rejection, multiple sclerosis, inflammatory bowel disease and AIDS), central nervous system diseases (e.g. Alzheimer's disease, stroke and trauma), septic shock, Parkinson's disease or hypertension. The peptides can also be used to produce antibodies which can be used to identify cells expressing the STK and to study the intracellular distribution of the STK. In addition, the peptides can be used to identify and quantitate ligands which bind the HJ loop of the STK from which the peptide was derived.

Query Match 83.7%; Score 41; DB 23; Length 8;
Best Local Similarity 87.5%; Pred. No. 9.3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPF 8
|||:||||
DB 1 MLLGKPPF 8

RESULT 18
AAU98316
ID AAU98316 standard; Peptide; 8 AA.

XX AC AAU98316;
XX DT 13-AUG-2002 (first entry)
XX DE Polo kinase serine-threonine kinase HJ loop peptide J-43.
XX KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
XX KW central nervous system disorder; inflammatory disorder;
XX KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
XX KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
XX KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
XX KW modulating STK activity; polo kinase; J-43.

XX CS Unidentified.
XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "N-terminal acetyl"
XX FT Modified-site 8 /note= "C-terminal amide"

XX PN US2002049201 A1.
XX PD 25-APR-2002.
XX FF 13-DEC-2000; 2000US-0736076.
XX PR 21-MAY-1997; 97US-0861338.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Ben-Sasson SA;
XX XX WPI; 2002-462787/49.
XX PT New peptide from the HJ loop of serine-threonine kinase, useful for treating e.g. cancer and for producing diagnostic antibodies -
XX PS Disclosure; Fig 4; 41pp; English.

XX CC The present invention relates to new peptides derived from the HJ loop of a serine/threonine kinase (STK). The peptides of the invention are used to modulate STK activity, especially for treating cancer, diabetes, obesity or a wide variety of central nervous system, inflammatory, autoimmune or cardiovascular disorders, also haemorrhagic shock, and for

CC regulating lipid metabolism. The peptides are also used to generate antibodies that bind specifically to the parent STK, used e.g. for identifying STK-expressing cells and to study intracellular distribution of STK, and to identify or quantify ligands that bind to the HJ loop. The present amino acid sequence represents the polo kinase serine-threonine kinase HJ loop peptide J-43. This sequence is one of the short peptides of the invention that selectively modulate the activity of STK.

XX XX Sequence 8 AA;
SQ Query Match 83.7%; Score 41; DB 23; Length 8;
Best Local Similarity 87.5%; Pred. No. 9.3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPF 8
|||:||||
DB 1 MLLGKPPF 8

RESULT 19
AAR92176
ID AAR92176 standard; Protein; 416 AA.

XX AC AAR92176;
XX DT 25-MAY-1996 (first entry)
XX DE Sak serine-threonine kinase N-terminus.
XX KW Sak; serine-threonine kinase; STK; agonist; antagonist;
XX KW proliferative disease; cancer; tumour; antisense; transgenic animal; therapy.

XX OS Mus musculus.
XX PN CA2150789-A.
XX PD 03-DEC-1995.

XX PF 01-JUN-1995; 95CA-2150789.
XX PR 02-JUN-1994; 94US-0252995.

XX PA (MOUN) MOUNT SINAI HOSPITAL CORP.
XX PI Dennis JW, Fode C, Heffernan M;
XX DR WPI; 1996-129817/14.
XX DR N-PSDB; AAT08710.

XX PT Nucleic acid encoding Sak serine-threonine kinase - useful for identifying modulators potentially useful in treatment or prevention of proliferative disease.

XX PS Claim 3; Page 46-49; 73pp; English.

XX CC 2 isoforms, sak-a and sak-b, of a novel serine/threonine kinase have an identical N-terminal sequence (AAR92176) that contains the kinase domain and that shows significant homology to the polo subfamily. The C-terminal sequences (each contg. 3 PEST regions) of the 2 isoforms differ (see AAR92177 and AAR92214). Sak-a and Sak-b are associated with mitotic and meiotic cell division, and may be involved in cell proliferation. They can be obtd. in recombinant form by expression of encoding sequences (see AAT08710-12) and used to test for inhibitory or stimulatory cpds. that may be useful in the treatment/diagnosis of proliferative disorders, such as cancer and viral (esp. HIV) infection.

XX SQ Sequence 416 AA;

Query Match 83.7%; Score 41; DB 17; Length 416;
Best Local Similarity 66.7%; Pred. No. 18;

XX Homo sapiens.
OS
XX WO200153312-A1.
XX
XX 26-JUN-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR N-PSDB; AAI58400.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PI such as central nervous system injuries -
XX
XX Example 4; SEQ ID NO 2389; 100789p; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX Sequence 970 AA;
SQ
Query Match 83.7%; Score 41; DB 22; Length 970;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
Db 204 LLIGRPPFD 212
RESULT 25
AAM79817
ID AAM79817 standard; Protein; 980 AA.
XX
XX AAM79817;
AC
XX
XX 06-NOV-2000 (first entry)
DT
XX
XX Human protein SEQ ID NO 2463.
DE
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04038.
XX
XX 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
XX 20-JUN-2000; 2000US-0598075.
XX 19-JUL-2000; 2000US-0620325.
XX 01-SEP-2000; 2000US-0654936.
XX 15-SEP-2000; 2000US-0663561.
XX 20-OCT-2000; 2000US-0693325.
XX 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
DR N-PSDB; AAK52950.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PI useful in diagnosis and gene therapy -
XX
XX Claim 20; Page 345; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX Sequence 980 AA;
SQ
Query Match 83.7%; Score 41; DB 22; Length 980;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
Db 214 LLIGRPPFD 222
RESULT 26
AAM41030
ID AAM41030 standard; Protein; 980 AA.
XX
XX AAM41030;
AC
XX
XX 22-OCT-2001 (first entry)
DT
XX
XX Human polypeptide SEQ ID NO 5961.
DE
XX
XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW Chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WC200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0498725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen P, Ma Y, Qian XR, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue A, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Oranag RC;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AA160186.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Example 2; SEQ ID NO 5961; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AA157038 AA161363) and
CC the encoded polypeptides (AA138642-AA42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activity, such as immune system suppression,
CC Activin/inhibin activity, chemotaxis/chemokine activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, antigenic and immunogenic, leukaemias and
CC CNS disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 980 AA;

Query Match 83.7%; Score 41; DB 22; Length 980;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
ID 214 LILGRPPFC 222

RESULT 27
AAW74162
ID AAW74162 standard; peptide; 9 AA.
XX
AC AAW74162;
XX
DT 05-MAY-1999 (first entry)
XX
DE HC loop peptide J-45.
XX
EW HC loop; serine/threonine kinase; cancer; diabetes; obesity, therapy.

KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
PH Key location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 9 /note= "amidated"
FT
XX
PN WC9853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10319.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CC.
XX
PI Ben-Sasson SA;
XX
DR WPI; 1999-070142/06.
XX
PT New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Claim 14; Fig 4; 70pp; English.
XX
CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HC loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 9 AA;

Query Match 81.6%; Score 40; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGRPPPE 9
ID 1 LGRPPPE 7

RESULT 28
AAJ98318
ID AAJ98318 standard; Peptide; 9 AA.
XX
AC AAJ98318;
XX
DT 13-AUG-2002 (first entry)
XX
DE Polo kinase serine-threonine kinase HC loop peptide J-45.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;

KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
KW modulating STK activity; polo kinase; J-45.
XX Unidentified.
OS Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Misc-difference 7
FT /note= "Benzyl ester of Glutamic acid"
FT Modified-site 9 /note= "C-terminal amide"
XX US2002049301-A1.
PN 25-APR 2002.
XX 13 DEC-2000; 2000US-0736076.
PF 21 MAY-1997; 97US-0861338.
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA Ben-Sasson SA;
XX WPI; 2002-462787/49.
XX New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies.
XX Disclosure; Fig 4; 4ipp; English.
XX The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J 45. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
SQ Sequence 9 AA;
Query Match 81.6%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 LGRPPFE 9
DB 1 LGRPPFE 7
RESULT 29
AAW74173
ID AAW74173 standard; peptide; 20 AA.
XX AAW74173;
AC
XX 05-MAY-1999 (first entry)
DT HJ loop peptide POLC.
DE
XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX Synthetic.
OS WO9853050-A2.
PN 26-NOV-1998.
XX 20-MAY-1998; 98WO-US10319.
PF 21-MAY-1997; 97US-0861338.
PR (CHIL-) CHILDRENS MEDICAL CENT.
XX (YISS) YISSUM RES & DEV CO.
PA Ben-Sasson SA;
XX WPI; 1999-070142/06.
DR New peptides for modulating serine/threonine kinase activity -
XX comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX Claim 41; Fig 3b; 70pp; English.
PS This sequence represents a peptide of the invention, and is a derivative
XX of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX Sequence 20 AA;
SQ Query Match 81.6%; Score 40; DB 20; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPFE 9
DB 3 LLVGKPPFE 11
RESULT 30
AAU98306
ID AAU98306 standard; Peptide; 20 AA.
XX AAU98306;
AC
XX 13-AUG-2002 (first entry)
DT Peptide sequence of HJ loop of serine-threonine kinase polo kinase.
XX
DE HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
XX central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
KW modulating STK activity; polo kinase.
XX Unidentified.

PT for therapeutic intervention, by inactivating in the strain one allele
PT of a gene and placing other allele of the gene under conditional
XX expression
PS Claim 44: SEQ ID NO 7571; 167pp + Sequence listing; English.
XX
CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of an
CC essential Candida albicans protein used in the method of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.
XX
SQ Sequence 528 AA;

Query Match 81.6% Score 40; DB 23; Length 528;
Best: Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 454 LNVGKPPFE 462

RESULT 3:
AAJ74656
ID AAJ74656 standard; Protein. 531 AA.
XX
AC AAJ74656;
XX
PT 09-APR 2002 (first entry)
XX
DE Mammalian polo-like kinase (Plk).
XX
KW Polo-like kinase; Plk; polo-box; cytoskeletal neoplasm;
KW hyperproliferative disorder; cytokinesis; solid tumour;
KW carcinoma; sarcoma; cancer; small cell carcinoma; adenocarcinoma;
KW Mullerian tumour; squamous cell carcinoma; protein.
XX
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Misc-difference 130 /label= Unknown
FT Misc-difference 131 /label= Unknown
FT Misc-difference 132 /label= Unknown
FT Misc-difference 133 /label= Unknown
FT Misc-difference 134 /label= Unknown
FT Misc-difference 135 /label= Unknown
FT Misc-difference 136 /label= Unknown

FT Misc-difference 136 /label= Unknown
FT Misc-difference 137 /label= Unknown
FT Misc-difference 138 /label= Unknown
FT Misc-difference 139 /label= Unknown
FT Misc-difference 140 /label= Unknown
FT Misc-difference 141 /label= Unknown
FT Misc-difference 142 /label= Unknown
FT Misc-difference 143 /label= Unknown
FT Misc-difference 144 /label= Unknown
FT Misc-difference 145 /label= Unknown
FT Misc-difference 146 /label= Unknown
FT Misc-difference 147 /label= Unknown
FT Misc-difference 148 /label= Unknown
FT Misc-difference 149 /label= Unknown
FT Misc-difference 150 /label= Unknown
FT Misc-difference 151 /label= Unknown
FT Misc-difference 152 /label= Unknown
FT Misc-difference 153 /label= Unknown
FT Misc-difference 154 /label= Unknown
FT Misc-difference 155 /label= Unknown
FT Misc-difference 156 /label= Unknown
FT Misc-difference 157 /label= Unknown
FT Misc-difference 158 /label= Unknown
FT Misc-difference 159 /label= Unknown
FT Misc-difference 160 /label= Unknown
FT Misc-difference 161 /label= Unknown
FT Misc-difference 162 /label= Unknown
FT Misc-difference 163 /label= Unknown
FT Misc-difference 164 /label= Unknown
FT Misc-difference 165 /label= Unknown
FT Region /label= Unknown
FT 410..439 /label= Polo-box
FT /note= "Core polo-box consensus sequence"
FT
XX WO200190401-A2.
PN 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US16903.
XX
PR 23-MAY-2000; 2000US-206588P.
XX
PA (HARD) HARVARD COLLEGE.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH) US NAT INST OF HEALTH.
XX
PI Lee KS, Song S, Erikson R;
XX WPI; 2002-106210/14.
DR
XX
PT Identifying polo-like kinase modulators by contacting eukaryotic cells
PT expressing polo-box peptides with test compounds and evaluating changes
PT in dominant negative cytokinesis-defective growth patterns -

XX Example 2; Fig 5; 57pp; English.

PS The invention describes a novel method of detecting compounds with

XX polo-like kinase (PLK) modulating activity. This comprises contacting

CC eukaryotic cells expressing polo-box or polo-box related peptides,

CC binding peptides comprising 25 contiguous residues from a polo-like

CC kinase C-terminal region, with a test compound. Ecopic expression of a

CC polo-box in a eukaryotic cell causes a severe cytokinetic defect in the

CC cell. These eukaryotic cells can also be tested with the test compound

CC used in the method of the invention. The polo-box related peptides and

CC polo-like kinase activity modulatory compounds can be used to inhibit or

CC enhance cellular proliferation and subsequently for treating

CC hyper-proliferative disorders including neoplasms, solid tumours,

CC carcinomas, sarcomas and cancers e.g. small cell carcinoma,

CC adenocarcinoma, Mullerian tumours and squamous cell carcinomas. This

CC is the amino acid sequence of a mammalian polo-like kinase (Plk),

CC uncontrolled expression of the plk family is implicated in the

CC development of human cancers, discussed in the method of the invention.

XX

SQ Sequence 531 AA;

Query Match 81.6%; Score 40; DB 23; Length 531;

Best Local Similarity 66.7%; Pred. No. 36;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGGRPPFE 9

Db 204 LLVGKPPFE 212

RESULT 34

AAU74420

ID AAR74620 standard; Protein: 603 AA.

XX

AC AAR74620;

XX

DT 25 MAR-2003 (updated)

DT 26-OCT-1995 (first entry)

XX

DE Human lung tumour Polo-like kinase.

XX

KW Polo-like kinase; Plk; serine threonine kinase; human; lung tumour;

KW autoimmune disease; lymphocyte activity

XX

OS Homo sapiens.

XX

EH Key Location/Qualifiers

FT Binding-site 60..86

FT /label= ATP binding site

FT Region 174..177

FT /note= "motif that is highly conserved in protein

FT kinases"

FT Region 194..196

FT /note= "motif that is highly conserved in protein

FT kinases"

XX

PN DE4329177-A1.

XX

PC 02-MAR-1995.

XX

PF 30 AUG-1993; 93DE-4329177.

XX

PR 30 AUG-1993; 93DE-4329177.

XX

PA (CHEM.) CHEMOTHERAPEUTISCHES FORSCHUNG

XX

PI Holtrich U, Rutsamen-Waigmann H, Stierwald H;

PI Rutsamen-Waigmann H;

XX

WR WP1; 1995-099454/14.

DR N-9508; AAQ88155.

XX

PT A polo-like serine threonine kinase-protein - isolated from

PT proliferating human tissue, useful in the determin of lymphocyte

PT activity, eg in auto-immune diseases

XX

PS Claim 1; Page 8-10; 11pp; German.

XX

CC A human lung tumour-derived cDNA (AAQ88155) was found to have high

CC homology with sequences from members of the serine/threonine kinase

CC family. Due to the strong homology with the Drosophila polo gene,

CC the protein encoded by the new cDNA (AAR74620) was designated a polo-

CC like kinase (PLK). PLK mRNA is expressed in proliferating cells such

CC as placenta, colon and tumours of the lung, oesophagus, gut and

CC intestine. Resting lymphocytes do not express the PLK gene but after

CC stimulation with phytohaemagglutinin, PLK is expressed and can be

CC used as an indicator of lymphocyte stimulation.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 603 AA;

Query Match 81.6%; Score 40; DB 16; Length 603;

Best Local Similarity 66.7%; Pred. No. 41;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGGRPPFE 9

Db 244 LLVGKPPFE 252

RESULT 35

AAU79306

ID AAU79306 standard; Peptide: 603 AA.

XX

AC AAU79306;

XX

DT 02-JUL-2002 (first entry)

XX

DE Mouse polo-like kinase (Plk).

XX

KW Polo box; Pbl; cytostatic; fungicide; protozoacide; antihelmintic;

KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;

KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;

KW cancer of the uterus; ovarian cancer; cervical cancer;

KW epithelial cancer; brain cancer; retina cancer; prostate cancer;

KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;

KW Epidermophyton; Microsporum; protozoan infection; helminthes infection;

KW arthropod infection; mouse; polo-like kinase; plk.

XX

OS Mus musculus.

XX

PN US6358738-B1.

XX

PD 19-MAR-2002.

XX

PF 13-MAY-1999; 99US-0311311.

XX

PR 13-MAY-1998; 98US-085296P.

XX

PA (HARD ; HARVARD COLLEGE.

XX

PI Erikson RL, Lee KS;

XX

DR WPI; 2002-314756/35.

XX

PT Administering polo kinase inhibitors for the treatment of cancers and

PT fungal infections

XX

PS Example 1; Column 59-64; 47pp; English.

XX

CC The invention describes a method of inhibiting growth of an isolated

CC population of cells by inhibiting a cell polo kinase by administering a

CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a

CC carboxy terminal domain of the polo kinase which excludes the polo

CC kinase catalytic domain. The method is used for the treatment of cancer

CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of the polo-like kinase (Plk), a
CC protein from which mitotic protein polo kinase inhibitory peptides are
CC derived.

XX
SQ Sequence 603 AA;
Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
:|:|:|:|
Db 244 LLVGKPPPE 252

RESULT 36
AAU79309
ID AAU79308 standard; Peptide; 603 AA.
XX
AC AAU79308;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T21ED mutant.
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelmintic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
XX
OS Mus musculus.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Misc-difference 21C /note= "Wild type Thr substituted by Asp"
FT
XX
PN US6358738-B1.
XX
PD 19-MAR-2002
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002 314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Page -; 47pp; English.

XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.

CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.

XX
SQ Sequence 603 AA;
Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
:|:|:|:|
Db 244 LLVGKPPPE 252

RESULT 37
AAU79309
ID AAU79309 standard; Peptide; 603 AA.
XX
AC AAU79309;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T21OE mutant.
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelmintic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
XX
OS Mus musculus.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Misc-difference 21C /note= "Wild type Thr substituted by Glu"
FT
XX
PN US6358738-B1.
XX
PD 19-MAR-2002
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Page -; 47pp; English.

XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.

CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy : MLLGRPPPE 9
Db 244 LLVGKPPPE 252

RESULT 38
AAU79310
ID AAU79310 standard; Peptide: 603 AA.
XX
AC AAU79310;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T210V mutant.
XX
KW Polo box; PBL; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Thr substituted by Val"
FT
XX
FN US6359738 B1.
FN
PD 19-MAR-2002.
PD
PF 13-MAY-1999; 99JS-0311311.
PF
XX
PR 13-MAY-1998; 98JS-085296P.
PR
XX
PA (HARD : HARVARD COLLEGE.
PA
XX
PI Erickson RL, Lee KS;
PI
XX
DR WPI; 2002-314756/35.
DR
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections
PT
XX
PS Example 1; Page : 47pp; English.
PS
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information

CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy : MLLGRPPPE 9
Db 244 LLVGKPPPE 252

RESULT 39
AAU79311
ID AAU79311 standard; Peptide: 603 AA.
XX
AC AAU79311;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) E236V mutant.
XX
KW Polo box; PBL; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Glu substituted by Val"
FT
XX
FN US6359738-B1.
FN
PD 19-MAR-2002.
PD
PF 13-MAY-1999; 99JS-0311311.
PF
XX
PR 13-MAY-1998; 98JS-085296P.
PR
XX
PA (HARD : HARVARD COLLEGE.
PA
XX
PI Erickson RL, Lee KS;
PI
XX
DR WPI; 2002-314756/35.
DR
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections
PT
XX
PS Example 1; Page : 47pp; English.
PS
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.

SQ Sequence 603 AA;
Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
:|:|:|
Db 244 LLVGKPPPE 252

RESULT 40
AAU79312
ID AAU79312 standard; Peptide; 603 AA;
XX
AC AAU79312;
XX
Pr 02-JUL 2002 (first entry);
XX
DE Mouse polo-like kinase (Plk) E206N mutant.
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Gln substituted by Asn"
FT
XX US6358735-B1.
XX 19 MAR-2002.
XX 13-MAY-1999; 99US-0311311.
XX 13-MAY-1998; 98US-085296P.
XX CHARD ; HARVARD COLLEGE.
XX Erikson Ed. Lee KS;
XX WPI; 2002-314756/35.
XX Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections .
XX Example 1; Page 4; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
:|:|:|
Db 244 LLVGKPPPE 252

Search completed: November 14, 2003, 13:25:19
Job time : 34.7143 secs

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OM protein - protein search, using sw model

Run on: November 14, 2003, 13:03:00 ; Search time 11.8286 Seconds
(without alignments)
32.193 Million cell updates/sec

Title: US-09-736-076-15
Perfect score: 49
Sequence: : MLLGRPPFE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 3
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/1aa/5R_COVB.pept*
3: /cgn2_6/ptodata/1/1aa/6A_COVB.pept*
4: /cgn2_6/ptodata/1/1aa/6B_COVB.pept*
5: /cgn2_6/ptodata/1/1aa/6C_US_COVB.pept*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pept*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	US-09-861-338-15	Sequence 15, Appl
2	49	100.0	11	US-09-861-338-15	Sequence 19, Appl
3	49	100.0	272	US-09-861-338-15	Sequence 12, Appl
4	49	100.0	272	US-09-861-338-15	Sequence 12, Appl
5	49	100.0	685	US-09-861-338-15	Sequence 11, Appl
6	49	100.0	685	US-09-861-338-15	Sequence 21, Appl
7	49	100.0	685	US-09-861-338-15	Sequence 11, Appl
8	49	100.0	685	US-09-861-338-15	Sequence 21, Appl
9	46	93.9	9	US-09-861-338-15	Sequence 17, Appl
10	41	83.7	8	US-09-861-338-15	Sequence 16, Appl
11	41	83.7	273	US-09-861-338-15	Sequence 10, Appl
12	41	83.7	273	US-09-861-338-15	Sequence 10, Appl
13	41	83.7	416	US-09-861-338-15	Sequence 2, Appl
14	41	83.7	416	US-09-861-338-15	Sequence 2, Appl
15	41	83.7	464	US-09-861-338-15	Sequence 6, Appl
16	41	83.7	464	US-09-861-338-15	Sequence 6, Appl
17	41	83.7	925	US-09-861-338-15	Sequence 4, Appl
18	41	83.7	925	US-09-861-338-15	Sequence 4, Appl
19	40	81.6	9	US-09-861-338-15	Sequence 18, Appl
20	40	81.6	20	US-09-861-338-15	Sequence 6, Appl
21	40	81.6	272	US-09-861-338-15	Sequence 14, Appl
22	40	81.6	272	US-09-861-338-15	Sequence 14, Appl
23	40	81.6	603	US-09-861-338-15	Sequence 3, Appl
24	40	81.6	603	US-09-861-338-15	Sequence 26, Appl
25	39	79.6	264	US-09-861-338-15	Sequence 17, Appl
26	39	79.6	271	US-09-861-338-15	Sequence 11, Appl
27	39	79.6	271	US-09-861-338-15	Sequence 11, Appl

28	39	79.6	303	4	US-09-739-455-12	Sequence 12, Appl
29	39	79.6	303	4	US-09-739-455-22	Sequence 22, Appl
30	38	77.6	259	4	US-09-252-991A-28679	Sequence 28679, A
31	38	77.6	275	1	US-08-252-995D-13	Sequence 13, Appl
32	38	77.6	275	2	US-08-834-108-13	Sequence 13, Appl
33	38	77.6	344	2	US-08-755-728-3	Sequence 3, Appl
34	38	77.6	344	2	US-08-974-655-3	Sequence 3, Appl
35	38	77.6	344	3	US-09-283-011-3	Sequence 3, Appl
36	38	77.6	347	2	US-09-216-000-1	Sequence 1, Appl
37	38	77.6	403	2	US-08-755-728-4	Sequence 4, Appl
38	38	77.6	403	2	US-08-974-655-4	Sequence 4, Appl
39	38	77.6	403	3	US-09-283-011-4	Sequence 4, Appl
40	38	77.6	737	4	US-09-772-647-4	Sequence 4, Appl
41	37	75.5	20	3	US-08-861-338-3	Sequence 3, Appl
42	37	75.5	182	4	US-09-134-01C-3742	Sequence 3742, Ap
43	37	75.5	220	1	US-08-233-146-2	Sequence 2, Appl
44	37	75.5	220	1	US-08-463-470-2	Sequence 2, Appl
45	37	75.5	264	2	US-07-857-224B-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-861-338-15
; Sequence 15, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DCS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; OTHER INFORMATION: Glutamic Acid-NH2"
US-08 861-338-15


```

Query Match      100.0%  Score 49; DB 3; Length 9;
Best Local Similarity 100.0%  Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      1 MLLGRPPPE 9
      |||||
DB      1 MLLGRPPPE 9

RESULT 2
US-08-861-338 19
; Sequence 19, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861-338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brock, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMDC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Serine NH2"
US-08-861-338 19

Query Match      100.0%  Score 49; DB 3; Length 11;
Best Local Similarity 100.0%  Pred. No. 3.0e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      1 MLLGRPPPE 9
      |||||
DB      1 MLLGRPPPE 9

RESULT 3
US-08-252-995D-12
; Sequence 12, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-252-995D-12

Query Match      100.0%  Score 49; DB 1; Length 272;
Best Local Similarity 100.0%  Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      1 MLLGRPPPE 9
      |||||
DB      199 MLLGRPPPE 207

RESULT 4
US-08-834-108-12
; Sequence 12, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdzyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US 08 834-108-12

Query Match 100.0%; Score 49; DB 2, Length 272;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGGRPPFE 9
|||
Db .99 MLGGRPPFE 207

RESULT 5
US 08-878-989-1
Sequence 1, Application US/08978989
Patent No. 5885803
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HUVENORC
CLONE: 39043
US-08-878-989-1

Query Match 100.0%; Score 49; DB 2; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGGRPPFE 9
|||
Db 273 MLGGRPPFE 281

RESULT 6
US-09-136-282-2
Sequence 2, Application US/09136282
Patent No. 6063609
GENERAL INFORMATION:
APPLICANT: ANDERSON, KAREN
APPLICANT: JACKSON, JEFFREY
APPLICANT: HANSBURY, MICHAEL
APPLICANT: NERURKAR, SANDHYA
APPLICANT: ROSHAK, AMY
APPLICANT: BOUZYK, MARK
TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,282
FILING DATE: 20-AUG-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/056,112
FILING DATE: 20-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-282-2

Query Match 100.0%; Score 49; DB 3; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MLLGRPPFE 9
Db      273 MLLGRPPFE 281

RESULT 7
US-09-272-796-1
; Sequence 1, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bardman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-032: US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENCB01
; CLONE: 39043
US-09-272-796-1

Query Match      100.0%; Score 49; DB 3; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 MLLGRPPFE 9
Db      273 MLLGRPPFE 281

RESULT 8
US-09-505-744-2
; Sequence 2, Application US/09505744
; Patent No. 6245544
; GENERAL INFORMATION:
; APPLICANT: Karen M. Anderson

```

```

; APPLICANT: Mark M. Bouzyk
; APPLICANT: Michael J. Hansbury
; APPLICANT: Jeffrey R. Jackson
; APPLICANT: Sandhya S. Nerurkar
; APPLICANT: Amy K. Roshak
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; FILE REFERENCE: GH-70231-D1
; CURRENT APPLICATION NUMBER: US/09/505,744
; CURRENT FILING DATE: 2000-02-16
; EARLIER APPLICATION NUMBER: 09/136,282
; EARLIER FILING DATE: 1998-09-20
; EARLIER APPLICATION NUMBER: 60/056,112
; EARLIER FILING DATE: 1997-09-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 685
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-505-744-2

Query Match      100.0%; Score 49; DB 3; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 MLLGRPPFE 9
Db      273 MLLGRPPFE 281

RESULT 9
US-08-861-338-17
; Sequence 17, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CWCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"

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FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "Gamma Benzyl Ester of
OTHER INFORMATION: Glutamine Acid-NH2"
US-08-861-338-17
Query Match 93.9%; Score 46; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.5e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 1 MLLGKPPFE 9

RESULT 10
US-08-861-338-16
Sequence 16, Application US/08861338
Patent No. 6174993
GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,338
FILING DATE: 21-MAY-1997
CLASSIFICATION: 514
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMC0-590
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "N-Acetyl Methionine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /note= "Phenylalanine-NH2"
US-08-861-338-16
Query Match 83.7%; Score 41; DB 3; Length 8;
Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPF 8
DB 1 MLLGKPPF 8

```

```

RESULT 11
US-08-252-995D-10
Sequence 10, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-252-995D-10
Query Match 83.7%; Score 41; DB 1; Length 273;
Best Local Similarity 66.7%; Pred. No. 3.3;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 200 LLIGRPPFD 208

RESULT 12
US-08-834-108-10
Sequence 10, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-834-108-10

Query Match 83.7%; Score 41; DB 2; Length 273;
Best Local Similarity 66.7%; Pred. No. 3.3;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRPPFE 9
Db 200 LLGRPPFD 208
RESULT 13
US-08-252-995D-2
Sequence 2, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-252-995D-2
Query Match 83.7%; Score 41; DB 1; Length 416;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGRPPFE 9
Db 204 LLGRPPFD 212

RESULT 14
US-08-834-108-2
Sequence 2, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-834-108-2

Query Match 83.7%; Score 41; DB 2; Length 416;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGRPPFE 9
Db 204 LLGRPPFD 212

RESULT 15
US-08-252-995D-6
Sequence 6, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR

STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-995D-6

Query Match 83.7% Score 41; DB 1; Length 464;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

DB 204 LLIGRPPFD 212

RESULT 16
US-08-834-108-6
Sequence 6, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-834-108-6

Query Match 83.7% Score 41; DB 2; Length 464;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

DB 204 LLIGRPPFD 212

RESULT 17
US-08-252-995D-4
Sequence 4, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-995D-4

Query Match 83.7% Score 41; DB 1; Length 925;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

DB 204 LLIGRPPFD 212

RESULT 18
US-08-834-108-4
Sequence 4, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

1 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
2 NUMBER OF SEQUENCES: 14
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: BERESKIN & PARR
5 STREET: 40 King Street West
6 CITY: Toronto
7 STATE: Ontario
8 COUNTRY: Canada
9 ZIP: M5H 3Y2
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: PatentIn Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/834,108
17 FILING DATE:
18 CLASSIFICATION: 536
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Kurdydyk, Linda M
21 REGISTRATION NUMBER: 34,972
22 REFERENCE/DOCKET NUMBER: 3,553 210
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (416) 364-7311
25 TELEFAX: (416) 361-1398
26 INFORMATION FOR SEQ ID NO: 4:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 925 amino acids
29 TYPE: amino acid
30 TOPOLOGY: linear
31 MOLECULE TYPE: protein
32
33 US 08-834-108-4

Query Match 83.7%; Score 41; DB 2; Length 925;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY : MLGRPPFE 9
: |||||
DB 204 LLGRPPFD 212

RESULT 19

US-08-861-338-18
1 Sequence 18, Application US/08861338
2 Patent No. 6174993
3 GENERAL INFORMATION:
4 APPLICANT: Ben-Sasson, Samuel A.
5 TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
6 TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
7 NUMBER OF SEQUENCES: 22
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
10 STREET: Two Militia Drive
11 CITY: Lexington
12 STATE: Massachusetts
13 COUNTRY: USA
14 ZIP: 02173
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.30
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/861,338
22 FILING DATE: 21-MAY-1997
23 CLASSIFICATION: 514
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Brook, David E.
26 REGISTRATION NUMBER: 22,592
27 REFERENCE/DOCKET NUMBER: CMCC-590
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (781) 861-6240
30 TELEFAX: (781) 861-9540
31 INFORMATION FOR SEQ ID NO: 6:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 20 amino acids
34 TYPE: amino acid
35 STRANDEDNESS: not relevant
36 TOPOLOGY: not relevant
37 MOLECULE TYPE: peptide
38 US-08-861-338-6

Query Match 81.6%; Score 40; DB 3; Length 20;

1 TELEFAX: (781) 861-9540
2 INFORMATION FOR SEQ ID NO: 18:
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 9 amino acids
5 TYPE: amino acid
6 STRANDEDNESS: not relevant
7 TOPOLOGY: not relevant
8 MOLECULE TYPE: peptide
9 FEATURE:
10 NAME/KEY: Modified-site
11 LOCATION: 1
12 OTHER INFORMATION: /note= "N-Acetyl Leucine"
13 FEATURE:
14 NAME/KEY: Modified site
15 LOCATION: 7
16 OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
17 FEATURE:
18 NAME/KEY: Modified-site
19 LOCATION: 9
20 OTHER INFORMATION: /note= "Serine-NH2"
21 US-08-861-338-18

Query Match 81.6%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGRPPFE 9
: |||||
DB 1 LGRPPFE 7

RESULT 20

US-08-861-338-6
1 Sequence 6, Application US/08861338
2 Patent No. 6174993
3 GENERAL INFORMATION:
4 APPLICANT: Ben-Sasson, Samuel A.
5 TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
6 TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
7 NUMBER OF SEQUENCES: 22
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
10 STREET: Two Militia Drive
11 CITY: Lexington
12 STATE: Massachusetts
13 COUNTRY: USA
14 ZIP: 02173
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.30
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/861,338
22 FILING DATE: 21-MAY-1997
23 CLASSIFICATION: 514
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Brook, David E.
26 REGISTRATION NUMBER: 22,592
27 REFERENCE/DOCKET NUMBER: CMCC-590
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (781) 861-6240
30 TELEFAX: (781) 861-9540
31 INFORMATION FOR SEQ ID NO: 6:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 20 amino acids
34 TYPE: amino acid
35 STRANDEDNESS: not relevant
36 TOPOLOGY: not relevant
37 MOLECULE TYPE: peptide
38 US-08-861-338-6

Query Match 81.6%; Score 40; DB 3; Length 20;

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Best Local Similarity 66.7%; Pred. No. 0.35;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
   :|:|:|
   3 LLVGKPPPE 11

RESULT 21
US-08-252-995D-14
; Sequence 14, Application US/08252995D
; Patent No. 5650531
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-252-995D-14

Query Match 81.6%; Score 40; DB 1; Length 272;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
   :|:|:|
   3 LLVGKPPPE 207

Db 199 LLVGKPPPE 207

RESULT 22
US-08-834-108-14
; Sequence 14, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR

```

```

; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-834-108-14

Query Match 81.6%; Score 40; DB 2; Length 272;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
   :|:|:|
   3 LLVGKPPPE 207

Db 199 LLVGKPPPE 207

RESULT 23
US-09-198-122-2
; Sequence 2, Application US/09198122
; Patent No. 6180380
; GENERAL INFORMATION:
; APPLICANT: Strebhardt, Klaus; Rubsamen-Waigmann, Helga;
; APPLICANT: Holtrich, Uwe
; TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE-
; TITLE OF INVENTION: THREONINE-KINASE FAMILY
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
; MEDIUM TYPE: storage
; COMPUTER: NEC Powermate SX-20
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/198,122
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/601,014
; FILING DATE: 23-FEB-1996
; APPLICATION NUMBER: PCT/EP94/02863
; FILING DATE: 30-AUG-1994

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4329177
; FILING DATE: 30-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 9518-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-09-198-122-2
;
Query Match 81.6%; Score 40; DB 3; Length 603;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db 244 LVLGKPPFE 252

RESULT 24
US-09-311-311C-26
; Sequence 26, Application US/09311311C
; Patent No. 6158738
; GENERAL INFORMATION:
; APPLICANT: Erikson, et al.
; TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS,
; TITLE OF INVENTION: METHODS, AND USES THEREFOR
; FILE REFERENCE: 1874/117
; CURRENT APPLICATION NUMBER: US/09/311,311C
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/285,296
; PRIOR FILING DATE: 1998-05-13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURES:
; NAME/KEY: DOMAIN
; LOCATION: (1).....(603)
; OTHER INFORMATION: Pk protein
US-09-311-311C-26

Query Match 81.6%; Score 40; DB 4; Length 603;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db 244 LVLGKPPFE 252

RESULT 25
US-07-857-224B-17
; Sequence 17, Application US/07857214B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Radlaubstrasse 151

```

```

; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; FEATURE: Protein kinase; Table 8 Column 18
; PUBLICATION INFORMATION:
; AUTHORS:
; AUTHORS: Hanks, S. K.
; AUTHORS: Quinn, A. M.
; AUTHORS: Hunter, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
US-07-857-224B-17

Query Match 79.6%; Score 39; DB 2; Length 264;
Best Local Similarity 66.7%; Pred. No. 7.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db 195 MLVGQPPFD 203

RESULT 26
US-08-252-995D-11
; Sequence 11, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Hefferman, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D

```

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; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdvyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; US-08-252-995D-11

Query Match: 79.6%; Score 39; DB 1; Length 271;
Best Local Similarity 66.7%; Pred. No. 7.7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db 198 LLVGQPPFE 206

RESULT 27
US-08-834-108-11
; Sequence 11, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3V2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdvyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; US-08-834-108-11

```

```

Query Match: 79.6%; Score 39; DB 2; Length 271;
Best Local Similarity 66.7%; Pred. No. 7.7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db 198 LLVGQPPFE 206

RESULT 28
US-09-739-455-12
; Sequence 12, Application US/09739455
; Patent No. 6413756
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000653
; CURRENT APPLICATION NUMBER: US/09/739,455
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Leishmania mexicana
; US-09-739-455-12

Query Match: 79.6%; Score 39; DB 4; Length 303;
Best Local Similarity 88.9%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db 207 MLLGRPLFE 215

RESULT 29
US-09-739-455-22
; Sequence 22, Application US/09739455
; Patent No. 6413756
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000653
; CURRENT APPLICATION NUMBER: US/09/739,455
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Leishmania mexicana
; US-09-739-455-22

Query Match: 79.6%; Score 39; DB 4; Length 303;
Best Local Similarity 88.9%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
Db 207 MLLGRPLFE 215

RESULT 30
US-09-252-991A-28679
; Sequence 28679, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

```


1 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

2 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

3 FILE REFERENCE: 107196.136

4 CURRENT APPLICATION NUMBER: US/09/252,991A

5 CURRENT FILING DATE: 1999-02-18

6 PRIOR APPLICATION NUMBER: US 60/074,788

7 PRIOR FILING DATE: 1998-02-18

8 PRIOR APPLICATION NUMBER: US 60/094,190

9 PRIOR FILING DATE: 1998-07-27

10 NUMBER OF SEQ ID NOS: 33142

11 SEQ ID NO 28673

12 LENGTH: 259

13 TYPE: PRT

14 ORGANISM: Pseudomonas aeruginosa

15 US-09-252-991A 28679

16 Query Match: 77.6%; Score 38; DB 4; Length 259;

17 Best Local Similarity: 100.0%; Pred. No. 11;

18 Matches: 7; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

19 QY 1 MLLGRPP 7

20 Db 152 MLLGRPP 158

21 RESULT 31

22 US-09-252-995D-13

23 Sequence 13, Application US/08252935D

24 Patent No. 5650501

25 GENERAL INFORMATION:

26 APPLICANT: Dennis, James W

27 APPLICANT: Heffernan, Mike

28 APPLICANT: Fode, Carol

29 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE

30 NUMBER OF SEQUENCES: 14

31 CORRESPONDENCE ADDRESS:

32 ADDRESSEE: BERESKIN & PARR

33 STREET: 40 King Street West

34 CITY: Toronto

35 STATE: Ontario

36 COUNTRY: Canada

37 ZIP: M5H 3Y2

38 COMPUTER READABLE FORM:

39 MEDIUM TYPE: Floppy disk

40 COMPUTER: IBM PC compatible

41 OPERATING SYSTEM: PC-DOS/MS-DOS

42 SOFTWARE: Patent in Release #1.0, Version #1.30

43 CURRENT APPLICATION DATA:

44 APPLICATION NUMBER: US/08/252,995D

45 FILING DATE: 02-JUN-1994

46 CLASSIFICATION: 536

47 ATTORNEY/AGENT INFORMATION:

48 NAME: Kurdydyk, Linda M

49 REGISTRATION NUMBER: 34,971

50 REFERENCE/DOCKET NUMBER: 3153-96

51 TELECOMMUNICATION INFORMATION:

52 TELEPHONE: (416) 364-7311

53 TELEFAX: (416) 361-1398

54 INFORMATION FOR SEQ ID NO: 13:

55 SEQUENCE CHARACTERISTICS:

56 LENGTH: 275 amino acids

57 TYPE: amino acid

58 STRANDEDNESS: single

59 TOPOLOGY: linear

60 MOLECULE TYPE: peptide

61 ORIGINAL SOURCE:

62 ORGANISM: Saccharomyces cerevisiae

63 US-09-252-995D-13

64 Query Match: 77.6%; Score 38; DB 1; Length 259;

65 Best Local Similarity: 55.6%; Pred. No. 11;

66 Matches: 5; Conservative: 4; Mismatches: 0; Indels: 0; Gaps: 0;

67 QY 1 MLLGRPP 9

68 Db 200 LLLGKPPFQ 208

69 RESULT 32

70 US-08-834-108-13

71 Sequence 13, Application US/08534108

72 Patent No. 5976893

73 GENERAL INFORMATION:

74 APPLICANT: Dennis, James W

75 APPLICANT: Heffernan, Mike

76 APPLICANT: Fode, Carol

77 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE

78 NUMBER OF SEQUENCES: 14

79 CORRESPONDENCE ADDRESS:

80 ADDRESSEE: BERESKIN & PARR

81 STREET: 40 King Street West

82 CITY: Toronto

83 STATE: Ontario

84 COUNTRY: Canada

85 ZIP: M5H 3Y2

86 COMPUTER READABLE FORM:

87 MEDIUM TYPE: Floppy disk

88 COMPUTER: IBM PC compatible

89 OPERATING SYSTEM: PC-DOS/MS-DOS

90 SOFTWARE: Patent in Release #1.0, Version #1.30

91 CURRENT APPLICATION DATA:

92 APPLICATION NUMBER: US/08/834,108

93 FILING DATE:

94 CLASSIFICATION: 536

95 ATTORNEY/AGENT INFORMATION:

96 NAME: Kurdydyk, Linda M

97 REGISTRATION NUMBER: 34,971

98 REFERENCE/DOCKET NUMBER: 3153-210

99 TELECOMMUNICATION INFORMATION:

100 TELEPHONE: (416) 364-7311

101 TELEFAX: (416) 361-1398

102 INFORMATION FOR SEQ ID NO: 13:

103 SEQUENCE CHARACTERISTICS:

104 LENGTH: 275 amino acids

105 TYPE: amino acid

106 STRANDEDNESS: single

107 TOPOLOGY: linear

108 MOLECULE TYPE: peptide

109 ORIGINAL SOURCE:

110 ORGANISM: Saccharomyces cerevisiae

111 US-08-834-108-13

112 Query Match: 77.6%; Score 38; DB 2; Length 275;

113 Best Local Similarity: 55.6%; Pred. No. 12;

114 Matches: 5; Conservative: 4; Mismatches: 0; Indels: 0; Gaps: 0;

115 QY 1 MLLGRPPF 9

116 Db 200 LLLGKPPFQ 208

117 RESULT 33

118 US-08-755-728-3

119 Sequence 3, Application US/08755728

120 Patent No. 5962312

121 GENERAL INFORMATION:

122 APPLICANT: Plowman, Gregory

123 APPLICANT: Mossie, Kevin

124 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1

125 TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS

126 NUMBER OF SEQUENCES: 29

127 CORRESPONDENCE ADDRESS:

128 ADDRESSEE: Lyon & Lyon

129 STREET: 633 West Fifth Street

130 STREET: Suite 4700

131 CITY: Los Angeles

STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/755,728
 FILING DATE: No. 5962312ember 25, 1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/008,809
 FILING DATE: December 18, 1995
 APPLICATION NUMBER: 60/023,943
 FILING DATE: August 14, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 223/113
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 344 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08 755-728-3

Query Match 77.6%; Score 38; DB 2; Length 344;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 1 MLJGRPPPE 9
 :|||
 Db 266 LLVGNPPPE 274

RESULT 14
 US-08 974-655-3
 Sequence 3, Application US/08974655
 Patent No. 5972676
 GENERAL INFORMATION:
 APPLICANT: Plowman, Gregory
 APPLICANT: Mossie, Kevin
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
 TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,655
 FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 38/755,728
 FILING DATE: No. 5972676ember 25, 1996
 APPLICATION NUMBER: 60/008,809
 FILING DATE: December 18, 1995
 APPLICATION NUMBER: 60/023,943
 FILING DATE: August 14, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 223/113
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 344 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-974-655-3

Query Match 77.6%; Score 38; DB 2; Length 344;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 1 MLJGRPPPE 9
 :|||
 Db 266 LLVGNPPPE 274

RESULT 35
 US-09-283-011-3
 Sequence 3, Application US/09283011
 Patent No. 6207401
 GENERAL INFORMATION:
 APPLICANT: Plowman, Gregory
 APPLICANT: Mossie, Kevin
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
 TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/283,011
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/012,135
 FILING DATE: January 22, 1998
 APPLICATION NUMBER: 08/755,728
 FILING DATE: No. 6207401ember 25, 1996
 APPLICATION NUMBER: 60/023,943
 FILING DATE: August 14, 1996
 APPLICATION NUMBER: 60/008,809
 FILING DATE: December 18, 1995

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-283-011-3

Query Match 77.6%; Score 38; DB 3; Length 344;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
Db 266 LLVGNPPPE 274

RESULT 36
US-09-016-000-1
; Sequence 1, Application US/09016000
; Patent No. 5962232
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Iat, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil G.
; APPLICANT: Guegler, Kari G.
; TITLE OF INVENTION: PROTEIN KINASE MOLECULES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,000
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0465 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HMCINOT01
; CLONE: 2940
US-09-016-000-1

Query Match 77.6%; Score 38; DB 2; Length 347;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
Db 269 LLVGNPPPE 277

RESULT 37
US-08-755-728-4
; Sequence 4, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,728
; FILING DATE: No. 5962312ember 25, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-755-728-4

Query Match 77.6%; Score 38; DB 2; Length 403;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 9

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SEQ ID NO 4
LENGTH: 737
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T7 tag and
OTHER INFORMATION: mouse protein kinase C epsilon coding sequence
CS 09 772 647-4

Query Match 77.6%; Score 38, DB 4; Length 737
Best Local Similarity 66.7%; Pred. No. 33
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLIGRPPE 9
Nb 600 MMAGQPPPE 608

Search completed: November 14, 2003, 13:29:49
Job time : 11.8286 secs

GenCore version 5.1.6
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QV protein - protein search, using sw model

Run on: November 14, 2003, 13:28:05 : Search time 22.3714 Seconds
(without alignments)
73.443 Million cell updates/sec

Title: US-09-736-076-15
Perfect score: 49
Sequence: 1 YLLGRPPFE 9

Scoring table: ELCSJM62
Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA*

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- 2: /cgn2_6/ptodata/1/pubpaa/PC01_NEW_PUB.pept.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pept.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pept.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pept.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pept.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pept.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pept.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pept.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pept.*

Pred. No. is the number of results predicted by the program to have a score greater than or equal to the score of the hit being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	US-09-736-076-15	Sequence 15, Appl
2	49	100.0	10	US-09-736-076-57	Sequence 57, Appl
3	49	100.0	11	US-09-736-076-19	Sequence 19, Appl
4	49	100.0	400	US-10-026-021-5	Sequence 5, Appl
5	49	100.0	469	US-10-059-585-14	Sequence 14, Appl
6	49	100.0	685	US-09-771-161A-249	Sequence 249, App
7	49	100.0	685	US-09-771-161A-250	Sequence 250, App
8	49	100.0	685	US-09-771-161A-251	Sequence 251, App
9	49	100.0	685	US-10-024-198A-101	Sequence 101, App
10	49	100.0	685	US-09-771-161A-101	Sequence 101, Appl
11	49	100.0	685	US-10-024-111A-101	Sequence 101, App
12	49	93.9	9	US-09-736-076-17	Sequence 17, Appl
13	49	83.7	8	US-09-736-076-16	Sequence 16, Appl
14	49	83.7	379	US-10-026-021-1	Sequence 3, Appl
15	49	83.7	970	US-10-026-021-2	Sequence 2, Appl

16	40	81.6	9	US-09-736-076-18	Sequence 18, Appl
17	40	81.6	20	US-09-736-076-6	Sequence 6, Appl
18	40	81.6	329	US-09-925-300-1268	Sequence 1268, Ap
19	40	81.6	367	US-10-026-021-6	Sequence 6, Appl
20	40	81.6	516	US-09-771-161A-123	Sequence 123, App
21	40	81.6	528	US-10-032-585-7571	Sequence 7571, Ap
22	40	81.6	603	US-09-771-161A-214	Sequence 214, App
23	40	81.6	603	US-10-171-311-186	Sequence 186, App
24	39	79.6	303	US-10-153-919-12	Sequence 12, Appl
25	39	79.6	303	US-10-153-919-22	Sequence 22, Appl
26	38	77.6	8	US-09-736-076-58	Sequence 58, Appl
27	38	77.6	256	US-09-898-837A-32	Sequence 32, Appl
28	38	77.6	344	US-09-012-135A-3	Sequence 3, Appl
29	38	77.6	344	US-10-059-585-34	Sequence 34, Appl
30	38	77.6	344	US-10-171-311-214	Sequence 214, App
31	38	77.6	347	US-09-974-298-136	Sequence 136, App
32	38	77.6	348	US-10-291-253A-16	Sequence 16, Appl
33	38	77.6	403	US-09-012-135A-4	Sequence 4, Appl
34	38	77.6	403	US-10-026-021-7	Sequence 7, Appl
35	38	77.6	403	US-10-059-585-33	Sequence 33, Appl
36	38	77.6	403	US-10-209-324-2	Sequence 2, Appl
37	38	77.6	737	US-09-771-161A-195	Sequence 195, App
38	38	77.6	737	US-10-228-931-4	Sequence 4, Appl
39	37	75.5	20	US-09-736-076-3	Sequence 3, Appl
40	37	75.5	445	US-09-836-392-15	Sequence 15, Appl
41	37	75.5	499	US-10-024-828-12	Sequence 12, Appl
42	37	75.5	505	US-10-156-761-14310	Sequence 14310, A
43	37	75.5	588	US-10-024-828-16	Sequence 16, Appl
44	37	75.5	672	US-08-681-219-29	Sequence 29, Appl
45	37	75.5	672	US-10-092-138-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-736-076-15
: Sequence 15, Application US/09736076
: Patent No. US2002004301A1
: GENERAL INFORMATION:
: APPLICANT: Ben-Sasson Shmuel A.
: TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
: FILE REFERENCE: 1242.1015-009
: CURRENT APPLICATION NUMBER: US/09/736,076
: CURRENT FILING DATE: 2000-12-13
: PRIOR APPLICATION NUMBER: US 08/861,338
: PRIOR FILING DATE: 1997-05-21
: NUMBER OF SEQ ID NOS: 68
: SOFTWARE: FastSeq for windows Version 4.0
: SEQ ID NO 15
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: ACETYLATION
: LOCATION: (1)...(9)
: OTHER INFORMATION: position 9 is benzylester
: NAME/KEY: AMIDATION
: LOCATION: (0)...(9)
: OTHER INFORMATION: J42
US-09-736-076-15

Query Match 100.0% Score 49; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.9e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGRPPFE 9
|||
Db : MLLGRPPFE 9

RESULT 2

US-09-736-076-57
 ; Sequence 57, Application US/09736076
 ; Patent No. US20020049301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; FILE REFERENCE: 1242.1015-009
 ; CURRENT APPLICATION NUMBER: US/09736,076
 ; CURRENT FILING DATE: 2000-12-13
 ; PRIOR APPLICATION NUMBER: US 08/561,212
 ; PRIOR FILING DATE: 1997-05-21
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 57
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: MYRISTATE
 ; LOCATION: 11...10
 ; OTHER INFORMATION: position 10 is benzylester
 ; NAME/KEY: AMIDATION
 ; LOCATION: (0)...(10)
 ; OTHER INFORMATION: SNK
 ; OTHER INFORMATION: SNK
 US-09-736-076-57

Query Match 100.0%; Score 49; DB 9; Length 10
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 DB 2 MLLGRPPPE 10

RESULT 1
 US-09-736-076-19
 ; Sequence 19, Application US/09736076
 ; Patent No. US20020049301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; FILE REFERENCE: 1242.1015-009
 ; CURRENT APPLICATION NUMBER: US/09736,076
 ; CURRENT FILING DATE: 2000-12-13
 ; PRIOR APPLICATION NUMBER: US 08/561,212
 ; PRIOR FILING DATE: 1997-05-21
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 19
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: ACETYLTATION
 ; LOCATION: (1)...(0)
 ; OTHER INFORMATION: position 9 is benzylester
 ; NAME/KEY: AMIDATION
 ; LOCATION: (0)...(11)
 ; OTHER INFORMATION: J46
 ; OTHER INFORMATION: J46
 US-09-736-076-19

Query Match 100.0%; Score 49; DB 9; Length 11
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 DB 1 MLLGRPPPE 9

RESULT 4
 US-10-026-021-5
 ; Sequence 5, Application US/10026021
 ; Publication No. US20030027756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hitoshi, Yasumichi
 ; APPLICANT: Demo, Susan
 ; APPLICANT: Jenkins, Yonchu
 ; APPLICANT: Rigel Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 ; TITLE OF INVENTION: Treatment of Cancer
 ; FILE REFERENCE: 021044-001210US
 ; CURRENT APPLICATION NUMBER: US/10/026,021
 ; CURRENT FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/309,632
 ; PRIOR FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 400
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (1)...(400)
 ; OTHER INFORMATION: human SNK mitotic kinase kinase domain
 US-10-026-021-5

Query Match 100.0%; Score 49; DB 15; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 DB 273 MLLGRPPPE 281

RESULT 5
 US-10-059-585-14
 ; Sequence 14, Application US/10059585
 ; Publication No. US20030082776A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ota, Toshio
 ; APPLICANT: Isogai, Takao
 ; APPLICANT: Nishikawa, Tetsuo
 ; APPLICANT: Hayashi, Koji
 ; APPLICANT: Otsuka, Kaoru
 ; APPLICANT: Yamamoto, Jun-ichi
 ; APPLICANT: Ishii, Shizuko
 ; APPLICANT: Sugiyama, Tomoyasu
 ; APPLICANT: Wakamatsu, Ai
 ; APPLICANT: Nagai, Keiichi
 ; APPLICANT: Otsuki, Tetsuji
 ; APPLICANT: Furahashi, Shin-ichi
 ; APPLICANT: Senoo, Chiaki
 ; APPLICANT: Nezu, Jun-ichi
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
 ; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
 ; FILE REFERENCE: 06501-098001
 ; CURRENT APPLICATION NUMBER: US/10/059,585
 ; CURRENT FILING DATE: 2002-01-29
 ; PRIOR APPLICATION NUMBER: PCT/JP00/05060
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: US 60/183,322
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: US 60/159,590
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: JP 2000-118776
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: JP 2000-183767
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: JP 11-248036
 ; PRIOR FILING DATE: 1999-07-29

NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585 14

Query Match 100.0%; Score 49; DB 15; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
|||
DB 57 MLLGRPPFE 65

RESULT 6
US-09-771-161A-249
; Sequence 249, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 249
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-249

Query Match 100.0%; Score 49; DB 10; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
|||
DB 273 MLLGRPPFE 281

RESULT 7
US-09-771-161A-250
; Sequence 250, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-250

Query Match 100.0%; Score 49; DB 10; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
|||
DB 273 MLLGRPPFE 281

RESULT 8
US-09-771-161A-251
; Sequence 251, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 251
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-251

Query Match 100.0%; Score 49; DB 10; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
|||
DB 273 MLLGRPPFE 281

RESULT 9
US-10-024-298A-101
; Sequence 101, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAH; KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JPC088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 685

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-101

Query Match      100.0%; Score 49; DB 12; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      : MLLGRPPPE 9
      : ||||| ||
DB      273 MLLGRPPPE 281

RESULT 10
US-09-769-970-1
; Sequence 1, Application US/09769970
; Publication No. US20030170219A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Corley, Neil C.
; Guegler, Karl G.
; Lal, Preeti
; Goli, Surya K.
; Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/769,970
; FILING DATE: 24-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/272,396
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy G J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: 16,121 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-3555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENOB01
; CLONE: 39043
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US 09-769-970-1

Query Match      100.0%; Score 49; DB 12; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      : MLLGRPPPE 9
      : ||||| ||

```

```

DB      273 MLLGRPPPE 281

RESULT 11
US-10-042-211A-101
; Sequence 101, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFκB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-101

Query Match      100.0%; Score 49; DB 12; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      1 MLLGRPPPE 9
      : ||||| |||
DB      273 MLLGRPPPE 281

RESULT 12
US-09-736-076-17
; Sequence 17, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015 039
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (9)...(9)
; OTHER INFORMATION: 343.1
US-09-736-076-17

Query Match      93.9%; Score 46; DB 9; Length 9;
Best Local Similarity 89.9%; Pred. No. 5.9e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY      : MLLGRPPPE 9
      : ||||| |||

```

QY 1 MLLGRPPFE 9
:|||||
Db 204 LLIGRPPFD 212

RESULT 13

US-09-736-076-16
; Sequence 16, Application US/09736076
; Publication No. US2002004931A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1315-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(8)
; NAME/KEY: AMIDATION
; LOCATION: (0)...(8)
; OTHER INFORMATION: J43
US-09-736-076-16

Query Match 83.7%; Score 41; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 5.9e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 8
:|||||
Db 1 MLLGKPPF 8

RESULT 14

US-10-026-021-3
; Sequence 3, Application US/10026021
; Publication No. US2003027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(379)
; OTHER INFORMATION: SAK serine/threonine kinase domain
US-10-026-021-3

Query Match 83.7%; Score 41; DB 15; Length 379;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
:|||||
Db 204 LLIGRPPFD 212

RESULT 15

US-10-026-021-2
; Sequence 2, Application US/10026021
; Publication No. US2003027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 970
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human SAK serine/threonine kinase
US-10-026-021-2

Query Match 83.7%; Score 41; DB 15; Length 970;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
:|||||
Db 204 LLIGRPPFD 212

RESULT 16

US-09-736-076-18
; Sequence 18, Application US/09736076
; Patent No. US2002004931A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1315-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 7 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (0)...(9)
; OTHER INFORMATION: J45
US-09-736-076-18

Query Match 81.6%; Score 40; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

QY      3 LGRPPPE 9
      |||||
Db      1 LGRPPPE 7

RESULT 17
US-09-736-076-6
; Sequence 6, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-039
; CURRENT APPLICATION NUMBER: US/09/736.076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: POLO
US-09-736-076-6

Query Match      81.6%  Score 40; DB 9; Length 20;
Best Local Similarity 66.7%; Pred. No. 21;
Matches      6; Conservative      3; Mismatches      0; Indels      0; Gaps      0;

QY      1 MLLGRPPPE 9
      |||||
Db      3 LLVGKPPPE 11

RESULT 18
US-09-925-300-1268
; Sequence 1268, Application US/09925100
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P4101
; CURRENT APPLICATION NUMBER: US/09/925.100
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/00488
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,276
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1690
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (307)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (338)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (314)

```

```

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (317)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (323)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (327)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (329)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1268

Query Match      81.6%  Score 40; DB 10; Length 329;
Best Local Similarity 66.7%; Pred. No. 31;
Matches      6; Conservative      3; Mismatches      0; Indels      0; Gaps      0;

QY      1 MLLGRPPPE 9
      |||||
Db      260 LLVGKPPPE 263

RESULT 19
US-10-026-021-6
; Sequence 6, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation Of Cellular Proliferation for
; TITLE OF INVENTION: Treatment Of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026.021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(367)
; OTHER INFORMATION: human pLk1 mitotic kinase kinase domain
US-10-026-021-6

Query Match      81.6%  Score 40; DB 15; Length 367;
Best Local Similarity 66.7%; Pred. No. 34;
Matches      6; Conservative      3; Mismatches      0; Indels      0; Gaps      0;

QY      1 MLLGRPPPE 9
      |||||
Db      244 LLVGKPPPE 252

RESULT 20
US-09-771-161A-123
; Sequence 123, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A

```

```
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 123
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-123

Query Match      81.6%; Score 40; DB 10; Length 516;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPFE 9
      :|:|:|
Db      157 LLVGKPPFE 165

RESULT 21
US-10-032-585-7571
; Sequence 7571, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7571
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7571

Query Match      81.6%; Score 40; DB 12; Length 528;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPFE 9
      :|:|:|
Db      454 LLVGKPPFE 462

RESULT 22
US-09-771-161A-214
; Sequence 214, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 214
```

```
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-214

Query Match      81.6%; Score 40; DB 10; Length 603;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPFE 9
      :|:|:|
Db      244 LLVGKPPFE 252

RESULT 23
US-10-171-311-186
; Sequence 186, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-186

Query Match      81.6%; Score 40; DB 15; Length 603;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPFE 9
      :|:|:|
Db      244 LLVGKPPFE 252

RESULT 24
US-10-153-919-12
; Sequence 12, Application US/10153919
; Publication No. US20030166219A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000653DIV
; CURRENT APPLICATION NUMBER: US/10/153,919
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/209,585
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 09/739,455
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Leishmania mexicana
US 10-153-919-12

Query Match      79.6%  Score 39; DB 12; Length 303;
Best Local Similarity 88.9%  Pred. No. 43;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
Db 207 MLLGRPLPE 215

RESULT 26
US-10-153-919-22
; Sequence 22, Application US/10153919
; Publication No. US20030166219A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: G000653D1V
; CURRENT APPLICATION NUMBER: US/10/153-919
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/209,585
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 09/739,455
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Leishmania mexicana
US-10-153-919-22

Query Match      79.6%  Score 39; DB 12; Length 303;
Best Local Similarity 88.9%  Pred. No. 43;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
Db 207 MLLGRPLPE 215

RESULT 26
US-09-736-076-58
; Sequence 58, Application US/09736058
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1C15-009
; CURRENT APPLICATION NUMBER: US/09/736-076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/841,000
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MYRISTATE
; LOCATION: (1)...(8)
; NAME/KEY: AMIDATION
; LOCATION: (1)...(19)
```

```
; OTHER INFORMATION: SNK
US-09-736-076-58

Query Match      77.6%  Score 38; DB 9; Length 8;
Best Local Similarity 100.0%  Pred. No. 5.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPP 7
Db 2 MLLGRPP 8

RESULT 27
US-09-898-837A-32
; Sequence 32, Application US/09898837A
; Publication No. US2003007697A1
; GENERAL INFORMATION:
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Herrmann, John L.
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Rastelli, Luca
; APPLICANT: CuraGen Corporation
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Macdougall, John R.
; TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: 15966-598 CIP
; CURRENT APPLICATION NUMBER: US/09/898,837A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
; PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-898-837A-32

Query Match      77.6%  Score 38; DB 11; Length 256;
Best Local Similarity 55.6%  Pred. No. 54;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
Db 193 LLLGKPPFQ 201

RESULT 28
US-09-012-135A-3
; Sequence 3, Application US/09012135A
; Patent No. US20020081576A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,268
; FILING DATE: January 9, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. US2002081578A September 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/292
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; US 09-012 135A-3

```

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Query Match 77.6%; Score 38; DB 9; Length 344;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MLLGRPPPE 9
Db 266 LLVGNPPPE 274

```

```

RESULT 29
US-10 059 585-34
; Sequence 34, Application US/10059585
; Publication No. US2003082776A1
; GENERAL INFORMATION:
; APPLICANT: Cta, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko

```

```

; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PC/JPC00/95060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-059-585-34

```

```

Query Match 77.6%; Score 38; DB 15; Length 344;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MLLGRPPPE 9
Db 266 LLVGNPPPE 274

```

```

RESULT 30
US-10-171-311-214
; Sequence 214, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerssh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: CF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-171-311-214

```

Query Match 77.6%; Score 38; DB 15; Length 344;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 266 LLVGNPPPE 274

RESULT 31
US-09-974-298-136
; Sequence 136, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hwei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-2037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 136
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 002940CD;
US 09 974-298-136

Query Match 77.6%; Score 38; DB 10; Length 347;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 269 LLVGNPPPE 277

RESULT 32
US 10 291-253A-16
; Sequence 16, Application US/10291253A
; Publication No. US20030150017A1
; GENERAL INFORMATION:
; APPLICANT: Botellia, Jose
; APPLICANT: Graham, Michael
; APPLICANT: Fairbairn, David
; TITLE OF INVENTION: A Method for Facilitating Patented Resistance
; FILE REFERENCE: Retatode
; CURRENT APPLICATION NUMBER: US/10/291,253A
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: PR8706
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: PR8802
; PRIOR FILING DATE: 2001-11-12
; PRIOR APPLICATION NUMBER: US60/341404
; PRIOR FILING DATE: 2001-12-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Meloidogyne incognita
US-10-291-253A-16

Query Match 77.6%; Score 38; DB 12; Length 348;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

Db 210 MMAGQPPPE 218
RESULT 33
US-09-012-135A-4
; Sequence 4, Application US/09012135A
; Patent No. US20020081578A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/035,268
; FILING DATE: January 9, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. US20020081578A1ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-012-135A-4

Query Match 77.6%; Score 38; DB 9; Length 403;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 9
DB 323 LVGKPPPE 330

RESULT 34
US-10-026-021-7
; Sequence 7, Application US/10026021
; Publication No. US20030027756A1


```

; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human ARK mitotic kinase
US-10-026-021-7

```

```

Query Match      77.6%; Score 38; DB 15; Length 403;
Best Local Similarity 75.0%; Pred. No. 84;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      2 LLGRPPPE 9
      |:::|
Db      323 LVGKPPPE 330

```

RESULT 15

```

US-10-059-585-33
; Sequence 33, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05860
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-116776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens

```

```

US-10-059-585-33
Query Match      77.6%; Score 38; DB 15; Length 403;
Best Local Similarity 75.0%; Pred. No. 84;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

QY      2 LLGRPPPE 9
      |:::|
Db      323 LVGKPPPE 330

RESULT 36
US-10-209-324-2
; Sequence 2, Application US/10209324
; Publication No. US20030108910A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA SAN FRANCISCO
; APPLICANT: TOLAND, Amanda E.
; APPLICANT: BALMAIN, Allan
; TITLE OF INVENTION: STK15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANCER
; FILE REFERENCE: UCSF1120-2
; CURRENT APPLICATION NUMBER: US/10/209,324
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/334,146
; PRIOR FILING DATE: 2002-11-28
; PRIOR APPLICATION NUMBER: US 60/308,911
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (31)..(31)
; OTHER INFORMATION: Xaa is Ile or Phe
US-10-209-324-2

```

```

Query Match      77.6%; Score 38; DB 15; Length 403;
Best Local Similarity 75.0%; Pred. No. 84;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      2 LLGRPPPE 9
      |:::|
Db      323 LVGKPPPE 330

```

RESULT 37

```

US-09-771-161A 195
; Sequence 195, Application US/09771161A
; Patent No. US2002011081A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 195
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-195

```

```

Query Match      77.6%; Score 38; DB 10; Length 737;

```

Best Local Similarity 66.7%; Score 38; DB 15; Length 237;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPF 9
DB 600 MMAGQPPF 608

RESULT 38
US-10-228-931-4
; Sequence 4, Application US/10228931
; Publication No. US20030051258A1
; GENERAL INFORMATION:
; APPLICANT: Verma, Ajit K
; APPLICANT: Reddig, Peter J
; APPLICANT: Jansen, Aaron P
; TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma
; FILE REFERENCE: 960236.97613
; CURRENT APPLICATION NUMBER: US/10/228,931
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US/09/772,647
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T tag and
; OTHER INFORMATION: mouse protein kinase C epsilon coding sequence
US 10-228-931-4

Query Match 77.6%; Score 38; DB 15; Length 237;
Best Local Similarity 66.7%; Score 38; DB 15; Length 237;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPF 9
DB 600 MMAGQPPF 608

RESULT 38
US-09-736-076-3
; Sequence 3, Application US/09736076
; Patent No. US20020049101A1
; GENERAL INFORMATION:
; APPLICANT: Ben Sasson, Samuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WITH SELECTIVE
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SE-10. 1100-1105 KINASES
; FILE REFERENCE: 124211015-004
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/841,104
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PKC
US-09-736-076-3

Query Match 75.5%; Score 37; DB 9; Length 20;
Best Local Similarity 66.7%; Score 37; DB 9; Length 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPF 9
DB 3 MMAGQPPF 11

RESULT 40
US-09-836-392-15
; Sequence 15, Application US/09836392
; Patent No. US20020173458A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptide
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: P202CP
; CURRENT APPLICATION NUMBER: US/09/836,392
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: PCT/US00/28066
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 60/159,542
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/165,914
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/189,027
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-392-15

Query Match 75.5%; Score 37; DB 10; Length 445;
Best Local Similarity 75.0%; Score 37; DB 10; Length 445;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPF 8
DB 263 MLVGQPPF 270

Search completed: November 14, 2003, 13:43:26
Job time : 22.3714 secs

GenCore version 5.1.6
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QM protein protein search, using sw model

Run on: November 14, 2003, 13:20:05 ; Search time 10.8 Seconds
(without alignment)
80.141 Million cell updates/sec

Title: US-09-736-076-15

Perfect score: 49

Sequence: 1 MLGRRPPE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96169682 residues

Total number of hits satisfying chosen parameters: 183308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match: 100%

Listing first 45 summaries

Database :

PIR 76:

1: pirl:

2: pirl:

3: pirl:

4: pirl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	682	2 A44493	serum-inducible ki
2	41	83.7	465	2 B55748	protein kinase (EC
3	41	83.7	521	2 D85640	Protein F55A8.2 (i
4	41	83.7	925	2 A55748	protein kinase (EC
5	40	81.6	603	2 S14133	serine/threonine-s
6	40	81.6	603	2 A47545	protein kinase (EC
7	40	81.6	603	2 A54538	protein kinase p02
8	39	79.6	576	2 S22127	protein kinase C (
9	39	79.6	639	2 A32545	protein kinase C (
10	38	77.6	305	2 T43221	serine/threonine-s
11	38	77.6	329	2 B87790	protein kinase B0207.4 (i
12	38	77.6	389	2 S52242	protein kinase (EC
13	38	77.6	403	2 JC5974	aurora-related kin
14	36	77.6	407	2 S52243	p463265 protein -
15	38	77.6	547	2 S44841	K05H7.1 protein -
16	38	77.6	547	2 T22856	hypothetical prote
17	38	77.6	634	1 B32392	protein kinase C (
18	38	77.6	648	2 T43337	pelo-like kinase-1
19	38	77.6	683	2 T38254	serine/threonine-s
20	38	77.6	705	2 A48144	protein kinase CDC
21	38	77.6	707	1 A53530	protein kinase C (
22	38	77.6	736	1 KIRBCE	protein kinase C (
23	38	77.6	737	1 S28942	protein kinase C (
24	38	77.6	737	1 KIRTC	protein kinase C (
25	38	77.6	737	1 KIMSC	protein kinase C (
26	37	75.5	220	1 B42725	multile hydratase
27	37	75.5	380	2 S70964	par5 protein - Myx
28	37	75.5	672	1 KIHUCA	protein kinase C (
29	37	75.5	672	1 KIRTC	protein kinase C (

RESULT 1

A44493

serum-inducible kinase - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 10-Sep-1997

C:Accession: A44493

R:Simmons, D.L.; Neel, B.G.; Stevens, R.; Evert, G.; Erikson, R.L.

Mol. Cell. Biol. 12, 4164-4169, 1992

A:Title: Identification of an early-growth-response gene encoding a novel putative p

A:Reference number: A44493; MUID:92375085; PMID:150821;

A:Accession: A44493

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-682 <SIM>

A:Experimental source: F-2 cells

A:Note: sequence extracted from NCBI backbone (NCBIN:111721, NCBI:P:111722)

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho

C:Keywords: ATP

F:77-331/Domain: protein kinase homology <KIN>

Query Match 100.0%; Score 49; DB 2; Length 682;

Best Local Similarity 100.0%; Pred. No. 0.24;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9

DB 270 MLGRRPPE 279

RESULT 2

B55748

protein kinase (EC 2.7.1.37) Sak-b - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Dec-1997

C:Accession: B55748

R:Podde, C.; Motro, B.; Yousefi, S.; Heffernan, M.; Dennis, J.W.

Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994

A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosop

A:Reference number: A55748; MUID:94294387; PMID:8022793

A:Accession: B55748

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-465 <FCD>

A:Cross-references: GB:L29480

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho

C:Keywords: ATP; phosphotransferase

F:10-265/Domain: protein kinase homology <KIN>

F:18-26/Region: protein kinase ATP-binding motif

Query Match 83.7%; Score 41; DB 2; Length 465;

Best Local Similarity 66.7%; Pred. No. 5.4;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 : : : : :
 Db 204 LLVGRPPFD 212

RESULT 3
 A47545
 protein f55a8.2 (imported) - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10 May-2001 #sequence_revision 10-May-2001 #text_change 17 May 2002
 C:Accession: D88640
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
 A:Reference numbers: A75000; MUID:99059611; PMID:9891916
 A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_elegans/
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: D88640
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-521 <STC>
 A:Cross-references: GB:chr_IV; PIDN:AA019186.1; PID:91931149; GSPDB:GN000022; CESP:F55A8.
 C:Genetics:
 A:Gene: F55A8.2
 A:Map position: 4
 C:Superfamily: cGMP-dependent protein kinase; cAMP receptor protein cyclic nucleotide-binding

Query Match 83.7%; Score 41; DB 2; Length 521;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 : : : : :
 Db 401 MLLGRPPPE 409

RESULT 4
 A47548
 protein kinase (EC 2.7.1.37) Sak-3 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Sep-1999
 C:Accession: A55748
 R:Fede, C.; Motro, B.; Yousefi, S.; Befferman, M.; Dennis, J.W.
 Proc. Natl. Acad. Sci. U.S.A. 91, 6389-6392, 1994
 A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosophila
 A:Reference numbers: A55748; MUID:94294380; PMID:8022793
 A:Accession: A55748
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-925 <PCN>
 A:Cross-references: GR:029479; NID:918484; PID:AA030144.1; PID:9487870
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C:Keywords: ATP; phosphotransferase
 F:10-265/Domain: protein kinase homology <KIN>
 F:18-265/Region: protein kinase ATP-binding motif

Query Match 83.7%; Score 41; DB 2; Length 925;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 : : : : :
 Db 204 LLVGRPPFD 212

RESULT 5
 S34130
 serine/threonine-specific protein kinase Plk (EC 2.7.1.37) - human
 N:Alternate names: polo-like protein kinase; protein kinase Plk-1
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
 C:Accession: S34130; I38123; S61543

R;Goisteyn, R.M.; Schultz, S.J.; Bartek, J.; Ziemiecki, A.; Ried, T.; Nigg, E.A.
 submitted to the EMBL Data Library, June 1993
 A:Description: Cloning and characterization of a novel human protein kinase plk-1 a
 through mitosis.
 A:Reference number: S34130
 A:Accession: S34130
 A:Molecule type: mRNA
 A:Residues: 1-603 <GC>
 A:Cross-references: EMBL:X73459; NID:9312997; PIDN:CAA51837.1; PID:9312998
 A:Experimental source: nasopharyngeal carcinoma
 R:Heinrich, U.; Wolf, G.; Brauning, A.; Karn, T.; Bohme, B.; Ruebsamen-Waigmann, H.
 Proc. Natl. Acad. Sci. U.S.A. 91, 1736-1740, 1994
 A:Title: Induction and down-regulation of PLK, a human serine/threonine kinase expre
 A:Reference number: A53134; MUID:94173904; PMID:8127874
 A:Accession: I38123
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-140, P, 142-226, E, 228-603 <RES>
 A:Cross-references: EMBL:X75932; NID:9460768; PIDN:CAA53536.1; PID:9460769
 A:Experimental source: lung tumor
 R:Brauning, A.; Strebhardt, K.; Ruebsamen-Waigmann, H.
 Oncogene 11, 1793-1800, 1995

A:Title: Identification and functional characterization of the human and murine polo
 A:Reference number: S61543; MUID:96568906; PMID:7479607
 A:Accession: S61543
 A:Molecule type: DNA
 A:Residues: 1-122, T, 124-136 <BRA>
 A:Cross-references: EMBL:X90725; NID:91061143; PIDN:CAA62260.1; PID:91061144
 A:Experimental source: placenta
 A:Note: the authors translated the codon AGC for residue 107 as Met
 C:Genetics:
 A:Gene: GDB:PLK
 A:Cross-references: GDB:331003
 A:Map position: 17pter-17p12
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hc
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:51-305/Domain: protein kinase homology <KIN>

Query Match 81.6%; Score 40; DB 2; Length 603;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 : : : : :
 Db 244 LLVGRPPPE 252

RESULT 6
 A47545
 protein kinase (EC 2.7.1.37) Plk - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
 C:Accession: A47545
 R:Clay, F.C.; McEwen, S.J.; Bertonecello, I.; Wilks, A.F.; Dunn, A.R.
 Proc. Natl. Acad. Sci. U.S.A. 90, 4882-4886, 1993
 A:Title: Identification and cloning of a protein kinase-encoding mouse gene, Plk, r
 A:Reference number: A47545; MUID:93281660; PMID:8099445
 A:Accession: A47545
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-603 <CLA>
 A:Cross-references: GB:L06144; NID:9309461; PIDN:AAA39948.1; PID:9309462
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase h
 C:Keywords: ATP; phosphotransferase
 F:51-305/Domain: protein kinase homology <KIN>

Query Match 81.6%; Score 40; DB 2; Length 603;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 : : : : :
 Db 244 LLVGRPPPE 252

A;Cross-references: GB:X05076; NID:g8352; PIDN:CAA28736.1; PID:g8353; GB:Y00042
C;Genetics:

A;Gene: FlyBase:Pkc53E

A;Cross-references: FlyBase:FBgn0003091

C;Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F;46-95/Domain: protein kinase C zinc-binding repeat homology <K21>

F;111-160/Domain: protein kinase C zinc-binding repeat homology <K22>

F;161-273/Domain: protein kinase C C2 region homology <K2>

F;339-599/Domain: protein kinase C C2 region homology <KIN>

F;347-355/Region: protein kinase ATP-binding motif

Query Match 79.6%; Score 39; DB 2; Length 639;

Best Local Similarity 66.7%; Pred. No. 18;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

|||:||||

Db 533 MLVGQPPFD 541

RESULT 10

T43221

serine/threonine-specific protein kinase (EC 2.7.1.1) 2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000

C;Accession: T43221

R;Schumacher, J.M.; Golden, A.; Donovan, P.J.

J. Cell Biol. 143, 1635-1646, 1998

A;Title: AIR-2: An aurora/ipll-related protein kinase associated with chromosomes and

A;Reference number: 222347; MUID:99069487; PMID:9852156

A;Accession: T43221

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-305 <SCH>

A;Cross-references: EMBL:AF071207; PIDN:AAC70945.1

C;Genetics:

A;Gene: AIR-2

A;Map position: 1

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: phosphotransferase

Query Match 77.6%; Score 38; DB 2; Length 305;

Best Local Similarity 75.0%; Pred. No. 13;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 9

|||:||||

Db 220 LVGKPPPE 227

RESULT 11

B87790

protein BC207.4 (imported) - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001

C;Accession: B87790

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;

A;Accession: B87790

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-329 <STO>

A;Cross-references: GB:chr_1; PIDN:AAB52459.1; PID:g1943805; GSPDB:GN00019; CESP:B020

C;Genetics:

A;Gene: B0207.4

A;Map position: 1

C;Superfamily: kinase-related transforming protein; protein kinase homology

RESULT 7

A54596

protein kinase - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C;Accession: A54596

R;Lake, R.J.; Jelinek, W.R.

Mol. Cell. Biol. 13, 7793-7801, 1993

A;Title: Cell cycle- and terminal differentiation-associated regulation of the mouse mRN

A;Reference number: A54596; MUID:94067140; PMID:7902533

A;Accession: A54596

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-603 <RES>

A;Cross-references: GB:L19558; NID:g403473; PIDN:AA16071.1; PID:g403474

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol

F;51-305/Domain: protein kinase homology <KIN>

Query Match 81.6%; Score 40; DB 2; Length 603;

Best Local Similarity 66.7%; Pred. No. 11;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

|||:||||

Db 244 LVGKPPPE 252

RESULT 8

S22127

protein kinase polo (EC 2.7.1.1) - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999

C;Accession: S22127

R;Sunkel, C.E.

Submitted to the EMBL Data Library, November 1991

A;Reference number: S22127

A;Accession: S22127

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-576 <SUN>

A;Cross-references: EMBL:X63361; NID:g8355; PIDN:CAA44963.3; PID:g8356

C;Genetics:

A;Gene: FlyBase:polo

A;Cross-references: FlyBase:FBgn0003124

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol

C;Keywords: ATP; phosphotransferase

F;21-277/Domain: protein kinase homology <KIN>

Query Match

79.6%; Score 40; DB 2; Length 603;

Best Local Similarity 66.7%; Pred. No. 11;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

|||:||||

Db 216 LVGQPPPE 224

RESULT 9

A32545

protein kinase C (EC 2.7.1.1) - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1999

C;Accession: A32545

R;Rosenblatt, A.; Rhee, L.; Yadegari, R.; Pato, R.; Ulrich, A.; Goeddel, D.V.

EMBO J. 6, 433-441, 1987

A;Title: Structure and nucleotide sequence of a Drosophila melanogaster protein kinase C

A;Reference number: A32545; MUID:87218499; PMID:3107983

A;Accession: A32545

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-539 <ROS>


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Query Match 77.6%; Score 38; DB 2; Length 329;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 9
   |||||
Db 244 LVGKPPPE 251

RESULT 13
S52242
protein kinase (EC 2.7.1.1) p46XlEq22 African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 18-Jun-1999
C:Accession: S52242
R:Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein kin
A:Reference number: S52242
A:Accession: S52242
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-389 <ROG>
A:Cross-references: EMBL:Z17206; NID:g609280; PIDN:CAA76914.1; PID:g609280
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:119-391/Domain: protein kinase homology <KIN>
F:127-135/Region: protein kinase ATP-binding motif

Query Match 77.6%; Score 38; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 9
   |||||
Db 311 LVGKPPPE 318

RESULT 13
JC5974
aurora related kinase 1 (EC 2.7.1.1) human
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jan-2000
C:Accession: JC5974
R:Shindou, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara, M.; Gilbert, D.J.; Jenk
Biochem. Biophys. Res. Commun. 244, 285-292, 1998
A:Title: cDNA cloning, expression, subcellular localization, and chromosomal assignment
A:Reference number: JC5974; MJD:98183439; PID:4514916
A:Accession: JC5974
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-403 <SHI>
A:Cross-references: GB:AF008551
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: phosphotransferase
F:131-383/Domain: protein kinase homology <KIN>

Query Match 77.6%; Score 38; DB 2; Length 403;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 9
   |||||
Db 323 LVGKPPPE 330

RESULT 14
S52243
p46Eg265 protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-May-1995 #sequence_revision 01-Aug-1995 #text_change 24-Sep-1999
C:Accession: S52243; S34642; I51695
R:Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
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submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein
A:Reference number: S52242
A:Accession: S52243
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-407 <ROG>
A:Cross-references: EMBL:Z17207; NID:g609281; PIDN:CAA78915.1; PID:g609282
R:Bouvet, P.; Omilli, F.; Arlot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Basset, T.;
submitted to the EMBL Data Library, June 1993
A:Description: Targetted deadenylation of specific mRNAs in Xenopus embryos by a mecl
A:Reference number: S34642
A:Accession: S34642
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 328-407 <BOU>
A:Cross-references: EMBL:Z24453; NID:g394756; PIDN:CAA80826.1; PID:g394757
R:Bouvet, P.; Omilli, F.; Arlot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Bassez, T.;
Mol. Cell. Biol. 14, 1893-1900, 1994
A:Title: The deadenylation conferred by the 3' untranslated region of a developmental
A:Reference number: I51695; MJD:94158861; PMID:8114721
A:Accession: I51695
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 328-407 <BO2>
A:Cross-references: EMBL:Z24453; NID:g394756; PIDN:CAA80826.1; PID:g394757
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; phosphotransferase; protein kinase
F:138-390/Domain: protein kinase homology <KIN>
F:146-154/Region: protein kinase ATP-binding motif

Query Match 77.6%; Score 38; DB 2; Length 407;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 9
   |||||
Db 330 LVGKPPPE 337

RESULT 15
S44841
K06H7.1 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C:Accession: S44841
R:Favella, A.D.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid K06H7.
A:Reference number: S44620
A:Accession: S44841
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-547 <FAV>
A:Cross-references: EMBL:L15314; NID:g289690; PIDN:AAA28084.1; PID:g289691
C:Genetics:
A:Introns: 25/3; 36/3; 80/3; 149/3; 186/2; 229/3; 311/3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
C:Keywords: ATP; serine/threonine-specific protein kinase
F:265-518/Domain: protein kinase homology <KIN>

Query Match 77.6%; Score 38; DB 2; Length 547;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
   |||||
Db 457 LLFGQPPPE 465

RESULT 16
T22856
hypothetical protein F57P5.5 - Caenorhabditis elegans
```

C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Jun-2002
 C;Accession: T22856
 R;Harris, B.
 Submitted to the EMBL Data Library, July 1996
 A;Reference number: Z19627
 A;Accession: T22856
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-547 <WIL>
 A;Cross references: EMBL:Z75953; PIDN:CAE00101.1; GSPDB:GN00023; CESP:F57F5.5
 A;Experimental source: clone F57F5
 C;Genetics:
 A;Gene: CESP:F57F5.5
 A;Map position: 5
 A;Introns: 43/1; 129/2; 166/3; 187/1; 289/2; 341/2; 450/3; 499/1
 A;Full-60/Domain: protein kinase C zinc binding repeat homology <K2N1>
 F;89-136/Domain: protein kinase C zinc-binding repeat homology <K2N2>

Query Match 77.6%; Score 38; DB 2; Length 547;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 : |||
 DB 410 MWAGQPPPE 418

RESULT 17
 E32392
 Protein kinase C (EC 2.7.1.1) epsilon related - fruit fly (Drosophila melanogaster)
 N;Alternate names: protein kinase C 98F
 C;Species: Drosophila melanogaster
 C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 11-Jun-1999
 C;Accession: B32392
 R;Schaeffer, E.; Smith, D.; Marden, G.; Quinn, W.; Zaker, C.
 Cell 57, 403-412, 1993
 A;Title: Isolation and characterization of two new Drosophila protein kinase C genes, in
 A;Reference number: A32392; MUID:89249300; PID:2720775

A;Accession: B32392
 A;Molecule type: mRNA
 A;Residues: 1-634 <SCH>
 A;Cross-references: GB:J04648; NID:G158128; PIDN:AAZ88.6.1; PID:G158129
 C;Genetics:
 A;Gene: FlyBase:PK03ae
 A;Cross-references: FlyBase:FBgn0003093
 C;Function:

A;Description: catalyzes the formation of peptidyl-serine phosphate or peptidyl-threonin
 A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
 C;Superfamily: protein kinase C delta; protein kinase C zeta binding repeat homology; pr
 C;Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransf
 F;58-63/Region: pseudophosphorylation motif
 F;72-131/Domain: protein kinase C zinc binding repeat homology <K21>
 F;147-196/Domain: protein kinase C zinc-binding repeat homology <K22>
 F;301-560/Domain: protein kinase homology <KIN>
 F;309-317/Region: protein kinase ATP-binding motif
 F;72-102/105-121/Binding site: zinc (Cys, Cys, Cys, His, Cys) #status predicted
 F;85-86-110-113/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F;147-172-180-196/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F;160-161-185-188/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F;332-351-427-429/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 77.6%; Score 38; DB 1; Length 634;
 Best Local Similarity 66.7%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 : |||
 DB 495 MWAGQPPPE 503

RESULT 18
 T43337

polo-like kinase-1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 01-Dec-2000
 C;Accession: T43337; S44761
 R;Chase, D.; Serafinas, C.; Ashcroft, N.; Kosinski, M.; Longo, D.; Ferris, D.K.; Gol
 Submitted to the EMBL Data Library, July 1998
 A;Description: The polo-like kinase PLK-1 is required for nuclear envelope breakdown
 A;Reference number: Z22438
 A;Accession: T43337
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-648 <CHA>
 A;Cross-references: EMBL:AF080581; PIDN:AAC34661.1
 R;Favella, A.D.
 Submitted to the EMBL Data Library, May 1993
 A;Description: Sequence of the C. elegans cosmid C14B9.
 A;Reference number: S44617
 A;Accession: S44761
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 'MKTL', 282-648 <PAV>
 A;Cross-references: EMBL:L15188; NID:g289640; PID:g289648
 C;Genetics:
 A;Gene: plk-1
 A;Map position: 3
 A;Introns: 391/3; 540/3; 578/3
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho

Query Match 77.6%; Score 38; DB 2; Length 648;
 Best Local Similarity 66.7%; Pred. No. 28;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 : |||
 DB 228 LFGQPPPE 236

RESULT 19
 T38254

serine/threonine-specific protein kinase plol (EC 2.7.1.1) - fission yeast (Schizosa
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
 C;Accession: T38254; T45128
 R;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 Submitted to the EMBL Data Library, August 1995
 A;Reference number: Z21781
 A;Accession: T38254

A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-683 <BRO>
 A;Cross-references: EMBL:Z58559; PIDN:CAB1167.1; GSPDB:GN00066; SPDB:SPAC23C11.16
 A;Experimental source: strain 972h-7 cosmid C23C11
 R;Ohkura, H.; Hagan, I.M.; Glover, D.M.
 Genes Dev. 9, 1059-1073, 1995

A;Title: The conserved Schizosaccharomyces pombe kinase plol, required to form a bip
 A;Reference number: Z22921; MUID:95262899; PMID:7744248

A;Accession: T45128
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-683 <OHK>
 A;Cross-references: EMBL:X85758; NID:g887640; PIDN:CAA59766.1; PID:g887641
 A;Experimental source: strain 972 derivative
 C;Genetics:

A;Gene: plol; SPAC23C11.16
 A;Map position: 1
 C;Function:

A;Description: required to form a bipolar spindle and early in the regulatory casc
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
 C;Keywords: phosphotransferase; protein kinase

Query Match 77.6%; Score 38; DB 2; Length 683;
 Best Local Similarity 55.6%; Pred. No. 30;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLJGRPPFE 9
 DB 243 MLJGRPPFE 241

RESULT 22
 A48144
 protein kinase CDC5 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein kinase PKX2; protein YMR201C; protein YMR001C
 C:Species: Saccharomyces cerevisiae
 C>Date: 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change 24-Sep-1999
 C:Accession: A48144, S53030; S27445
 R:Kitada, K.; Johnson, A.L.; Johnston, B.H.; Sugino, A
 Mol. Cell. Biol. 13, 4445-4457, 1993
 A:Title: A multicopy suppressor gene of the Saccharomyces cerevisiae G 1 cell cycle mutant
 A:Reference number: A48144; MUID:93309473; PMID:8321244
 A:Accession: A48144
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-705 <KIT>
 A:Cross-references: EXBL:M84220; NID:q172186; PID:AAA02576.1; PID:q172187
 R:Devlin, K.; Churcher, C.M.
 Submitted to the EMBL Data Library, March 1995
 A:Reference number: S53028
 A:Accession: S53030
 A:Molecule type: DNA
 A:Residues: 1-705 <DEV>
 A:Cross-references: EXBL:Z48613; NID:q728645; PID:CAAE516.1; PID:q728648; MIPS:YMR001C
 A:Experimental source: strain AB972
 C:Genetics:
 A:Gene: SCD1CDC5; PKX2
 A:Cross-references: SCD:SC004603; MIPS:YMP001C
 A:Map position: 13K
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C:Keywords: ATP; cell cycle control; phosphotransferase; protein kinase
 F:80-337/Domain: protein kinase homology <KIN>

Query Match 77.6% Score 38; DB 2; Length 705;
 Best Local Similarity 55.6% Pred. No. 31;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLJGRPPFE 9
 DB 274 MLJGRPPFE 282

RESULT 22
 A53530
 protein kinase C (EC 2.7.1.1) epsilon-related - Caenorhabditis elegans
 N:Alternate names: protein kinase C PKC1B; neuronal
 C:Species: Caenorhabditis elegans
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jun-1999
 C:Accession: A53530
 R:Land, M.; Islas-Trejo, A.; Freedman, J.H.; Rucin, G.
 C. Biol. Chem. 269, 9234-9244, 1994
 A:Title: Structure and expression of a novel, neuronal protein kinase C (PKC1B) from Caenorhabditis elegans
 A:Keywords: signals
 A:Reference number: A53530; MUID:94179345; PMID:8132661
 A:Accession: A53530
 A:Molecule type: mRNA
 A:Residues: 1-707 <LAN>
 A:Cross-references: GB:J000181; NID:q494065; PID:AAA1816.1; PID:q392435
 C:Genetics:
 A:Gene: kin-13
 A:Map position: V
 A:Note: located near myo-3, col-1, and CPE37/2 genes
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 A:Note: activity is calcium-independent, phospholipid-dependent, and activated by diacylglycerol
 C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; phospholipid binding; phosphotransferase
 C:Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransferase
 F:157-162/Region: pseudophosphorylation motif

F:171-220/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:249-298/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:376-638/Domain: protein kinase homology <KIN>
 F:384-392/Region: protein kinase ATP-binding motif
 F:171,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:184,187,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:249,279,282,298/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:262,265,287,290/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:407,426,502,504/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 77.6% Score 38; DB 1; Length 707;
 Best Local Similarity 66.7% Pred. No. 31;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLJGRPPFE 9
 DB 570 MMAGQPPFE 578

RESULT 22
 KIRBC2
 protein kinase C (EC 2.7.1.1) epsilon - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
 C:Accession: A29880
 R:Ohno, S.; Akita, Y.; Konno, Y.; Imajoh, S.; Suzuki, K.
 Cell. 53, 731-741, 1988
 A:Title: A novel phorbol ester receptor/protein kinase, nPKC, distantly related to protein kinase C
 A:Reference number: A29880; MUID:8823367; PMID:3370672
 A:Accession: A29880
 A:Molecule type: mRNA
 A:Residues: 1-736 <OHN>
 A:Cross-references: GB:M20014
 C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
 A:Note: activity is calcium-independent, phospholipid-dependent, and activated by diacylglycerol
 C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology
 C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid binding; phosphotransferase
 F:156-161/Region: pseudophosphorylation motif
 F:170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:405-667/Domain: protein kinase homology <KIN>
 F:413-421/Region: protein kinase ATP-binding motif
 F:170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:436,455,531,533/Active site: Lys, Glu, Asp, Lys #status predicted
 F:702,709/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status

Query Match 77.6% Score 38; DB 1; Length 736;
 Best Local Similarity 66.7% Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLJGRPPFE 9
 DB 599 MMAGQPPFE 607

RESULT 23
 S28942
 protein kinase C (EC 2.7.1.1) epsilon - human
 C:Species: Homo sapiens (man)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999
 C:Accession: S28942
 R:Basta, P.; Strickland, M.B.; Holmes, W.; Loomis, C.R.; Ballas, L.M.; Burns, D.J.
 Biochim. Biophys. Acta 1132, 154-160, 1992
 A:Title: Sequence and expression of human protein kinase C-epsilon.
 A:Reference number: S28942; MUID:93003318; PMID:1382605
 A:Accession: S28942
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-737 <BAS>

A/Cross-references: EMBL:X65293; NID:935494; PID:CAA46388.1; PID:935495
 A/Comments: This is a calcium-independent, phospholipid-dependent, serine- and threonine-
 of inositol phospholipids. This protein is a receptor for tumor promoting phorbol ester
 C/Genetics:
 A/Gene: GDB:PKCE
 A/Cross-references: GDB:128039; OMIM:176975
 A/Map position: 3pter-3qter
 C/Function:
 A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 A/Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
 C/Superfamily: protein kinase C delta; protein kinase C zinc binding repeat homology; p
 C/Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransf
 F/156-161/Region: pseudophosphorylation motif
 F/170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
 F/243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
 F/406-668/Domain: protein kinase homology <KIN>
 F/414-422/Region: protein kinase ATP-binding motif
 F/170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F/183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F/243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F/256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F/437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
 Query Match 77.6%; Score 38; DB 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 | : : : : :
 Db 600 MMAGQPPPE 608
 RESULT 24
 KIRTCF
 A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Sep-1992 #sequence_revision 30 Sep-1992 #text_change 11-Jun-1999
 C/Accession: P28163; B26408; S00216
 R/Obo: Y. Fujita, T. Ogita, K. Kikkawa, J. Igarashi, K. Nishizuka, Y
 J. Biol. Chem. 263, 6927-6932, 1988
 A/Title: The structure, expression, and properties of additional members of the protein
 A/Reference number: A92717; MUID:88198270; PMID:2634397
 A/Accession: B28163
 A/Molecule type: DNA
 A/Residues: 1-737 <ON>
 A/Cross-references: GB:M18331; NID:9206192; PID:AAA41872.1; PID:9206193
 R/Housey, G.M.; O'Brian, C.A.; Johnson, M.D.; Kirschmeier, P.; Weinstein, I.B.
 Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987
 A/Title: Isolation of cDNA clones encoding protein kinase C evidence for a protein kin
 A/Reference number: A94145; MUID:87147193; PMID:3466647
 A/Accession: B26403
 A/Molecule type: mRNA
 A/Residues: 397-447; GSRGHDREDFGSGAET...; GSRGHDREDFGSGAET...; GSRGHDREDFGSGAET...
 A/Cross-references: GB:M15523; NID:9206192; PID:AAA41872.1; PID:9206193
 C/Comment: Protein kinase C epsilon and epsilon' appear to be encoded by the same gene a
 C/Function:
 A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 A/Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
 C/Superfamily: protein kinase C delta; protein kinase C zinc binding repeat homology; p
 C/Keywords: alternative splicing; ATP; autophosphorylation; duplication; phorbol ester b
 C/156-161/Region: pseudophosphorylation motif
 F/170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
 F/243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
 F/406-668/Domain: protein kinase homology <KIN>
 F/414-422/Region: protein kinase ATP-binding motif
 F/170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F/183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F/243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F/256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F/437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
 F/703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match 77.6%; Score 38; DB 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 | : : : : :
 Db 600 MMAGQPPPE 608
 RESULT 25
 KIMSCE
 A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
 A/Note: activity is calcium-independent, phospholipid-dependent, and activated by dia
 C/Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology;
 C/Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholip
 F/156-161/Region: pseudophosphorylation motif
 F/170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
 F/243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
 F/406-668/Domain: protein kinase homology <KIN>
 F/414-422/Region: protein kinase ATP-binding motif
 F/170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F/183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F/243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F/256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F/437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
 F/703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p
 Query Match 77.6%; Score 38; DB 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 | : : : : :
 Db 600 MMAGQPPPE 608
 RESULT 26
 B42725
 A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
 C/Species: Pseudomonas chlororaphis
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C/Accession: B42725
 R/Nishiyama, M.; Horinouchi, S.; Kobayashi, M.; Nagasawa, T.; Yamada, H.; Beppu, T.
 J. Bacteriol. 173, 2465-2472, 1991
 A/Title: Cloning and characterization of genes responsible for metabolism of nitrile
 A/Reference number: A42725; MUID:91193202; PMID:2013568
 A/Accession: B42725
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-220 <NIS>
 A/Cross-references: GB:D90216; NID:9216850; PIDN:BAA14246.1; PID:9216853
 C/Superfamily: nitrile hydratase beta chain
 C/Keywords: carbon-oxygen lyase; hydro-lyase
 Query Match 75.5%; Score 37; DB 1; Length 220;
 Best Local Similarity 75.0%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LLGRPPPE 9
 | : : : : :
 Db 200 MMAGQPPPE 208

Db 118 ITGRPPFE 125

RESULT 29

S70964

pkns protein - Myxococcus xanthus
N:Alternate names: serine protein kinase homolog
C:Species: Myxococcus xanthus
C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
C:Accession: S70964
R:Zhang, W.; Inouye, M.; Inouye, S.
Mol. Microbiol. 20, 435-447, 1996
A:Title: Reciprocal regulation of the differentiation of Myxococcus xanthus by Pkn5 and A:Reference number: S70964; MUID:96310360; PMID:8733241
A:Accession: S70964
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-380 <ZHA>
A:Cross-references: EMBL:U40656; NID:G1113924; PIDN:AAB40049.1; PID:G1113925
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C:Genetics:
A:Gene: pkn5

Query Match. 75.5%; Score 37; DB 2; Length 380;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

Db 314 LLSGRPPFD 322

RESULT 28

K:HUCA

protein kinase C (EC 2.7.1.1-) alpha - human
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: S09496
R:Finkezeiler, G.; Varne, D.; Hug, H.
Nucleic Acids Res. 18, 2183, 1990
A:Title: Sequence of human protein kinase C alpha.
A:Reference number: S09496; MUID:90245676; PMID:2336401
A:Accession: S09496
A:Molecule type: mRNA
A:Residues: 1-672 <FIN>
A:Cross-references: EMBL:X52479; NID:G35482; PIDN:CAA36718.1; PID:G35483
C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-sp
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters,
C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
C:Comment: the zinc stabilized regions bind diacylglycerol and phorbol esters.
C:Genetics:
A:Gene: GDB:PRKCA
A:Cross-references: GDB:128015; OMIM:176900
A:Map position: 17q22-17q23.2
C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase
C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding
F:19-29/Region: phospholipid binding #status experimental
F:22-27/Region: pseudophosphorylation motif
F:37-86/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F:102-151/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F:152-264/Domain: protein kinase C C2 region homology <K2>
F:337-597/Domain: protein kinase homology <KIN>
F:345-353/Region: protein kinase ATP-binding motif
F:368/Active site: Lys #status predicted
F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match. 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

Db 531 MLACQPPFD 539

RESULT 29

K:IRTC

protein kinase C (EC 2.7.1.1-) alpha - rat
N:Alternate names: protein kinase C type III
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: S02248; SC2620
R:Ono, Y.; Fujii, T.; Igarashi, K.; Kikkawa, U.; Ogita, K.; Nishizuka, Y.
Nucleic Acids Res. 16, 5199-5200, 1988
A:Title: Nucleotide sequences of cDNAs for alpha and gamma subspecies of rat brain pr
A:Reference number: S02129; MUID:88262515; PMID:3387228
A:Accession: S02248
A:Molecule type: mRNA
A:Residues: 1-672 <ONO>
A:Cross-references: EMBL:X07286; NID:G56913; PIDN:CAA30266.1; PID:G56914
C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol este
C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k
C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin
F:19-29/Region: phospholipid binding #status experimental
F:22-27/Region: pseudophosphorylation motif
F:37-86/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F:102-151/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F:152-264/Domain: protein kinase C C2 region homology <K2>
F:337-597/Domain: protein kinase homology <KIN>
F:345-353/Region: protein kinase ATP-binding motif
F:368/Active site: Lys #status predicted
F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status F

Query Match. 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

Db 531 MLACQPPFD 539

RESULT 30

K:IMSCA

protein kinase C (EC 2.7.1.1-) alpha - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: S07104; JSC078
R:Megidish, T.; Mazurek, N.
Nature 342, 807-811, 1989
A:Title: A mutant protein kinase C that can transform fibroblasts.
A:Reference number: S07104; MUID:90098082; PMID:2601739
A:Accession: S07104
A:Molecule type: mRNA
A:Residues: 1-672 <MEG>
A:Cross-references: GB:X52685; GB:X51603; NID:G49938; PIDN:CAA36908.1; PID:G49939
A:Experimental source: strain Balb/c
R:Rose-John, S.; Dietrich, A.; Marks, F.
Gene 74, 465-471, 1988
A:Title: Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss 3T3 fibro
A:Reference number: JS0078; MUID:89232737; PMID:2469625
A:Accession: JS0078
A:Molecule type: mRNA
A:Residues: 1-146, 'D', '148-217, 'N', '219-276, 'AH', '279-312, 'V', '314-466, 'N', '468-471, 'N', '4
A:Cross-references: GB:M25811
A:Note: the authors translated the codon AAC for residue 141 as Lys; the sequence sh
C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonin
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol est
C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane

C;Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C;Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C;Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding
F;19-29/Region: phospholipid binding #status experimental
F;22-27/Region: pseudophosphorylation motif
F;37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
F;102-151/Domain: protein kinase C zinc binding repeat homology <K22>
F;152-264/Domain: protein kinase C C2 region homology <K2>
F;337-597/Domain: protein kinase homology <KIN>
F;345-353/Region: protein kinase ATP-binding motif
F;37,67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;50,53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;102,132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;368/Active site: Lys #status predicted
F;631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 75.5% Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
|||:
Db 531 MLAGQPPFD 539

RESULT 31
KIRBC
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C;Accession: C26037
R;Chino, S.; Kawasaki, H.; Imaoh, S.; Suzuki, K.; Inagaki, M.; Yokokura, H.; Sakoh, T.; Nature 325, 161-166, 1987
A;Title: Tissue-specific expression of three distinct types of rabbit protein kinase C.
A;Reference number: A26037; MUID:87115883; PMID:3808073
A;Accession: C26037
A;Molecule type: mRNA
A;Residues: 1-672 <CHN>
A;Cross-references: EMBL:X04796; NID:G1672; PIDN:CAA28483.1; PID:G1673
C;Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters, C;Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may C;Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C;Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C;Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding
F;19-29/Region: phospholipid binding #status experimental
F;22-27/Region: pseudophosphorylation motif
F;37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
F;102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
F;152-264/Domain: protein kinase C C2 region homology <K2>
F;337-597/Domain: protein kinase homology <KIN>
F;345-353/Region: protein kinase ATP-binding motif
F;37,67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;50,53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;102,132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;368/Active site: Lys #status predicted
F;631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 75.5% Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
|||:
Db 531 MLAGQPPFD 539

RESULT 32
K;BOC
protein kinase C (EC 2.7.1.1) alpha - bovine
C;Species: Bos primigenius taurus (cattle)

C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 11-Jun-1999
C;Accession: A00621
R;Parker, P.J.; Coussens, L.; Totty, N.; Rhee, L.; Young, S.; Chen, E.; Stabel, S.; W Science 233, 853-859, 1986
A;Title: The complete primary structure of protein kinase C - the major phorbol ester A;Reference number: A00621; MUID:86289425; PMID:3755547
A;Accession: A00621
A;Molecule type: mRNA
A;Residues: 1-672 <PAR>
A;Cross-references: GB:M13973; NID:G163529; PIDN:AAA30706.1; PID:G163530
A;Experimental source: brain
C;Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester C;Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane C;Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C;Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C;Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding
F;19-29/Region: phospholipid binding #status experimental
F;22-27/Region: pseudophosphorylation motif
F;37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
F;102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
F;152-264/Domain: protein kinase C C2 region homology <K2>
F;337-597/Domain: protein kinase homology <KIN>
F;345-353/Region: protein kinase ATP-binding motif
F;37,67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;50,53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;102,132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;368/Active site: Lys #status predicted
F;631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 75.5% Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
|||:
Db 531 MLAGQPPFD 539

RESULT 33
A37237
protein kinase C (EC 2.7.1.1) I - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 28-Feb-1997
C;Accession: A37237
R;Chen, K.; Peng, Z.; Lavi, S.; Kung, H.
Second Messengers Phosphoproteins 12, 251-260, 1989
A;Title: Molecular cloning and sequence analysis of two distinct types of Xenopus lae A;Reference number: A37237; MUID:90572230; PMID:3272298
A;Accession: A37237
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A;Molecule type: mRNA
A;Residues: 1-676 <CHE>
C;Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C;Keywords: ATP; phosphotransferase
F;42-91/Domain: protein kinase C zinc-binding repeat homology <K21>
F;107-156/Domain: protein kinase C zinc-binding repeat homology <K22>
F;157-267/Domain: protein kinase C C2 region homology <K2>
F;341-601/Domain: protein kinase homology <KIN>
F;349-357/Region: protein kinase ATP-binding motif

Query Match 75.5% Score 37; DB 2; Length 676;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
|||:
Db 535 MLAGQPPFD 543

RESULT 34
KIBOGC

protein kinase C (EC 2.7.1.1-) gamma - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C/Accession: C24664
R/Coussens, L.; Parker, P.J.; Rhee, L.; Yang-Feng, T.L.; Chen, E.; Waterfield, M.D.; Fra
Science 213, 859-866, 1986
A/Title: Multiple, distinct forms of bovine and human protein kinase C suggest diversity
A/Reference number: A94291; MUID:86289426; PMID:3755549
A/Accession: C24664
A/Molecule type: mRNA
A/Residues: 1-682 <OHN>
A/Cross-references: GB:M13976; NID:g163525; PIDN:AAA30704.1; PID:g163526
C/Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-sp
f inositol phospholipids. This protein is a receptor for tumor promoting phorbol esters,
C/Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
C/Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C/Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kin
C/Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bindin
F/3-11/Region: phospholipid binding #status predicted
F/6-11/Region: pseudophosphorylation motif
F/21-70/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F/86-135/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F/136-249/Domain: protein kinase C C2 region homology <KC2>
F/334-599/Domain: protein kinase C C2 region homology <KIN>
F/342-353/Region: protein kinase ATP-binding motif
F/2-51-54,70/Binding site: zinc (His, Cys, Cys) #status predicted
F/34,37,59,62/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F/86,116,119,135/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F/99,102,124,127/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F/365/Active site: Lys #status predicted
F/633,640/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match 75.5%; Score 37; DB 1; Length 682;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB 533 MLAGQPPFC 541

RESULT 35
KIRTCG
Protein kinase C (EC 2.7.1.1-) gamma rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C/Accession: A35105; S02129; I55317
R/Knopf, J.L.; Lee, M.H.; Salzman, L.A.; Kikkawa, K.; Hewick, R.W.; Bell,
Cell 46, 491-502, 1986
A/Title: Cloning and expression of multiple protein kinase C cDNAs.
A/Reference number: A90883; MUID:86272097; PMID:3759377
A/Accession: A35105
A/Molecule type: mRNA
A/Residues: 1-697 <KNC>
A/Cross-references: GB:M13707; NID:g206186; PIDN:AAA41874.1; PID:g206187
A/Note: the authors translated the codon JGU for residue 432 as Glu
R/Ono, Y.; Fujii, T.; Igarashi, K.; Kikkawa, K.; Ogita, K.; Nishizuka, Y.
Nucleic Acids Res. 16, 5199-5200, 1988
A/Title: Nucleotide sequences of cDNAs for alpha and gamma subtypes of rat brain prote
A/Reference number: S02129; MUID:89262515; PMID:3397229
A/Accession: S02129
A/Molecule type: mRNA
A/Residues: 1-697 <ONC>
A/Cross references: EMBL:X07287; NID:g56917; PIDN:CAA30267.1; PID:g56918
R/Chen, K.
J. Biol. Chem. 265, 19961-19965, 1990
A/Title: Characterization of the 5'-flanking region of the rat protein kinase C gamma ge
A/Reference number: I55317; MUID:91060619; PMID:2246211
A/Accession: I55317
A/Status: translated from GB/EMBL/DDBC
A/Molecule type: DNA
A/Residues: 1-56 <RES>
A/Cross references: GB:M55417; NID:g206184; PIDN:AAA41873.1; PID:g554487

C/Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonin
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol est
C/Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
C/Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C/Genetics:
A/Gene: PRKC-gamma
C/Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein
C/Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bi
F/18-28/Region: phospholipid binding #status predicted
F/21-26/Region: pseudophosphorylation motif
F/36-85/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F/101-150/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F/151-264/Domain: protein kinase C C2 region homology <KC2>
F/349-614/Domain: protein kinase homology <KIN>
F/357-365/Region: protein kinase ATP-binding motif
F/36,66,69,85/Binding site: zinc (His, Cys, Cys) #status predicted
F/49,52,74,77/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F/101,131,134,150/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F/114,117,139,142/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F/380/Active site: Lys #status predicted
F/648,655/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status

Query Match 75.5%; Score 37; DB 1; Length 697;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB 548 MLAGQPPFD 556

RESULT 36
KIRBGC
Protein kinase C (EC 2.7.1.1-) gamma - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C/Accession: A28708
R/Ohno, S.; Kawasaki, H.; Konno, Y.; Inagaki, M.; Hidaka, H.; Suzuki, K.
Biochemistry 27, 2083-2087, 1988
A/Title: A fourth type of rabbit protein kinase C.
A/Reference number: A28708; MUID:88241036; PMID:2837282
A/Accession: A28708
A/Molecule type: mRNA
A/Residues: 1-697 <OHN>
A/Cross-references: GB:M19338; NID:g165651; PIDN:AAA31449.1; PID:g165652
C/Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonin
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol est
C/Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
C/Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C/Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein
C/Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bi
F/18-28/Region: phospholipid binding #status predicted
F/21-26/Region: pseudophosphorylation motif
F/36-85/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F/101-150/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F/151-264/Domain: protein kinase C C2 region homology <KC2>
F/349-614/Domain: protein kinase homology <KIN>
F/357-365/Region: protein kinase ATP-binding motif
F/36,66,69,85/Binding site: zinc (His, Cys, Cys) #status predicted
F/49,52,74,77/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F/101,131,134,150/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F/114,117,139,142/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F/380/Active site: Lys #status predicted
F/648,655/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status

Query Match 75.5%; Score 37; DB 1; Length 697;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB 548 MLAGQPPFD 556

XX SQ Sequence 329 AA;
Query Match 87.8%; Score 43; DB 21; Length 129;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPPE 9
DB 260 LLVGKPPPE 268
RESULT 20
ABF73734
ID ABP73734 standard; Protein; 528 AA.
XX AC ABP73734;
XX DT 30-JAN-2003 (first entry)
XX DE Candida albicans essential protein SEQ ID NO 7571.
XX KW Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal.
XX OS Candida albicans.
XX PN WC200253728-A2.
XX PD 11-JUL-2002.
XX PF 26-DEC-2001; 2001WO-US49486.
XX PR 29-DEC-2000; 2000US-259128P.
XX PR 20-FEB-2001; 2001US-C792024.
XX PR 22-AUG-2001; 2001US-314050P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX WP1; 2002-566694/60.
XX DR N-PSDB; ABZ32284.
XX CC Constructing strains for identifying gene products as effective targets
PR for therapeutic intervention, by inactivating in the strain one allele
PR of a gene and placing other allele of the gene under conditional
PR expression.
XX Claim 44; SEQ ID NO 7571; 167pp * Sequence listing; English.
XX The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of an

CC essential Candida albicans protein used in the method of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.
XX SQ Sequence 528 AA;
Query Match 87.8%; Score 43; DB 23; Length 528;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPPE 9
DB 454 LLVGKPPPE 462
RESULT 21
AAU74656
ID AAU74656 standard; Protein; 531 AA.
XX AC AAU74656;
XX DT 09-APR-2002 (first entry)
XX DE Mammalian polo-like kinase (Plk).
XX KW Polo-like kinase; PLK; polo-box; cytostatic; neoplasm;
KW hyperproliferative disorder; cytokinesis; solid tumour;
KW carcinoma; sarcoma; cancer; small cell carcinoma; adenocarcinoma;
KW Mullerian tumour; squamous cell carcinoma; protein.
XX OS Mammalia.
XX FH Key Location/Qualifiers
FT Misc-difference 130 /label= Unknown;
FT Misc-difference 131 /label= Unknown
FT Misc-difference 132 /label= Unknown
FT Misc-difference 133 /label= Unknown
FT Misc-difference 134 /label= Unknown
FT Misc-difference 135 /label= Unknown
FT Misc-difference 136 /label= Unknown
FT Misc-difference 137 /label= Unknown
FT Misc-difference 138 /label= Unknown
FT Misc-difference 139 /label= Unknown
FT Misc-difference 140 /label= Unknown
FT Misc-difference 141 /label= Unknown
FT Misc-difference 147 /label= Unknown
FT Misc-difference 148 /label= Unknown
FT Misc-difference 149 /label= Unknown
FT Misc-difference 150 /label= Unknown
FT Misc-difference 151 /label= Unknown
FT Misc-difference 152 /label= Unknown
FT Misc-difference 153 /label= Unknown
FT Misc-difference 154

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FT FT Misc difference 355 /label= Unknown
FT FT /label= Unknown
FT FT Misc-difference 356 /label= Unknown
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FT FT /label= Unknown
FT FT Misc-difference 365 /label= Unknown
FT FT /label= Unknown
FT FT Region 410..439
FT FT /label= Polo-box
FT FT /note= "Core polo box consensus sequence"
XX
XX
XX PN WC200190401 A2.
XX PD 29 NOV-2001.
XX
XX PF 23-MAY-2001; 2001WO-US16903.
XX PR 23-MAY 2000; 2000JS-206588P.
XX
XX (HARD : HARVARD COLLEGE.
PA (USSH : US DEPT HEALTH & HUMAN SERVICES.
PA (USSH : US NAT INST OF HEALTH.
XX
XX Lee KS, Song S, Erikson R;
XX WFT; 2000-106210/14.
XX
XX Identifying polo-like kinase modulators by contacting eukaryotic cells
XX expressing polo box peptides with test compounds and evaluating changes
XX in dominant negative cytokinesis-defective growth patterns .
XX
XX Example 2; Fig 5; 57pp; English.
XX
XX The invention describes a novel method of detecting compounds with
XX polo-like kinase (PLK) modulating activity. This comprises contacting
XX eukaryotic cells expressing polo-box or polo-box related peptides,
XX binding peptides comprising 25 contiguous residues from a polo-like
XX kinase C-terminal region, with a test compound. Ectopic expression of a
XX polo-box in a eukaryotic cell causes a severe cytokinetic defect in the
XX cell. These eukaryotic cells can also be tested with the test compound
XX used in the method of the invention. The polo-box related peptides and
XX polo-like kinase activity modulatory compounds can be used to inhibit or
XX enhance cellular proliferation and subsequently for treating
XX hyper-proliferative disorders including neoplasia, solid tumours,
XX carcinomas, sarcomas and cancers e.g. small cell carcinoma,
XX adenocarcinoma, Mullerian tumours and squamous cell carcinomas. This
XX is the amino acid sequence of a mammalian polo like kinase (plk),
XX uncontrolled expression of the plk family is implicated in the
XX development of human cancers, discussed in the method of the invention.
XX
XX Sequence 531 AA;
XX
XX Query Match: 87.8%; Score 43; DB 03; Length 531;
XX Best Local Similarity 77.8%; Pred. No. 11;
XX Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
XX : MLGKTFE 9

```



```

RESULT 23
AAU79306
ID AAU79306 standard; Peptide; 603 AA.
XX
AC AAU79306;
XX
DT 02 JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk);
XX
KW Polo box; PBL; cytostatic; fungicide; protozoacide; antihelmintic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk;
XX
OS Mus musculus.
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI, 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Column 59-64; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of the polo like kinase (Plk), a
CC protein from which mitotic protein polo kinase inhibitory peptides are
CC derived.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
|||
Db 244 LLVGKPPFE 252
|||

RESULT 24
AAU79308
ID AAU79308 standard; Peptide; 603 AA.
XX
AC AAU79308;
XX
DT 02 JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T210E mutant.
XX
```

```

DE Mouse polo-like kinase (Plk) T210D mutant.
XX
KW Polo box; PBL; cytostatic; fungicide; protozoacide; antihelmintic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Thr substituted by Asp"
FT
XX US6358738-B1.
XX
PN 19-MAR-2002.
XX
PD 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI, 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
|||
Db 244 LLVGKPPFE 252
|||

RESULT 25
AAU79309
ID AAU79309 standard; Peptide; 603 AA.
XX
AC AAU79309;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T210E mutant.
XX
```


KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
XX
OS Mus musculus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Thr substituted by Glu"
FT
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections .
XX
PS Example 1; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79310 using information
CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
Db 244 LLVGKPPFE 252
RESULT 26
AAU79310
ID AAU79310 standard; Peptide; 603 AA.
XX
AC AAU79310;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T210V mutant.
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
XX
OS Mus musculus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Thr substituted by Glu"
FT
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections .
XX
PS Example 1; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79310 using information
CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
Db 244 LLVGKPPFE 252
RESULT 26
AAU79310
ID AAU79310 standard; Peptide; 603 AA.
XX
AC AAU79310;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T210V mutant.
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
XX
OS Mus musculus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Thr substituted by Val"
FT
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections .
XX
PS Example 1; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
OS Mus musculus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Thr substituted by Val"
FT
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections .
XX
PS Example 1; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
Db 244 LLVGKPPFE 252
RESULT 27
AAU79311
ID AAU79311 standard; Peptide; 603 AA.
XX
AC AAU79311;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) E206V mutant.
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;

KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Glu substituted by Val"
FT XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Page 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY : MLLGKPPFE 9
: |||||
Db 244 LLVGKPPFE 252
RESULT 28
AAU79312
ID AAU79312 standard; Peptide; 603 AA.
XX
AC AAU79312;
XX
DT 02-JUL-2002 (first entry);
XX
DE Mouse polo-like kinase (Plk) E206N mutant.
XX
KW Polo box; PB1; cytosolic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.

KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Glu substituted by Asn"
FT XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Page 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY : MLLGKPPFE 9
: |||||
Db 244 LLVGKPPFE 252
RESULT 29
AAU79313
ID AAU79313 standard; Peptide; 603 AA.
XX
AC AAU79313;
XX
DT 02-JUL-2002 (first entry);
XX
DE Mouse polo-like kinase (Plk) E206V/T210V mutant.
XX
KW Polo box; PB1; cytosolic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.

XX Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Glu substituted by Val"
FI Misc-difference 210 /note= "Wild type Thr substituted by Val"
FT
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Page -; 47pp; English.

CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
: : : : :
DB 244 LLVGKPPFE 252

RESULT 20
AAU79314
ID AAU79314 standard; Peptide; 603 AA.
XX
AC AAU79314;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) D194N mutant.

XX Polo box; PBl; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelia; cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.

XX Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 194 /note= "Wild type Asp substituted by Asn"
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Page -; 47pp; English.

CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
: : : : :
DB 244 LLVGKPPFE 252

RESULT 31
AAU79315
ID AAU79315 standard; Peptide; 603 AA.
XX
AC AAU79315;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) D194R mutant.

XX Polo box; PBl; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.

```
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc difference 194
FT /note= "Wild type Asp substituted by Arg"
FT
XX
PN US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections -
XX
XX Example 1; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Sequence 603 AA;
SQ
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 3; Gaps 0;
QY 1 MLLGKPPFE 9
Db 244 LLVGKPPFE 252
RESULT 32
AAU79316
ID AAU79316 standard; Peptide; 603 AA.
XX
XX AAU79316;
XX
XX 02 JUL-2002 (first entry)
XX
XX Mouse polo-like kinase (Plk) K28M mutant.
XX
XX Polo box; Pbl; cytostatic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Plk; mutant; mutetr.
XX
XX Mus musculus.
XX Synthetic.
XX
```

```
FH Key Location/Qualifiers
FT Misc-difference 28
FT /note= "Wild type Lys substituted by Met"
XX
XX US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections -
XX
XX Example 2; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Sequence 603 AA;
SQ
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
Db 244 LLVGKPPFE 252
RESULT 33
AAU79317
ID AAU79317 standard; Peptide; 603 AA.
XX
XX AAU79317;
XX
XX 02-JUL-2002 (first entry)
XX
XX Mouse polo-like kinase (Plk) V415A mutant.
XX
XX Polo box; Pbl; cytostatic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Plk; mutant; mutetr.
XX
XX Mus musculus.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 415
XX
```

/note= "Wild type Val substituted by Ala"

PT US6358738-B1.
XX 19-MAR-2002.
XX 13-MAY-1999; 99US-0311311.
XX 13-MAY-1998; 98US-085296P.
XX (HARD) HARVARD COLLEGE.
XX Erikson RL, Lee KS;
XX WPI; 2002-314756/35.
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections -
XX Example 7; Page -: 47pp; English.
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk);
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX Sequence 603 AA;
SQ
Query Match: 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
Db 244 LLVGKPPFE 252
RESULT 34
AAU79318
ID AAU79318 standard; Peptide; 603 AA.
XX
AC AAU79315;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo like kinase (Plk); L427A mutant.
XX
KW Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 427 /note= "Wild type Lys substituted by Ala"
XX

PN US6358738-B1.
XX 19-MAR-2002.
XX 13-MAY-1999; 99US-0311311.
XX 13-MAY-1998; 98US-085296P.
XX (HARD) HARVARD COLLEGE.
XX Erikson RL, Lee KS;
XX WPI; 2002-314756/35.
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections -
XX Example 7; Page -: 47pp; English.
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk);
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX Sequence 603 AA;
SQ
Query Match: 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
Db 244 LLVGKPPFE 252
RESULT 35
AAU79319
ID AAU79319 standard; Peptide; 603 AA.
XX
AC AAU79319;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk); N437I mutant.
XX
KW Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 437 /note= "Wild type Asn substituted by Ile"
XX
PN US6358738-B1.
XX

PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WP1; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections .
XX
PS Example 7; Page 7; 47pp; English.
XX

CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match: 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
Db 244 LLVGKPPFE 252

RESULT 36
AAU79320
IF AAU79320 standard; Peptide; 603 AA.

XX
AC AAU79320;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) W414F/T210D mutant.

XX Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.

XX Mus musculus.
OS Synthetic.
XX

FH Key Location/Qualifiers

FT Misc-difference 4:4 /note= "Wild type Trp substituted by Phe"

FT Misc difference 2:0

FT /note= "Wild type Thr substituted by Asp"

XX US6358738-B1.

XX

PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WP1; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections .
XX
PS Example 10; Page 7; 47pp; English.
XX

CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match: 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
Db 244 LLVGKPPFE 252

RESULT 37
ABR48196
ID ABR48196 standard; Protein; 603 AA.

XX
AC ABR48196;

XX
DT 12-JUN-2003 (first entry)

XX Human bladder cancer associated protein sequence SEQ ID NO:110.

XX Human; bladder cancer; cytostatic; gene therapy; vaccine.

XX Homo sapiens.

XX WO2003003906-A2.

XX 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US21338.

XX 03-JUL-2001; 2001US-302814P.

XX 03-AUG-2001; 2001US-310099P.

XX 08-NOV-2001; 2001US-343705P.

XX 13-NOV-2001; 2001US-350666P.

XX 12-APR-2002; 2002US-372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Mack DH, Aziz N;

XX

DR WPI: 2003-201532/19.
DR N-PSDB; ACC51009.
XX
PT Detecting a bladder cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with
PT a bladder cancer-associated polynucleotide or antibody
XX
XX
ES Claim 10; Page 269; 307pp; English.
XX
CC The present invention describes a method for detecting a bladder cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with a polynucleotide
CC that selectively hybridises to a sequence that is 80 % identical to a
CC table of sequences (see ACC5095; to ACC51059). ACC5095; to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
CC ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications.
XX
SQ Sequence 603 AA;

Query Match 87.8%; Score 43; DB 24; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLIGKPPFE 9
DB 244 LVGKPPFE 252

RESULT 38
AAW18084
ID AAW18084 standard; Protein; 403 AA.
XX
AC AAW18084;
XX
DT 07-SEP-1997 (first entry)
XX
DE Human Aurora-2.
KW Aurora-2; AUR-2, signal transduction; protein kinase; tumour;
KW cancer; protein kinase; gene therapy; diagnosis; antibody.
XX
CS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..130
FT /label= N-terminal_domain
FT Domain 131..403
FT /label= Kinase_domain
FT Misc-difference 50
FT /note= "deduced residue from some cDNA clones is
FT Leu"
FT
FT Misc-difference 57
FT /note= "deduced residue from some cDNA clones is
FT Ile"
FT
FT Modified-site 288
FT /label= Phosphorylation
FT /note= "cAMP-dependent protein kinase
FT phosphorylation site conserved in AUR-2
FT and yeast and Drosophila homologues"
FT
FT Modified-site 334
FT /label= Phosphorylation
FT /note= "tyrosine phosphorylation consensus site
FT conserved in Drosophila aurora but not
FT in AUR-; c: yeast IPLI"
FT
FT Modified-site 342

FT /label= Phosphorylation
FT /note= "cAMP-dependent protein kinase
FT phosphorylation site conserved in AUR-2
FT and yeast and Drosophila homologues"
FT
FT Misc-difference 50
FT /note= "deduced residue from some cDNA clones is
FT Leu"
FT
FT Misc-difference 57
FT /note= "deduced residue from some cDNA clones is
FT Ile"
FT
XX WO9722702-A1.
PN
XX 26-JUN-1997.
PD
XX 25-NOV-1996; 96WO-US:8859.
XX
XX 14-AUG-1996; 96US-0023943.
PR
XX 18-DEC-1995; 95US-0008809.
XX
XX (SUGEN) SUGEN INC.
XX
XX Mossie KG, Plowman GD;
PI
XX WPI; 1997-341693/31.
DR
DR N-PSDB; AAT67290.
XX
PT Aurora-1 and Aurora-2 and related genes - useful in tumour gene
PT therapy
XX
PS Claim 3; Page 83-85; 98pp; English.
XX
CC Novel human proteins, termed Aurora-1 (AAW18083) and Aurora-2
CC (AAW18084) (AUR-1 and AUR-2), are related serine/threonine kinases
CC with short N-terminal extensions that appear to be involved in
CC cancer and/or signal transduction disorders. Their amino acid
CC sequences were deduced from pancreatic tumour cDNA clones (AAT67289-
CC 90). AUR-1 and AUR-2 appear to regulate nuclear division, with
CC disruption of their signaling resulting in polyploid cells. AUR-2
CC RNA is low or absent in most normal tissues, and abundant in a
CC subset of tumour-derived cell lines, partic. those of colorectal
CC origin. AUR polypeptides can be expressed in host cells and used
CC to raise diagnostic antibodies and to screen for compounds that
CC interact with AUR-1 and/or AUR-2.
XX
SQ Sequence 403 AA;

Query Match 83.7%; Score 41; DB 18; Length 403;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPFE 9
DB 323 LVGKPPFE 330

RESULT 39
AAW22476
ID AAY22476 standard; Protein; 403 AA.
XX
XX AAY22476;
XX
XX
DT 29-SEP-1999 (first entry)
XX
DE Human AUR2 protein sequence.
XX
KW AUR1; AUR2; human; AUR modulator; cancer; glioma; medullablastoma;
KW chondrosarcoma; pancreatic tumour; proliferative disease; diagnosis;
KW therapy.
XX
XX Homo sapiens.
OS
XX WO9937788-A2.
PN

XX 29-JUL-1999.
PD
XX
FF 21 JAN-1999; 99WO-US01283.
XX
XX 22-JAN-1998; 98US-0012135.
PR
XX (SUGEN-) SUGEN INC.
PA
XX
PI Mossie K, Plowman GD;
XX
XX WPI: 1999-458699/38.
DR N-PSDB; AAX99725.
DR
XX New nucleic acid encoding human AUR1 and 2 polypeptides, used to
PT identify specific modulators for treating cancer or for diagnosis
PT
XX Claim 1; Page 141-142; 153pp; English.
PS
XX This sequence is the human AUR2 protein of the invention. The AUR1
CC and AUR2 proteins can be used to identify specific modulators of, and to
CC generate specific antibodies recognising AUR1 and AUR2. The modulators
CC can be used for treating conditions involving abnormal AUR signal
CC transduction, specifically cancer (of colon, breast, kidney, ovary,
CC bladder, head or neck, also glioma, medulloblastoma, chondrosarcoma and
CC pancreatic tumours, particularly of colon (specifically), breast or
CC kidney). The modulators can also be used for studying their effects in
CC animal models of proliferative disease. Probes, based on the coding
CC sequences are used, diagnostically, to detect or quantify AUR mRNA, by
CC hybridisation or polymerase chain reaction (PCR). The DNA, optionally
CC mutated, are useful in gene therapy. Ab are used as diagnostic
CC immunoassay reagents for detecting the proteins.
XX
SQ Sequence 403 AA;

Query Match 83.7%; Score 41; DB 20; Length 403;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLGKPPFE 9
Db 323 LVGKPPFE 330

RESULT 40
AAG67435
ID AAG67435 standard; Protein: 403 AA.
XX
AC AAG67435;
XX
DT 26-NOV 2001 (first entry)
XX
DE Amino acid sequence of a human polypeptide.
XX
KW Human; protein kinase; protein phosphatase; signal transduction;
KW intracellular signalling pathway.
XX
OS Homo sapiens.
XX
FN WC200109345 A1.
XX
PD 08-FEB-2001.
XX
PF 28 JUL-2000; 2000WO-JP05060.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 18-OCT-1999; 99US-0159590.
PR 11-JAN-2000; 2000JP-0118776.
PR 17-FEB-2000; 2000US-0183322.
PR 02 MAY-2000; 2000JP-0183767.
XX
XX (HELI-) HELIX RES INST.
XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
PI Senoo C, Nezu J;
XX
DR WPI: 2001-564736/63.
XX
XX New genes encoding protein kinase and protein phosphatase, useful for
PT identifying modulators which can be used to treat human or animal
PT disorders associated with the expression or function of these enzymes -
XX
XX Example 4; Page 196-199; 336pp; Japanese.
XX
CC The specification describes human protein kinase/protein phosphatases.
CC The polypeptides are expected to participate in signal transduction
CC in cells. The kinase phosphatases are connected with intracellular
CC signalling pathways. Antisense oligonucleotides and compounds
CC identified by screening (agonists or antagonists) can be used to
CC treat human or animal disorders associated with the expression
CC or function of the protein. In addition, the polypeptides may be used
CC as target molecules for drug development. The present sequence
CC represents a polypeptide, used in the course of the invention.
XX
SQ Sequence 403 AA;

Query Match 83.7%; Score 41; DB 22; Length 403;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLGKPPFE 9
Db 323 LVGKPPFE 330

Search completed: November 14, 2003, 13:25:21
Job time : 35.7143 secs

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OM protein - protein search, using sw model

Run on: November 14, 2003, 13:23:00 ; Search time 11.8286 Seconds
(without alignments)
32.193 Million cell updates/sec

Title: US-09-736-076-17
Perfect score: 49
Sequence: : MLLGKPPFE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/1aa/PC-US_COMB.pep:
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	3 US-08-861-338-17	Sequence 17, Appl
2	46	93.9	9	3 US-08-861-338-15	Sequence 15, Appl
3	46	93.9	11	3 US-08-861-338-13	Sequence 13, Appl
4	46	93.9	272	1 US-08-252-995D-12	Sequence 12, Appl
5	46	93.9	272	2 US-08-834-108-12	Sequence 12, Appl
6	46	93.9	685	2 US-08-878-989-1	Sequence 1, Appl
7	46	93.9	685	3 US-09-136-282-2	Sequence 2, Appl
8	46	93.9	685	3 US-09-272-796-1	Sequence 1, Appl
9	46	93.9	685	3 US-09-505-744-2	Sequence 2, Appl
10	44	89.8	8	3 US-08-861-338-16	Sequence 16, Appl
11	43	87.8	20	3 US-08-861-338-6	Sequence 6, Appl
12	43	87.8	272	1 US-08-252-995D-14	Sequence 14, Appl
13	43	87.8	272	2 US-08-834-108-14	Sequence 14, Appl
14	43	87.8	603	3 US-09-198-122-2	Sequence 2, Appl
15	43	87.8	603	4 US-09-311-311C-26	Sequence 26, Appl
16	41	83.7	275	1 US-08-252-995D-13	Sequence 13, Appl
17	41	83.7	275	2 US-08-834-108-13	Sequence 13, Appl
18	41	83.7	403	2 US-08-755-728-4	Sequence 4, Appl
19	41	83.7	403	2 US-08-974-655-4	Sequence 4, Appl
20	41	83.7	403	3 US-09-283-011-4	Sequence 4, Appl
21	39	79.6	264	2 US-07-857-224B-17	Sequence 17, Appl
22	39	79.6	271	1 US-08-252-995D-11	Sequence 11, Appl
23	39	79.6	271	2 US-08-834-108-11	Sequence 11, Appl
24	38	77.6	273	1 US-08-252-995D-10	Sequence 10, Appl
25	38	77.6	273	2 US-08-834-108-10	Sequence 10, Appl
26	38	77.6	344	2 US-08-755-728-3	Sequence 3, Appl
27	38	77.6	344	2 US-08-974-655-3	Sequence 3, Appl

28	38	77.6	344	3 US-09-283-011-3	Sequence 3, Appl
29	38	77.6	347	2 US-09-016-000-1	Sequence 1, Appl
30	38	77.6	416	1 US-08-252-995D-2	Sequence 2, Appl
31	38	77.6	416	2 US-09-834-108-2	Sequence 2, Appl
32	38	77.6	464	1 US-08-252-995D-6	Sequence 6, Appl
33	38	77.6	464	2 US-09-834-108-6	Sequence 6, Appl
34	38	77.6	737	4 US-09-772-647-4	Sequence 4, Appl
35	38	77.6	925	1 US-08-252-995D-4	Sequence 4, Appl
36	38	77.6	925	2 US-08-834-108-4	Sequence 4, Appl
37	38	77.6	1037	4 US-09-428-71A-21	Sequence 21, Appl
38	37	75.5	9	3 US-08-861-338-18	Sequence 18, Appl
39	37	75.5	20	3 US-08-861-338-3	Sequence 3, Appl
40	37	75.5	264	2 US-07-857-224B-10	Sequence 10, Appl
41	37	75.5	264	2 US-07-857-224B-15	Sequence 15, Appl
42	37	75.5	269	2 US-07-857-224B-14	Sequence 14, Appl
43	37	75.5	269	2 US-07-857-224B-16	Sequence 16, Appl
44	37	75.5	499	4 US-09-509-902A-12	Sequence 12, Appl
45	37	75.5	588	4 US-09-509-902A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-861-338-17
; Sequence 17, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: ~~Ben-Sasson, Shmuel-A.~~
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861.338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; OTHER INFORMATION: Glutamine Acid-NH2"
US-08-861-338-17

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Query Match 100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
DB 1 MLLGKPPFE 9

RESULT 2
US-08-861-338-15
; Sequence 15, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; OTHER INFORMATION: Glutamic Acid-NH2"
US-08-861-338-15

Query Match 93.9%; Score 46; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.5e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
DB 1 MLLGKPPFE 9

RESULT 3
US-08-861-338-19
; Sequence 19, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
```

```
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Serine-NH2"
US-08-861-338-19

Query Match 93.9%; Score 46; DB 3; Length 11;
Best Local Similarity 88.9%; Pred. No. 0.013;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
DB 1 MLLGKPPFE 9

RESULT 4
US-08-252-995D-12
; Sequence 12, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
```



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; ZIP: MSH 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-08-252-995D-12
```

```
Query Match 93.9% Score 46; DB 1; Length 272;
Best Local Similarity 88.9% Pred. No. 0.35;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MLJGKPPPE 9
   |||:||||
Db 199 MLJGRPPE 207
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```
RESULT 3
US-08-834-108-12
; Sequence 12, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; City: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: MSH 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
```

```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-08-834-108-12
```

```
Query Match 93.9% Score 46; DB 2; Length 272;
Best Local Similarity 88.9% Pred. No. 0.35;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MLJGKPPPE 9
   |||:||||
Db 199 MLJGRPPE 207
```

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RESULT 6
US-08-878-989-1
; Sequence 1, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVEBOB01
; CLONE: 39043
; US-08-878-989-1
```

```
Query Match 93.9% Score 46; DB 2; Length 685;
Best Local Similarity 88.9% Pred. No. 0.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLLGKPPFE 9
 |||:||||
 Db 273 MLLGRPPFE 281

RESULT 7

US-09-136-282 2
 ; Sequence 2, Application US/09136282
 ; Patent No. 6063609
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDERSON, KAREN
 ; APPLICANT: JACKSON, JEFFREY
 ; APPLICANT: HANSBURY, MICHAEL
 ; APPLICANT: NERURKAR, SANDHYA
 ; APPLICANT: ROSHAK, AMY
 ; APPLICANT: BOUZYK, MARK
 ; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ratner & Prestia
 ; STREET: P.O. Box 980
 ; CITY: Valley Forge
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/136,282
 ; FILING DATE: 20-AUG-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/056,112
 ; FILING DATE: 20-AUG-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Prestia, Paul F
 ; REGISTRATION NUMBER: 23,031
 ; REFERENCE/DOCKET NUMBER: GH-70211
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0700
 ; TELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 685 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-136-282-2

Query Match 93.9% Score 46; DB 3; Length 685;
 Best Local Similarity 88.9% Pred. No. 0.9;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 |||:||||
 Db 273 MLLGRPPFE 281

RESULT 8

US-09-272-796-1
 ; Sequence 1, Application US/09272796
 ; Patent No. 6207148
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl G.

APPLICANT: Lal, Preeti
 APPLICANT: Goli, Surya K.
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 TITLE OF INVENTION: KINASES
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/272,796
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/878,989
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0321 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 685 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: HUVEBO01
 CLONE: 39043
 US-09-272-796-1

Query Match 93.9% Score 46; DB 3; Length 685;
 Best Local Similarity 88.9% Pred. No. 0.9;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 |||:||||
 Db 273 MLLGRPPFE 281

RESULT 9

US-09-505-744-2
 ; Sequence 2, Application US/09505744
 ; Patent No. 6245544
 ; GENERAL INFORMATION:
 ; APPLICANT: Karen M. Anderson
 ; APPLICANT: Mark M. Bouzyk
 ; APPLICANT: Michael J. Hansbury
 ; APPLICANT: Jeffrey R. Jackson
 ; APPLICANT: Sandhya S. Nerurkar
 ; APPLICANT: Amy K. Roshak
 ; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
 ; FILE REFERENCE: GH-70231-D1
 ; CURRENT APPLICATION NUMBER: US/09/505,744
 ; CURRENT FILING DATE: 2000-02-16
 ; EARLIER APPLICATION NUMBER: 09/136,282
 ; EARLIER FILING DATE: 1998-08-20
 ; EARLIER APPLICATION NUMBER: 60/056,112
 ; EARLIER FILING DATE: 1997-08-20
 ; NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2
LENGTH: 685
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-505-744-2

Query Match 93.9%; Score 46; DB 3; Length 685;
Best Local Similarity 88.9%; Pred. No. 0.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
DB 273 MLLGKPPFE 281

RESULT 10

US-08-861-338-16
Sequence 16, Application US/08861338
Patent No. 6174993

GENERAL INFORMATION:

APPLICANT: Ben-Sasson, Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,338
FILING DATE: 21-MAY-1997

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC-590

TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids

TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide

FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "N-Acetyl Methionine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /note= "Phenylalanine-NH2"

US-08-861-338-16

Query Match 89.8%; Score 44; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 8
DB 1 MLLGKPPFE 8

RESULT 11

US-08-861-338-6
Sequence 6, Application US/08861338
Patent No. 6174993

GENERAL INFORMATION:

APPLICANT: Ben-Sasson, Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,338
FILING DATE: 21-MAY-1997

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC-590

TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide

US-08-861-338-6

Query Match 87.8%; Score 43; DB 3; Length 20;
Best Local Similarity 77.8%; Pred. No. 0.087;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
DB 3 LLVGKPPFE 11

RESULT 12

US-08-252-995D-14
Sequence 14, Application US/08252995D
Patent No. 5650501

GENERAL INFORMATION:

APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto

STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

US-08-834-108-14
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdzyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-252-995D-14

Query Match 87.8% Score 43; DB 1; Length 272;
Best Local Similarity 77.8% Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
Db 199 LLVGKPPFE 207

RESULT 13
US-08-834-108-14
Sequence 14, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: HRESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdzyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-2.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus

US-08-834-108-14
Query Match 87.8% Score 43; DB 2; Length 272;
Best Local Similarity 77.8% Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
Db 199 LLVGKPPFE 207
RESULT 14
US-09-198-122-2
Sequence 2, Application US/09198122
Patent No. 6180380
GENERAL INFORMATION:
APPLICANT: Streibhardt, Klaus; Rubsamen-Waigmann, Helga;
APPLICANT: Holtrich, Uwe
TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE-
TITLE OF INVENTION: THREONINE-KINASE FAMILY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HORN KRAMER & WOODS
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
MEDIUM TYPE: storage
COMPUTER: NEC Powermate SX-20
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,122
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/601,014
FILING DATE: 23-FEB-1996
APPLICATION NUMBER: PCT/EP94/02863
FILING DATE: 30-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4329177
FILING DATE: 30-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9516-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-09-198-122-2

Query Match 87.8% Score 43; DB 3; Length 603;
Best Local Similarity 77.8% Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
Db 244 LLVGKPPFE 252

RESULT 15
US-09-311-311C-24

```

; Sequence 26, Application US/09311111C
; Patent No. 6358738
; GENERAL INFORMATION:
; APPLICANT: Erikson, et al.
; TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS.
; TITLE OF INVENTION: METHODS, AND USES THEREFOR
; FILE REFERENCE: 1874/117
; CURRENT APPLICATION NUMBER: US/09/311,111C
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/385,296
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(603)
; OTHER INFORMATION: Plk protein
US-09-311-311C-26

```

```

Query Match      87.8%; Score 43; DB 4; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPFE 9
       1:|||||
Db      244 LLLGKPPFE 252

```

```

RESULT 16
US-08-252-995D-13
; Sequence 13, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:

```

```

; ORGANISM: Saccharomyces cerevisiae
US-08-252-995D-13
Query Match      83.7%; Score 41; DB 1; Length 275;
Best Local Similarity 66.7%; Pred. No. 3.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY      1 MLLGKPPFE 9
       1:|||||
Db      200 LLLGKPPFE 208

```

```

RESULT 17
US-08-834-108-13
; Sequence 13, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
US-08-834-108-13

```

```

Query Match      83.7%; Score 41; DB 2; Length 275;
Best Local Similarity 66.7%; Pred. No. 3.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPFE 9
       1:|||||
Db      200 LLLGKPPFE 208

```

```

RESULT 18
US-08-755-728-4
; Sequence 4, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1

```



```

; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,728
; FILING DATE: No. 5962312ember 25, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-755-728-4

```

```

Query Match 83.7% Score 41; DB 2; Length 403;
Best Local Similarity 87.5%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 2 LKGPPE 9
|:|:|:|
Db 323 LVGKPPPE 330

```

```

RESULT 14
US-08-974 655-4
; Sequence 4, Application US/08974655
; Parent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

```

```

; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 5972676ember 25, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-974-655-4

```

```

Query Match 83.7% Score 41; DB 2; Length 403;
Best Local Similarity 87.5%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 LKGPPE 9
|:|:|:|
Db 323 LVGKPPPE 330

```

```

RESULT 20
US-09-283-011-4
; Sequence 4, Application US/09283011
; Patent No. 6207401
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/283,011
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/012,135

```

```

; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: NO. 6207401ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-09-283-011-4

```

```

Query Match 83.7%; Score 41; DB 3; Length 403;
Best Local Similarity 87.5%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 LLLGKPPFE 9
Db 323 LVGQPPFE 330

```

```

RESULT 21
US 07 857-224B-17
; Sequence 17, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting folded structures of proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) 8000 8002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster

```

```

; FEATURE: Protein kinase; Table 8 Column 18
; PUBLICATION INFORMATION:
; AUTHORS:
; AUTHORS: Hanks, S. K.
; AUTHORS: Quinn, A. M.
; AUTHORS: Hunter, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
; US-07-857-224B-17

```

```

Query Match 79.6%; Score 39; DB 2; Length 264;
Best Local Similarity 66.7%; Pred. No. 7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGKPPFE 9
Db 195 MLVGQPPFD 203

```

```

RESULT 22
US-08-252-995D-11
; Sequence 11, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; City: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
US-08-252-995D-11

```

```

Query Match 79.6%; Score 39; DB 1; Length 271;
Best Local Similarity 66.7%; Pred. No. 7.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGKPPFE 9
Db 198 LLVGQPPFE 206

```

```
RESULT 23
US-08-834-108-11
; Sequence 11, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
US-08-834-108-11
Query Match 79.6%; Score 39; DB 2; Length 271;
Best Local Similarity 66.7%; Pred. No. 7.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGKPPFE 9
Db 198 LLVGQPPFE 206

RESULT 24
US-08-252-995D-10
; Sequence 10, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-252-995D-10
Query Match 77.6%; Score 38; DB 1; Length 273;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
Db 200 LLIGRPPFD 208

RESULT 25
US-08-834-108-10
; Sequence 10, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-834-108-10

Query Match 77.6%; Score 38; DB 2; Length 273;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
:|:|:|:
DB 200 LLVGPPPE 208

RESULT 26

US-08-755-728-3
; Sequence 3, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,728
; FILING DATE: December 18, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US 08-755-728-3

Query Match 77.6%; Score 38; DB 2; Length 344;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
:|:|:|:
DB 200 LLVGPPPE 208

Db 266 LLVGPPPE 274

RESULT 27

US-08-974-655-3
; Sequence 3, Application US/08974655
; Patent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 5972676ember 25, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-08-974-655-3

Query Match 77.6%; Score 38; DB 2; Length 344;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
:|:|:|:
DB 266 LLVGPPPE 274

RESULT 28

US-09-283-011-3
; Sequence 3, Application US/09283011
; Patent No. 6207401
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin

```

; TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF AUR
; TITLE OF INVENTION:  AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES:  39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Lyon & Lyon
; STREET:  633 West Fifth Street
; STREET:  Suite 4700
; CITY:  Los Angeles
; STATE:  California
; COUNTRY:  U.S.A.
; ZIP:  90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  3.5" Diskette, 1.44 MB
; MEDIUM TYPE:  storage
; COMPUTER:  IBM Compatible
; OPERATING SYSTEM:  IBM P.C. DOS 5.0
; SOFTWARE:  FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/09/283,011
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  09/012,135
; FILING DATE:  January 22, 1998
; APPLICATION NUMBER:  08/755,728
; FILING DATE:  NO. 6207401ember 25, 1996
; APPLICATION NUMBER:  60/023,943
; FILING DATE:  August 14, 1996
; APPLICATION NUMBER:  60/008,809
; FILING DATE:  December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME:  Warburg, Richard J.
; REGISTRATION NUMBER:  32,327
; REFERENCE/DOCKET NUMBER:  231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (213) 489-1600
; TELEFAX:  (213) 955-3440
; TELEX:  67-3510
; INFORMATION FOR SEQ ID NO:  3:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  344 amino acids
; TYPE:  amino acid
; STRANDEDNESS:  single
; TOPOLOGY:  linear
; MOLECULE TYPE:  protein
; HYPOTHEICAL:  NO
; ANTI-SENSE:  NO
;
US 09-283 011.3

Query Match      77.6%  Score 38;  DB 1;  Length 344;
Best Local Similarity 66.7%  Pred. No. 14;
Matches      6;  Conservative      2;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  MLLGKPPFE 9
      :  |  |  |  |
Db      269  LLVGNPPFE 274

RESULT 29
US-09-016-000-1
; Sequence 1, Application US/09016000
; Patent No. 5962232
; GENERAL INFORMATION:
; APPLICANT:  Hillman, Jennifer L.
; APPLICANT:  Lai, Preeti
; APPLICANT:  Bandman, Olga
; APPLICANT:  Akerblom, Ingrid E.
; APPLICANT:  Shah, Purvi
; APPLICANT:  Corley, Neil C.
; APPLICANT:  Guegler, Karl G.
; TITLE OF INVENTION:  PROTEIN KINASE MOLECULES
; NUMBER OF SEQUENCES:  12
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE:  Incyte Pharmaceuticals, Inc.
; STREET:  3174 Porter Drive
; CITY:  Palo Alto
; STATE:  CA
; COUNTRY:  USA
; ZIP:  94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Diskette
; COMPUTER:  IBM Compatible
; OPERATING SYSTEM:  DOS
; SOFTWARE:  FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/09/016,000
; FILING DATE:  HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:  Billings, Lucy J.
; REGISTRATION NUMBER:  36,749
; REFERENCE/DOCKET NUMBER:  PF-0465 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  650-855-0555
; TELEFAX:  650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO:  1:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  347 amino acids
; TYPE:  amino acid
; STRANDEDNESS:  single
; TOPOLOGY:  linear
; IMMEDIATE SOURCE:
; LIBRARY:  HMCINCT01
; CLONE:  2940
;
US-09-016-000-1

Query Match      77.6%  Score 36;  DB 2;  Length 347;
Best Local Similarity 66.7%  Pred. No. 14;
Matches      6;  Conservative      2;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  MLLGKPPFE 9
      :  |  |  |  |
Db      269  LLVGNPPFE 277

RESULT 30
US-08-252-995D-2
; Sequence 2, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT:  Dennis, James W
; APPLICANT:  Heffernan, Mike
; APPLICANT:  Fode, Carol
; TITLE OF INVENTION:  NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES:  14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  BERESKIN & PARR
; STREET:  40 King Street West
; CITY:  Toronto
; STATE:  Ontario
; COUNTRY:  Canada
; ZIP:  M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/252,995D
; FILING DATE:  02-JUN-1994
; CLASSIFICATION:  536
; ATTORNEY/AGENT INFORMATION:

```



```

; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-252-995D-2

```

```

Query Match 77.6%; Score 38; DB 1; Length 416;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MLLGKPPFE 9
Db 204 LLIGRPFFD 212

```

```

RESULT 31
US-08-834-108-2
; Sequence 2, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-834-108-2

```

```

Query Match 77.6%; Score 38; DB 2; Length 416;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MLLGKPPFE 9
Db 204 LLIGRPFFD 212

```

```

RESULT 32
US-08-252-995D-6
; Sequence 6, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-252-995D-6

```

```

Query Match 77.6%; Score 38; DB 1; Length 464;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MLLGKPPFE 9
Db 204 LLIGRPFFD 212

```

```

RESULT 33
US-08-834-108-6
; Sequence 6, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-834-108-6

Query Match 77.6%; Score 38; DB 2; Length 464;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
   :|:|:|:|:
Db 204 LLGRPPFD 212

RESULT 34
US-09-772 647-4
; Sequence 4, Application US/09772647
; Patent No. 6521815
; GENERAL INFORMATION:
; APPLICANT: Verma, Ajit K
; APPLICANT: Reddig, Peter J
; APPLICANT: Jansen, Aaron P
; TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma
; FILE REFERENCE: 960296.97613
; CURRENT APPLICATION NUMBER: US/39/772,647
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P7 tag and
; OTHER INFORMATION: mouse protein kinase C epsilon coding sequence
US-09 772 647-4

Query Match 77.6%; Score 38; DB 4; Length 737;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
   :|:|:|:|
Db 600 MMAGQPPPE 608

RESULT 35
US-08-252-995D-4
; Sequence 4, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto

```

```

; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 925 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-252-995D-4

Query Match 77.6%; Score 38; DB 1; Length 925;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
   :|:|:|:|:
Db 204 LLGRPPFD 212

RESULT 36
US-08-834-108-4
; Sequence 4, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 925 amino acids
; TYPE: amino acid

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-834-108-4

Query Match      77.6%; Score 38; DB 2; Length 925;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPPFE 9
Db      204 LLIGRPPFD 212

RESULT 37
US-09-428-711A-21
; Sequence 21, Application US/C9428711A
; Patent No. 6358720
; GENERAL INFORMATION:
; APPLICANT: Muramatsu, Masaaki
; APPLICANT: Shirasawa, Takuji
; APPLICANT: Tokumitsu, Hiroshi
; APPLICANT: No. 6358720uchi, Teruhisa
; TITLE OF INVENTION: SERINE/THREONINE PROTEIN KINASE
; FILE REFERENCE: C6501-C45001
; CURRENT APPLICATION NUMBER: US/C9/428,711A
; CURRENT FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: PCT/JP98/C1246
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: JP 9/124796
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1037
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-428-711A-21

Query Match      77.6%; Score 38; DB 4; Length 1037;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LGLKPPFE 9
Db      208 LVGKPPFQ 215

RESULT 38
US-08-861-338-18
; Sequence 18, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.3, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant

```

Search completed: November 14, 2003, 13:29:50
Job time : 11.8286 secs

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/      TOPOLOGY: not relevant
/      MOLECULE TYPE: peptide
US-08-861-338-3
Query Match: 75.5%; Score 37; DB 3; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 MLLGKPPFE 9
      |||
Db       3 MLAGQPPFD 11
```

```

RESULT 40
US-07-857-224B-10
/ Sequence 10, Application US/07857224B
/ Patent No. 5958784
/ GENERAL INFORMATION:
/ APPLICANT: Benner, Steven A.
/ TITLE OF INVENTION: Predicting Folded Structures of Proteins
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Steven A. Benner
/ STREET: Hadlaubstrasse 15;
/ CITY: Zurich
/ STATE: none
/ COUNTRY: Switzerland
/ ZIP: (note: this is an international post code) CH-8092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh 7.0
/ SOFTWARE: Microsoft Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/857,224B
/ FILING DATE: 03/25/92
/ CLASSIFICATION: 436
/ PRIOR APPLICATION DATA: none
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (International) 41 1 632 2820
/ TELEFAX: (International) 41 1 262 2437
/ TELEX: none
```

```

/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 264
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE:
/ DESCRIPTION: protein
/ ORIGINAL SOURCE:
/ ORGANISM: bovine
/ FEATURE: Protein kinase; Table 8 Column 1;
/ PUBLICATION INFORMATION:
/ AUTHORS:
/ AUTHORS: Hanks, S. K.
/ AUTHORS: Quinn, A. M.
/ AUTHORS: Hunter, T.
/ TITLE: The protein kinase family
/ JOURNAL: Science
/ VOLUME: 241
/ PAGES: 42-52
/ DATE: 1988
US-07-857-224B-10
```

```

Query Match: 75.5%; Score 37; DB 2; Length 264;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 MLLGKPPFE 9
      |||
Db      195 MLAGQPPFD 203
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model:

Run on: November 14, 2003, 13:28:05 / Search time 22.39.4 Seconds
(without alignments)
73.443 Million cell updates/sec

Title: US-09-736-076-17
Perfect score: 49
Sequence: 1 MLLGKPPFE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCCMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCN_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCCMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCNUS_PUBCCMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCCMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCCMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCCMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCCMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCCMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCCMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCCMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US06_PUBCCMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	49	100.0	9	9	US-09-736-076-17 Sequence 17, Appl
2	46	93.9	9	9	US-09-736-076-15 Sequence 15, Appl
3	46	93.9	10	9	US-09-736-076-57 Sequence 57, Appl
4	46	93.9	11	9	US-09-736-076-19 Sequence 19, Appl
5	46	93.9	400	15	US-10-026-021-5 Sequence 5, Appl
6	46	93.9	469	15	US-10-059-585-14 Sequence 14, Appl
7	46	93.9	685	10	US-09-771-161A-249 Sequence 249, Appl
8	46	93.9	685	10	US-09-771-161A-250 Sequence 250, Appl
9	46	93.9	685	10	US-09-771-161A-251 Sequence 251, Appl
10	46	93.9	685	12	US-10-024-298A-101 Sequence 101, Appl
11	46	93.9	685	12	US-09-769-970-1 Sequence 1, Appl
12	46	93.9	685	12	US-10-042-211A-101 Sequence 16, Appl
13	44	89.8	8	9	US-09-736-076-16 Sequence 6, Appl
14	43	87.8	20	9	US-09-736-076-6
15	43	87.8	329	10	US-09-925-300-1268

16	43	87.8	367	15	US-10-026-021-6	Sequence 6, Appl
17	43	87.8	516	10	US-09-771-161A-123	Sequence 123, App
18	43	87.8	528	12	US-10-032-585-7571	Sequence 7571, Ap
19	43	87.8	603	10	US-09-771-161A-214	Sequence 214, App
20	43	87.8	603	15	US-10-171-311-186	Sequence 186, App
21	41	83.7	256	11	US-09-898-837A-32	Sequence 32, Appl
22	41	83.7	403	9	US-09-012-135A-4	Sequence 4, Appl
23	41	83.7	403	15	US-10-026-021-7	Sequence 7, Appl
24	41	83.7	403	15	US-10-059-585-33	Sequence 33, Appl
25	41	83.7	403	15	US-10-209-324-2	Sequence 2, Appl
26	39	79.6	40	10	US-09-842-582-9	Sequence 9, Appl
27	39	79.6	122	10	US-09-515-806-24	Sequence 24, Appl
28	39	79.6	183	15	US-10-172-088-12	Sequence 12, Appl
29	38	77.6	8	9	US-09-736-076-55	Sequence 55, Appl
30	38	77.6	344	9	US-09-012-135A-3	Sequence 3, Appl
31	38	77.6	344	15	US-10-059-585-34	Sequence 34, Appl
32	38	77.6	344	15	US-10-171-311-214	Sequence 214, App
33	38	77.6	347	10	US-09-974-298-136	Sequence 136, App
34	38	77.6	348	12	US-10-291-253A-16	Sequence 16, Appl
35	38	77.6	379	15	US-10-026-021-3	Sequence 3, Appl
36	38	77.6	419	10	US-09-893-737-106	Sequence 106, App
37	38	77.6	627	9	US-09-949-970-2	Sequence 2, Appl
38	38	77.6	627	9	US-09-949-970-4	Sequence 4, Appl
39	38	77.6	646	10	US-09-738-626-3546	Sequence 3546, Ap
40	38	77.6	737	10	US-09-771-161A-195	Sequence 195, App
41	38	77.6	737	15	US-10-228-931-4	Sequence 4, Appl
42	38	77.6	970	15	US-10-026-021-2	Sequence 2, Appl
43	37	75.5	9	9	US-09-736-076-18	Sequence 18, Appl
44	37	75.5	20	9	US-09-736-076-3	Sequence 3, Appl
45	37	75.5	445	10	US-09-836-392-15	Sequence 15, Appl

ALIGNMENTS

RESULT :

US-09-736-076-17
; Sequence 17, Application US/C9736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: ~~SHORT PEPTIDES~~ WHICH SELECTIVELY
; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (9)...(9)
; OTHER INFORMATION: J43.1
US-09-736-076-17

Query Match : 100.0%; Score 49; DB 9; Length 9;
Best Local Similarity : 100.0%; Pred. No. 5.9e+05;
Matches : 9; Conservative : 0; Mismatches : 0; Indels : 0; Gaps : 0;

QY 1 MLLGKPPFE 9

DB 1 MLLGKPPFE 9

RESULT 2


```

US-09-736-076-15
; Sequence 15, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: J42
US-09-736-076-15

```

```

Query Match      93.9%; Score 46; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. 5.8e+05;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MLLGKPPFE 9
      1 MLLGKPPFE 9
DB      1 MLLGKPPFE 9
      1 MLLGKPPFE 9

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```

RESULT 3
US-09-736-076-57
; Sequence 57, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MYRISTATE
; LOCATION: (1)...(10)
; OTHER INFORMATION: position 10 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (1)...(10)
; OTHER INFORMATION: SNK
US-09-736-076-57

```

```

Query Match      93.9%; Score 46; DB 9; Length 10;
Best Local Similarity 88.9%; Pred. No. 6.077;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPFE 9
      1 MLLGKPPFE 9
DB      2 MLLGKPPFE 10
      2 MLLGKPPFE 10

```

```

RESULT 4
US-09-736-076-19
; Sequence 19, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(11)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (1)...(11)
; OTHER INFORMATION: J46
US-09-736-076-19

```

```

Query Match      93.9%; Score 46; DB 9; Length 11;
Best Local Similarity 88.9%; Pred. No. 0.085;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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QY      1 MLLGKPPFE 9
      1 MLLGKPPFE 9
DB      1 MLLGKPPFE 9
      1 MLLGKPPFE 9

```

```

RESULT 5
US-10-026-021-5
; Sequence 5, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasunichi;
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(400)
; OTHER INFORMATION: human SNK mitotic kinase kinase domain
US-10-026-021-5

```

```

Query Match      93.9%; Score 46; DB 15; Length 400;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPFE 9
      1 MLLGKPPFE 9
DB      273 MLLGKPPFE 281
      273 MLLGKPPFE 281

```

```

RESULT 6
US-10-059-585-14
; Sequence 14, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US 10-059-585 14

```

```

Query Match          93.9%; Score 46; DB 15; Length 469;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MLLGKPPFE 9
      |||:||||
Db      57 MLLGRPPFE 65

RESULT 7
US-09-771-161A-249
; Sequence 249, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 249

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```

; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-249

Query Match          93.9%; Score 46; DB 10; Length 685;
Best Local Similarity 88.9%; Pred. No. 5.2;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPFE 9
      |||:||||
Db      273 MLLGRPPFE 281

RESULT 8
US-09-771-161A-250
; Sequence 250, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-250

```

```

Query Match          93.9%; Score 46; DB 10; Length 685;
Best Local Similarity 88.9%; Pred. No. 5.2;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPFE 9
      |||:||||
Db      273 MLLGRPPFE 281

RESULT 9
US-09-771-161A-251
; Sequence 251, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 251
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-251

```

```

Query Match          93.9%; Score 46; DB 10; Length 685;
Best Local Similarity 88.9%; Pred. No. 5.2;

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Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
|||:||||
DB 273 MLLGRPPFE 281

RESULT 10

US-10-024-298A 101
; Sequence 101, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP2540318/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101:
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024 298A-101

Query Match 93.9%; Score 46; DB 12; Length 685;
Best Local Similarity 88.9%; Pred. No. 5.2;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
|||:||||
DB 273 MLLGRPPFE 281

RESULT 11

US-09-769-970-1
; Sequence 1, Application US/09769970
; Publication No. US20030170219A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Corley, Neil C.
; Czegler, Karl G.
; Lal, Preeti
; Goli, Surya K.
; Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,970
FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/272,796
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321; US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-3555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
TYPE: aminc acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HUVEHOB01
CLONE: 39043
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-769-970-1

Query Match 93.9%; Score 46; DB 12; Length 685;
Best Local Similarity 88.9%; Pred. No. 5.2;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
|||:||||
DB 273 MLLGRPPFE 281

RESULT 12

US-10-042-211A-101
; Sequence 101, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-101

Query Match 93.9%; Score 46; DB 12; Length 685;
Best Local Similarity 88.9%; Pred. No. 5.2;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 Db 273 MLLGRPPFE 281

RESULT 13
 US-09-736-076-16
 ; Sequence 16, Application US/09736076
 ; Patent No. US2002049301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; FILE REFERENCE: 1242.1015-009
 ; CURRENT APPLICATION NUMBER: US/09/736,076
 ; CURRENT FILING DATE: 2000-12-13
 ; PRIOR APPLICATION NUMBER: US 08/861,338
 ; PRIOR FILING DATE: 1997-05-21
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: ACETYLATION
 ; LOCATION: (1)...(8)
 ; NAME/KEY: AMIDATION
 ; LOCATION: (1)...(8)
 ; OTHER INFORMATION: G43
 US-09-736-076-16

Query Match 89.8%; Score 44; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 Db 1 MLLGKPPF 8

RESULT 14
 US-09-736-076-6
 ; Sequence 6, Application US/09736076
 ; Patent No. US2002049301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; FILE REFERENCE: 1242.1015-009
 ; CURRENT APPLICATION NUMBER: US/09/736,076
 ; CURRENT FILING DATE: 2000-12-13
 ; PRIOR APPLICATION NUMBER: US 08/861,338
 ; PRIOR FILING DATE: 1997-05-21
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: POLO
 US-09-736-076-6

Query Match 87.8%; Score 43; DB 9; Length 20;
 Best Local Similarity 77.8%; Pred. No. 0.52;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 Db 3 LLVGKPPFE 11

RESULT 15
 US-09-925-300-1268
 ; Sequence 1268, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben,
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/USCO/05988
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1268
 ; LENGTH: 329
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (3)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (59)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (307)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (308)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (314)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (317)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (323)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (327)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (328)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (329)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-925-300-1268

Query Match 87.8%; Score 43; DB 10; Length 329;
 Best Local Similarity 77.8%; Pred. No. 8.5;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 Db 260 LLVGKPPFE 268

RESULT 16
 US-10-026-021-6
 ; Sequence 6, Application US/10026021
 ; Publication No. US2003027756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hitoshi, Yasumichi
 ; APPLICANT: Demo, Susan
 ; APPLICANT: Jenkins, Yonchu
 ; APPLICANT: Rigel Pharmaceuticals, Inc.

```

; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(367)
; OTHER INFORMATION: human PKC mitotic kinase kinase domain
US-10-026-021-6

```

```

Query Match      87.8%   Score 43; DB 15; Length 367;
Best Local Similarity 77.8%   Pred. No. 9.5;
Matches      7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPFE 9
      :|||:|
DB      244 LLVGKPPFE 252

```

```

RESULT 19
US-09-771-161A-123
; Sequence 123, Application US/09771:161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771:161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 123
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US 09-771 161A 123

```

```

Query Match      87.8%   Score 43; DB 10; Length 516;
Best Local Similarity 77.8%   Pred. No. 13;
Matches      7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPFE 9
      :|||:|
DB      157 LLVGKPPFE 165

```

```

RESULT 18
US-10-032-585-7571
; Sequence 7571, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Technologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585

```

```

; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7571
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7571

```

```

Query Match      87.8%   Score 43; DB 12; Length 528;
Best Local Similarity 77.8%   Pred. No. 14;
Matches      7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPFE 9
      :|||:|
DB      454 LLVGKPPFE 462

```

```

RESULT 19
US-09-771-161A-214
; Sequence 214, Application US/09771:161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771:161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 214
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-214

```

```

Query Match      87.8%   Score 43; DB 10; Length 603;
Best Local Similarity 77.8%   Pred. No. 16;
Matches      7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLLGKPPFE 9
      :|||:|
DB      244 LLVGKPPFE 252

```

```

RESULT 20
US-10-171-311-186
; Sequence 186, Application US/10171311
; Publication No. US2003087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Ganavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155

```


; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/335,936
 ; PRIOR FILING DATE: 2001-11-14
 ; NUMBER OF SEQ ID NOS: 238
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 186
 ; LENGTH: 603
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-171-311-186

Query Match 87.8%; Score 41; DB 15; Length 603;
 Best Local Similarity 77.8%; Pred. No. 16;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLGKPPFE 9
 Db 244 LVGKPPFE 252

RESULT 21

US-09-898-837A-32
 ; Sequence 32, Application US/09898837A
 ; Publication No. US20030077697A;
 ; GENERAL INFORMATION:
 ; APPLICANT: Quinn, Kerry E.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Majumder, Kumud
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Herrmann, John L.
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Fernandes, Elma
 ; APPLICANT: Taupier Jr., Raymond
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: CuraGen Corporation
 ; APPLICANT: Gerlach, Valerie L.
 ; APPLICANT: MacDougall, John R.
 ; TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN KINASE LIKE PROTEINS AND
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
 ; FILE REFERENCE: 15966-598 CIP
 ; CURRENT APPLICATION NUMBER: US/09/898,837A
 ; CURRENT FILING DATE: 2001-07-03
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
 ; PRIOR FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,819
 ; PRIOR FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,600
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,630
 ; PRIOR FILING DATE: 2000-04-13
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/214,600
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
 ; PRIOR FILING DATE: 2000-04-03
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,936
 ; PRIOR FILING DATE: 2000-07-03
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
 ; PRIOR FILING DATE: 2000-11-16
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 32
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 US-09-898-837A-32

Query Match 83.7%; Score 41; DB 11; Length 256;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLGKPPFE 9

Db 193 LLGKPPFE 201
 ; Sequence 4, Application US/09012135A
 ; Patent No. US20020081578A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Plowman, Gregory
 ; APPLICANT: Mossie, Kevin
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
 ; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSeq for Windows 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/012,135A
 ; FILING DATE: January 22, 1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/005,269
 ; FILING DATE: January 9, 1998
 ; APPLICATION NUMBER: 08/755,728
 ; FILING DATE: No. US20020081578A1ember 25, 1996
 ; APPLICATION NUMBER: 60/023,943
 ; FILING DATE: August 14, 1996
 ; APPLICATION NUMBER: 60/008,809
 ; FILING DATE: December 18, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 231/282
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 403 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 US-09-012-135A-4

Query Match 83.7%; Score 41; DB 9; Length 403;
 Best Local Similarity 87.5%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLGKPPFE 9
 Db 323 LVGKPPFE 330

RESULT 23

US-10-026-021-7
 ; Sequence 7, Application US/10026021
 ; Publication No. US20030027756A1

; GENERAL INFORMATION:
 ; APPLICANT: Hitechi, Yasumichi
 ; APPLICANT: Demo, Susan
 ; APPLICANT: Jenkins, Yonchu
 ; APPLICANT: Rigel Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 ; TITLE OF INVENTION: Treatment of Cancer
 ; FILE REFERENCE: 021044-001210US
 ; CURRENT APPLICATION NUMBER: US/10/026,021
 ; CURRENT FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/309,632
 ; PRIOR FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human ARK mitotic kinase
 US-10-026-021-7

Query Match 83.7%; Score 41; DB 15; Length 403;
 Best Local Similarity 87.5%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPFE 9
 |:|:|:|:
 DB 323 LVGKPPFE 330

RESULT 24
 US-10-059-585-33
 ; Sequence 33, Application US/10059585
 ; Publication No. US20030082776A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ota, Toshio
 ; APPLICANT: Isogai, Takao
 ; APPLICANT: Nishikawa, Tetsuo
 ; APPLICANT: Hayashi, Koji
 ; APPLICANT: Otsuka, Kaoru
 ; APPLICANT: Yamamoto, Jun-ichi
 ; APPLICANT: Ishii, Shizuko
 ; APPLICANT: Sugiyama, Tomoyasu
 ; APPLICANT: Wakamatsu, Ai
 ; APPLICANT: Nagai, Keiichi
 ; APPLICANT: Otsuki, Tetsuji
 ; APPLICANT: Funahashi, Shin-ichi
 ; APPLICANT: Seroo, Chiaki
 ; APPLICANT: Nezu, Jun-ichi
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
 ; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
 ; FILE REFERENCE: 36501-098001
 ; CURRENT APPLICATION NUMBER: US/10/059,585
 ; CURRENT FILING DATE: 2002-01-29
 ; PRIOR APPLICATION NUMBER: PCT/JP00/05060
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: US 60/183,322
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: US 60/159,590
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: JP 2000-118776
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: JP 2000-183767
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: JP 11-248036
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 33
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-059-585-33
 Query Match 83.7%; Score 41; DB 15; Length 403;
 Best Local Similarity 87.5%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLGKPPFE 9
 |:|:|:|:
 DB 323 LVGKPPFE 330
 RESULT 25
 US-10-209-324-2
 ; Sequence 2, Application US/10209324
 ; Publication No. US20030108910A1
 ; GENERAL INFORMATION:
 ; APPLICANT: UNIVERSITY OF CALIFORNIA SAN FRANCISCO
 ; APPLICANT: TOLAND, Amanda E.
 ; APPLICANT: BALMAIN, Allan
 ; TITLE OF INVENTION: STK15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANCER
 ; FILE REFERENCE: UCSF1120-2
 ; CURRENT APPLICATION NUMBER: US/10/209,324
 ; CURRENT FILING DATE: 2002-07-29
 ; PRIOR APPLICATION NUMBER: US 60/334,146
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: US 60/308,911
 ; PRIOR FILING DATE: 2001-07-27
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (31)-(31)
 ; OTHER INFORMATION: Xaa is Ile or Phe
 US-10-209-324-2

Query Match 83.7%; Score 41; DB 15; Length 403;
 Best Local Similarity 87.5%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPFE 9
 |:|:|:|:
 DB 323 LVGKPPFE 330

RESULT 26
 US-09-842-582-9
 ; Sequence 9, Application US/09842582
 ; Patent No. US2002015570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Meyers, Rachel
 ; TITLE OF INVENTION: 2246, NOVEL PROTEIN KINASE MOLECULES AND
 ; TITLE OF INVENTION: USES THEREFOR
 ; FILE REFERENCE: 38155-20054.00
 ; CURRENT APPLICATION NUMBER: US/09/842,582
 ; CURRENT FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: US 60/199,391
 ; PRIOR FILING DATE: 2000-04-25
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 40
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Consensus amino acid
 US-09-842-582-9
 Query Match 79.6%; Score 39; DB 10; Length 40;

FILING DATE: December 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-012-135A-3

Query Match 77.6%; Score 38; DB 9; Length 344;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLGKPPFE 9
:|:| |:
Db 266 LLVGNPPFE 274

RESULT 31
US-10-059-585-34

; Sequence 34, Application US/10053585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-ichi
; APPLICANT: Senco, Chiaki
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-34

Query Match 77.6%; Score 38; DB 15; Length 344;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLGKPPFE 9
:|:| |:
Db 266 LLVGNPPFE 274

RESULT 32

US-10-171-311-214
; Sequence 214, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-214

Query Match 77.6%; Score 38; DB 15; Length 344;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLGKPPFE 9
:|:| |:
Db 266 LLVGNPPFE 274

RESULT 33

US-09-974-298-136
; Sequence 136, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Huei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 136
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 002940CD1
US-09-974-298-136

Query Match 77.6%; Score 38; DB 10; Length 247;
 Best Local Similarity 66.7%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 :|||
 Db 269 LLVGNPPE 277

RESULT 34
 US-10-291-253A-16
 ; Sequence 16, Application US/1029:253A
 ; Publication No. US20030150017A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Botella, Jose
 ; APPLICANT: Graham, Michael
 ; APPLICANT: Fairbairn, David
 ; TITLE OF INVENTION: A Method for Facilitating Pathogen Resistance
 ; FILE REFERENCE: nematode
 ; CURRENT APPLICATION NUMBER: US/10/291:253A
 ; CURRENT FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: PR8706
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: PR8802
 ; PRIOR FILING DATE: 2001-11-12
 ; PRIOR APPLICATION NUMBER: US60/341404
 ; PRIOR FILING DATE: 2001-12-14
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Meloidogyne incognita
 US-10-291-253A-16

Query Match 77.6%; Score 38; DB 12; Length 348;
 Best Local Similarity 66.7%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 :|||
 Db 210 MXAGQPPFE 219

RESULT 35
 US-10-026-021 3
 ; Sequence 3, Application US/100260:1
 ; Publication No. US20030027756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hitoshi, Yasumichi
 ; APPLICANT: Demo, Susan
 ; APPLICANT: Jenkins, Yonchu
 ; APPLICANT: Rigel Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 ; TITLE OF INVENTION: Treatment of Cancer
 ; FILE REFERENCE: 021044-001210US
 ; CURRENT APPLICATION NUMBER: US/10/026:021
 ; CURRENT FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/309,632
 ; PRIOR FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 379
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (1)...(379)
 ; OTHER INFORMATION: SAK serine/threonine kinase kinase domain
 US-10-026-021-3

Query Match 77.6%; Score 38; DB 15; Length 379;
 Best Local Similarity 55.6%; Pred. No. 74;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 :|||
 Db 204 LLIGRPPFD 212

RESULT 36
 US-09-893-737-106
 ; Sequence 106, Application US/09893737
 ; Patent No. US20020110855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul C.
 ; APPLICANT: Presnell, Scott R.
 ; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
 ; FILE REFERENCE: 00-41
 ; CURRENT APPLICATION NUMBER: US/09/893,737
 ; CURRENT FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US 60/215,446
 ; PRIOR FILING DATE: 2000-06-30
 ; NUMBER OF SEQ ID NOS: 329
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 106
 ; LENGTH: 419
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-893-737-106

Query Match 77.6%; Score 38; DB 10; Length 419;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPP 7
 :|||
 Db 170 MLLGKPP 176

RESULT 37
 US-09-949-970-2
 ; Sequence 2, Application US/09949970
 ; Patent No. US20020042105A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BATHE, BRIGITTE
 ; APPLICANT: HANS, STEPHAN
 ; APPLICANT: FARWICK, MIKE
 ; APPLICANT: HERMANN, THOMAS
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE PCNB GENE
 ; FILE REFERENCE: 213734US0X
 ; CURRENT APPLICATION NUMBER: US/09/949,970
 ; CURRENT FILING DATE: 2001-09-12
 ; PRIOR APPLICATION NUMBER: DE 10044912.3
 ; PRIOR FILING DATE: 2000-09-12
 ; PRIOR APPLICATION NUMBER: DE 10120095.1
 ; PRIOR FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: US 60/297,250
 ; PRIOR FILING DATE: 2001-06-12
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 627
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-09-949-970-2

Query Match 77.6%; Score 38; DB 9; Length 627;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 :|||
 Db 198 LVTGKPPFE 196

RESULT 38
US-09-949-970-4
; Sequence 4, Application US/09949970
; Patent No. US20020342105A1
; GENERAL INFORMATION:
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEPHAN
; APPLICANT: FARWICK, MIKE
; APPLICANT: HERMANN, THOMAS
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE PDR GENE
; FILE REFERENCE: 213734JUSX
; CURRENT APPLICATION NUMBER: US/09/949,970
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: DE 10044912.3
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: DE 10120095.1
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/297,250
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2343)..(2343)
; OTHER INFORMATION: C-T transition
US-09-949-970-4

Query Match 77.6%; Score 38; DB 9; Length 627;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CY 1 MLLGKPPPE 9
DB 158 LVTKGPPPE 196

RESULT 39
US-09-738-626-3546
; Sequence 3546, Application US/0973862-
; Publication No. US20020197635A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NACKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280928
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent in ver. 3.0
; SEQ ID NO 3546
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum

US-09-738-626-3546

Query Match 77.6%; Score 38; DB 10; Length 646;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CY 1 MLLGKPPPE 9
DB 207 LVTKGPPPE 215

RESULT 40
US-09-771-161A-195
; Sequence 195, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802623-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 195
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-195

Query Match 77.6%; Score 38; DB 10; Length 737;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CY 1 MLLGKPPPE 9
DB 600 MWAGQPPPE 608

Search completed: November 14, 2003, 13:43:27
Job time : 22.3714 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 14, 2003, 13:20:05 ; Search time 10.8 Seconds
(without alignments:
80.14; Million cell updates/sec

Title: US-09-736-076-17
Perfect score: 49
Sequence: 1 MLLGKPPPE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	93.9	682	2 A44493	serum-inducible ki
2	43	87.8	603	2 S34130	serine/threonine-s
3	43	87.8	603	2 A47545	protein kinase (EC
4	43	87.8	603	2 A54596	protein kinase - m
5	41	83.7	305	2 T43221	serine/threonine-s
6	41	83.7	329	2 B87790	protein B8207.4 [i
7	41	83.7	389	2 S52242	protein kinase (EC
8	41	83.7	403	2 JCS974	aurora-related kin
9	41	83.7	407	2 S52243	p46Eg265 protein -
10	41	83.7	693	2 T38254	serine/threonine-s
11	41	83.7	705	2 A48144	protein kinase CDC
12	40	81.6	766	2 S69657	hypothetical prote
13	39	79.6	371	2 T16391	hypothetical prote
14	39	79.6	465	2 S68462	protein kinase ATP
15	39	79.6	472	2 S68463	protein kinase ATP
16	39	79.6	480	2 S56639	ribosomal protein
17	39	79.6	576	2 S22127	protein kinase pol
18	39	79.6	592	2 T43402	probable protein k
19	39	79.6	639	2 A32545	protein kinase C (
20	38	77.6	465	2 B55748	protein kinase (EC
21	38	77.6	521	2 D88640	protein F55A8.2 [i
22	38	77.6	525	2 S45884	probable serine/th
23	38	77.6	547	2 S44841	K06H7.1 protein -
24	38	77.6	547	2 T22856	hypothetical prote
25	38	77.6	634	1 B32392	protein kinase C (
26	38	77.6	648	2 T43337	polo-like kinase-1
27	38	77.6	707	1 A53530	protein kinase C (
28	38	77.6	736	1 KIRBCE	protein kinase C (
29	38	77.6	737	1 S28942	protein kinase C (

30	38	77.6	737	1 KIRTCE	protein kinase C (
31	38	77.6	737	1 KIMSCE	protein kinase C (
32	38	77.6	925	2 A55748	protein kinase (EC
33	38	77.6	1081	2 S51899	probable protein k
34	37	75.5	615	2 T29223	hypothetical prote
35	37	75.5	664	2 G89894	protein kinase lam
36	37	75.5	672	1 KIHUCA	protein kinase C (
37	37	75.5	672	1 KIRTC	protein kinase C (
38	37	75.5	672	1 KIMSCA	protein kinase C (
39	37	75.5	672	1 KIRBC	protein kinase C (
40	37	75.5	672	1 KIBOC	protein kinase C (
41	37	75.5	676	2 A37237	protein kinase C (
42	37	75.5	682	1 KIBOGC	protein kinase C (
43	37	75.5	697	1 KIRTC	protein kinase C (
44	37	75.5	697	1 KIRBGC	protein kinase C (
45	37	75.5	697	2 JN0548	protein kinase C (

ALIGNMENTS

RESULT 1

A44493
serum-inducible kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 10-Sep-1997
C;Accession: A44493
R;Simmons, D.L.; Neel, B.G.; Stevens, R.; Evett, G.; Erikson, R.L.
Mol. Cell. Biol. 12, 4164-4169, 1992
A;Title: Identification of an early-growth-response gene encoding a novel putative pr
A;Reference number: A44493; MUID:92375085; PMID:1508211
A;Accession: A44493
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-682 <SIM>
A;Experimental source: F-2 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:111721, NCBIPI:111722)
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
C;Keywords: ATP
F;77-331/Domain: protein kinase homology <KIN>

Query Match 93.9%; Score 46; DB 2; Length 682;
Best Local Similarity 88.9%; Pred. No. 0.86;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPPE 9
DB 270 MLLGRPPPE 278

RESULT 2

S34130
serine/threonine-specific protein kinase PLK (EC 2.7.1.1) - human
N;Alternate names: polo-like protein kinase; protein kinase plx-1
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C;Accession: S34130; I38123; S61543
R;Golsteyn, R.M.; Schultz, S.J.; Bartek, J.; Ziemiecki, A.; Ried, T.; Nigg, E.A.
submitted to the EMBL Data Library, June 1993
A;Description: Cloning and characterization of a novel human protein kinase plx-1 a p
through mitosis.
A;Reference number: S34130
A;Accession: S34130
A;Molecule type: mRNA
A;Residues: 1-603 <COL>
A;Cross-references: EMBL:X73458; NID:g312997; PIDN:CAA51837.1; PID:g312998
A;Experimental source: nasopharyngeal carcinoma
R;Holttrich, U.; Wolf, G.; Brauning, A.; Karn, T.; Bohme, B.; Rubsamen-Waigmann, H.,
Proc. Natl. Acad. Sci. U.S.A. 91, 1736-1740, 1994
A;Title: Induction and down-regulation of PLK, a human serine/threonine kinase expres
A;Reference number: A53134; MUID:94173904; PMID:8127874
A;Accession: I38123
A;Status: preliminary; nucleic acid sequence not shown

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A;Molecule type: mRNA
A;Residues: 1-140, 'P', 142-226, 'E', 228-603 <RES>
A;Cross-references: EMBL:X75932; NID:g460768; PIDN:CAA53536.1; PID:g460769
A;Experimental source: lung tumor
R;Braeuninger, A.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Oncogene 11, 1793-1800, 1995
A;Title: Identification and functional characterization of the human and murine polo-like
A;Reference number: S61543; MUID:96068906; PMID:7478607
A;Accession: S61543
A;Molecule type: DNA
A;Residues: 1-122, 'T', 124-136 <BRA>
A;Cross-references: EMBL:X90725; NID:g1061143; PIDN:CAA62260.1; PID:g1061144
A;Experimental source: placenta
A;Note: the authors translated the codon AGC for residue 107 as Met
C;Genetics:
A;Gene: GDB:PLK
A;Cross-references: GDB:331003
A;Map position: 17pter-17p12
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;51-305/Domain: protein kinase homology <KIN>

Query Match      87.8%; Score 43; DB 2; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPPPE 9
Db      244 LLVGKPPPE 252

RESULT 2
A47545
protein kinase (EC 2.7.1.37) Plk - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: A47545
R;Clay, F.J.; McEwen, S.J.; Bertoncello, I.; Wilks, A.F.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4882-4886, 1993
A;Title: Identification and cloning of a protein kinase encoding mouse gene, Plk, related
A;Reference number: A47545; MUID:93281660; PMID:8099445
A;Accession: A47545
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-603 <CLA>
A;Cross-references: GBL06144; NID:g309461; PIDN:AAA39946.1; PID:g309462
C;Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolog
C;Keywords: ATP; phosphotransferase
F;51-305/Domain: protein kinase homology <KIN>

Query Match      87.8%; Score 43; DB 2; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPPPE 9
Db      244 LLVGKPPPE 252

RESULT 4
A54596
protein kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: A54596
R;Lake, R.J.; Celinek, W.R.
Mol. Cell. Biol. 13, 7793-7801, 1993
A;Title: Cell cycle- and terminal differentiation-associated regulation of the mouse mRN
A;Reference number: A54596; MUID:94067140; PMID:7902533
A;Accession: A54596
A;Status: preliminary; translated from GB/EMBL/CDJ
A;Molecule type: mRNA
A;Residues: 1-603 <RES>

A;Molecule type: mRNA
A;Residues: 1-140, 'P', 142-226, 'E', 228-603 <RES>
A;Cross-references: EMBL:X75932; NID:g460768; PIDN:CAA53536.1; PID:g460769
A;Experimental source: lung tumor
R;Braeuninger, A.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Oncogene 11, 1793-1800, 1995
A;Title: Identification and functional characterization of the human and murine polo-like
A;Reference number: S61543; MUID:96068906; PMID:7478607
A;Accession: S61543
A;Molecule type: DNA
A;Residues: 1-122, 'T', 124-136 <BRA>
A;Cross-references: EMBL:X90725; NID:g1061143; PIDN:CAA62260.1; PID:g1061144
A;Experimental source: placenta
A;Note: the authors translated the codon AGC for residue 107 as Met
C;Genetics:
A;Gene: GDB:PLK
A;Cross-references: GDB:331003
A;Map position: 17pter-17p12
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;51-305/Domain: protein kinase homology <KIN>

Query Match      87.8%; Score 43; DB 2; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPPPE 9
Db      244 LLVGKPPPE 252

RESULT 5
T43221
serine/threonine-specific protein kinase (EC 2.7.1.-) 2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Accession: T43221
R;Schumacher, J.M.; Golden, A.; Donovan, P.J.
J. Cell Biol. 143, 1635-1646, 1998
A;Title: AIR-2: An aurora/Ipl1-related protein kinase associated with chromosomes an
A;Reference number: Z22347; MUID:99069487; PMID:9852156
A;Accession: T43221
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-305 <SCH>
A;Cross-references: EMBL:AF071207; PIDN:AAC70945.1
C;Genetics:
A;Gene: AIR-2
A;Map position: 1
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: phosphotransferase

Query Match      83.7%; Score 41; DB 2; Length 305;
Best Local Similarity 87.5%; Pred. No. 3.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLGKPPPE 9
Db      220 LVGKPPPE 227

RESULT 6
B87790
protein B0207.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: B87790
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating br
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999,
A;Accession: B87790
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-329 <STO>
A;Cross-references: GB:chr_I; PIDN:AAB52459.1; PID:g1943805; GSPDB:GN00019; CESP:B02
C;Genetics:
A;Gene: B0207.4
A;Map position: 1
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match      83.7%; Score 41; DB 2; Length 329;
Best Local Similarity 87.5%; Pred. No. 3.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLGKPPPE 9
Db      244 LVGKPPPE 251
```

```

RESULT 7
S52242
A:Title: protein kinase (EC 2.7.1.1.) p46XlEg2 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 18-Jun-1999
C:Accession: S52242
R;Roghi, C.; le Gueliec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein kin
A:Reference number: S52242
A:Accession: S52242
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-389 <ROG>
A:Cross-references: EMBL:Z17206; NID:G609279; PIDN:CAA78914.1; PID:G609280
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:119-171/Domain: protein kinase homology <KIN>
F:127-135/Region: protein kinase ATP-binding motif

Query Match      83.7%; Score 41; DB 2; Length 389;
Best Local Similarity 87.5%; Pred. No. 4.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLGKPPFE 9
DB      311 LVGKPPFE 318

RESULT 8
JC5974
A:Title: aurora-related kinase 1 (EC 2.7.1.1.) - human
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jan-2000
C:Accession: JC5974
R;Shirado, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara, M.; Gilbert, D.J.; Jenk
Biochem. Biophys. Res. Commun. 244, 285-292, 1998
A:Title: cDNA cloning, expression, subcellular localization, and chromosomal assignment
A:Reference number: JC5974; MUID:98183439; PMID:9514916
A:Accession: JC5974
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-403 <SH1>
A:Cross-references: GB:AF008551
C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolo
C:Keywords: phosphotransferase
F:131-383/Domain: protein kinase homology <KIN>

Query Match      83.7%; Score 41; DB 2; Length 403;
Best Local Similarity 87.5%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLGKPPFE 9
DB      323 LVGKPPFE 330

RESULT 9
S52243
p46Eg265 protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1999
C:Accession: S52243; S34642; I51695
R;Roghi, C.; le Gueliec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein kin
A:Reference number: S52242
A:Accession: S52243
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-407 <ROG>
A:Cross-references: EMBL:Z17207; NID:G60928; PIDN:CAA78915.1; PID:G609282

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R;Bouvet, P.; Omilli, F.; Arlot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Basset, T.;
submitted to the EMBL Data Library, June 1993
A:Description: Targetted deadenylation of specific mRNAs in Xenopus embryos by a mech
A:Reference number: S34642
A:Accession: S34642
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 328-407 <BOU>
A:Cross-references: EMBL:Z24453; NID:G394756; PIDN:CAA80826.1; PID:G394757
R;Bouvet, P.; Omilli, F.; Arlot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Bassez, T.;
Mol. Cell. Biol. 14, 1893-1900, 1994
A:Title: The deadenylation conferred by the 3' untranslated region of a developmental
A:Reference number: I51695; MUID:94158861; PMID:8114721
A:Accession: I51695
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 328-407 <BO2>
A:Cross-references: EMBL:Z24453; NID:G394756; PIDN:CAA80826.1; PID:G394757
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; phosphotransferase; protein kinase
F:138-390/Domain: protein kinase homology <KIN>
F:146-154/Region: protein kinase ATP-binding motif

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Query Match      83.7%; Score 41; DB 2; Length 407;
Best Local Similarity 87.5%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      2 LLGKPPFE 9
DB      330 LVGKPPFE 337

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RESULT 10
T38254
serine/threonine-specific protein kinase plol (EC 2.7.1.1.) - fission yeast (Schizosac
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T38254; T45128
R;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z21781
A:Accession: T38254
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-683 <BRC>
A:Cross-references: EMBL:Z98559; PIDN:CAB11167.1; GSPDB:GN00066; SPDB:SPAC23C11.16
A:Experimental source: strain 972h-; cosmid c23C11
R;Ohkura, H.; Hagan, I.M.; Glover, D.M.
Genes Dev. 9, 1059-1073, 1995
A:Title: The conserved Schizosaccharomyces pombe kinase plol, required to form a bipo
A:Reference number: Z22921; MUID:95262899; PMID:7744248
A:Accession: T45128
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-683 <OHK>
A:Cross-references: EMBL:X85758; NID:G887640; PIDN:CAA59766.1; PID:G887641
A:Experimental source: strain 972 derivative
C:Genetics:
A:Gene: plol; SPAC23C11.16
A:Map position: 1
C:Function:
A:Description: required to form a bipolar spindle and early in the regulatory cascade
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: phosphotransferase; protein kinase

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Query Match      83.7%; Score 41; DB 2; Length 683;
Best Local Similarity 66.7%; Pred. No. 7.8;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MLGKPPFE 9
DB      233 LLGKPPFE 241

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RESULT 11
A48144
protein kinase CDC5 (EC 2.7.1.1) - Yeast (Saccharomyces cerevisiae)
N;Alternate names: protein kinase PKX2; Protein YM8270.03C; protein YMR001c
C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change 24-Sep-1999
C;Accession: A48144; S53030; S27445
R;Kitada, K.; Johnson, A.L.; Johnston, L.H.; Sugino, A.
Mol. Cell. Biol. 13, 4445-4457, 1993
A;Title: A multicopy suppressor gene of the Saccharomyces cerevisiae G-1 cell cycle mutation
A;Reference number: A48144; MUID:93309479; PMID:8321244
A;Accession: A48144
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-705 <KIT>
A;Cross-references: EMBL:M84220; NID:gl72186; PIDN:AAAC2576.1; PID:gl72187
R;Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53028
A;Accession: S53030
A;Molecule type: DNA
A;Residues: 1-705 <DEV>
A;Cross-references: EMBL:Z48613; NID:q728645; PIDN:CAAR8516.1; PID:q728648; MIPS:YMR001c
A;Experimental source: strain AB972
C;Genetics:
A;Gene: SGD:CDC5; PKX2
A;Cross-references: SGD:S0004603; MIPS:YMR001c
A;Map position: 13R
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP; cell cycle control; phosphotransferase; protein kinase
F;8C-337/Domain: protein kinase homology <KIN>

Query Match      83.7%; Score 41; DB 2; Length 705;
Best Local Similarity 66.7%; Pred. No. 9;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPPFE 9
      1 11111
Db      274 LLLGKPPFQ 282

RESULT 12
S69657
hypothetical protein YDR490C - Yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 10-Sep-1996 #text_change 10-Apr-2002
C;Accession: S69657
R;Dietrich, F.S.
submitted to the EMBL Data Library, August 1995
A;Description: The sequence of S. cerevisiae cosmids 9410, 9035, 8166, and 9787.
A;Reference number: S69554
A;Accession: S69657
A;Molecule type: DNA
A;Residues: 1-766 <DIE>
A;Cross-references: EMBL:U33050; NID:q927726; PIDN:AA564917.1; PID:q927745; MIPS:YDR490C
C;Genetics:
A;Gene: SGD:PKH1
A;Cross-references: SGD:S0002898
A;Map position: 4R
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP
F;123-391/Domain: protein kinase homology <KIN>
F;131-139/Region: protein kinase ATP-binding motif

Query Match      81.6%; Score 40; DB 2; Length 766;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 MLLGKPPFE 9
      1 11111
Db      330 MLAGKPPFK 339
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RESULT 13
T16391
hypothetical protein F47F2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C;Accession: T16391
R;Bentley, D.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F47F2.
A;Reference number: Z18506
A;Accession: T16391
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-371 <BEN>
A;Cross-references: EMBL:U40943; NID:glC72202; PID:gl072204; PIDN:AAA8j716.1; CESP:F
C;Genetics:
A;Gene: CESP:F47F2.1
A;Introns: 39/3; 70/1; 126/2; 156/2; 182/3; 214/2; 286/2; 331/3
C;Superfamily: kinase-related transforming protein; protein kinase homology
F;61-317/Domain: protein kinase homology <KIN>

Query Match      79.6%; Score 39; DB 2; Length 371;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPPF 8
      1 11111
Db      251 MMLVGKPPF 258

RESULT 14
S68462
protein kinase ATPK6/ATPK1 (EC 2.7.1.1) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
C;Accession: S68462; A54141
R;Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 359, 199-204, 1995
A;Title: Two genes that encode ribosomal protein S6 kinase homologs are induced by cold
A;Reference number: S68462; MUID:95129712; PMID:7828736
A;Accession: S68462
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-465 <MIZ>
A;Cross-references: EMBL:D42056; NID:q867996; PIDN:BAA07656.1; PID:dl008238; PID:q86
R;Zhang, S.H.; Lawton, M.A.; Hunter, T.; Lamb, C.J.
J. Biol. Chem. 269, 17586-17592, 1994
A;Title: atpk1, a novel ribosomal protein kinase gene from Arabidopsis. I. Isolation
A;Reference number: A54141; MUID:94292519; PMID:7912697
A;Contents: ecotype Landsberg erecta
A;Accession: A54141
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-465 <ZHA>
A;Cross-references: GB:L29030; NID:q508307; PIDN:AAA21142.1; PID:q508308
A;Note: sequence extracted from NCBI backbone (NCBIN:149344, NCBIPI:149415)
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;132-389/Domain: protein kinase homology <KIN>
F;140-148/Region: protein kinase ATP-binding motif

Query Match      79.6%; Score 39; DB 2; Length 465;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLLGKPPF 8
      1 11111
Db      324 MMLVGKPPF 331

RESULT 15
S68463
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protein kinase ATPK19 (EC 2.7.1.1) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Dec-1996 #sequence_revision 27-Feb-1997 #text_change 24-Sep-1999
C:Accession: S68463
R:Mizoguchi, T.; Hayashida, N.; Yamaguchi Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 358, 199-204, 1995
A:Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold
A:Reference number: S68462; MUID:95129713; PMID:7828736
A:Accession: S68463
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-471 <M12>
A:Cross-references: EMBL:D42061; NID:q1526412; PIDN:BAAN7661.1; PID:d1008243; PID:g86799
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:138-395/Domain: protein kinase homology <KIN>
F:146-154/Region: protein kinase ATP-binding motif
Query Match 79.6%; Score 39; DB 2; Length 471;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 330 MLTGKPPF 337
RESULT 16
S6639
ribosomal protein S6 kinase homolog (clone AspK11) - oat
N:Alternate names: mitogen-activated protein kinase pp70 homolog
C:Species: Avena sativa (oat)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
C:Accession: S56639
R:Buttery, A.K.; Phillips, A.L.
Plant Mol. Biol. 27, 1043-1052, 1995
A:Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that show
A:Reference number: S56638; MUID:95284341; PMID:7766874
A:Accession: S56639
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-480 <HUT>
A:Cross-references: EMBL:X79992; NID:g871985; PIDN:CAA56313.1; PID:g971986
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase; protein kinase
F:149-407/Domain: protein kinase homology <KIN>
F:157-165/Region: protein kinase ATP-binding motif
Query Match 79.6%; Score 39; DB 2; Length 480;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 341 MLTGKPPF 348
RESULT 17
S22127
protein kinase polo (EC 2.7.1.1) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999
C:Accession: S22127
R:Sunkel, C.E.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22127
A:Accession: S22127
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-576 <SUN>
A:Cross-references: EMBL:X63361; NID:g8355; PIDN:CAA44943.1; PID:g8356
C:Genetics:
A:Gene: FlyBase:polo

A:Cross-references: FlyBase:FBgn0003124
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; phosphotransferase
F:23-277/Domain: protein kinase homology <KIN>
Query Match 79.6%; Score 39; DB 2; Length 576;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 9
DB 216 LLVGQPPF 224
RESULT 18
T43402
probable protein kinase (EC 2.7.1.1) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T43402; T41425
R:Niederberger, C.
submitted to the EMBL Data Library, July 1998
A:Reference number: Z22486
A:Accession: T43402
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-592 <NIE>
A:Cross-references: EMBL:X99280; PIDN:CAA67672.1
A:Experimental source: strain h9C
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21954
A:Accession: T41425
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-592 <WOO>
A:Cross-references: EMBL:AL031799; PIDN:CAA21194.1; GSPDB:GN00068; SPDB:SPCC576.15c
A:Experimental source: strain 972h-; cosmid c576
C:Genetics:
A:Gene: XSG1; SPCC576.15c
A:Map position: 3
A:Introns: 191/3
C:Keywords: phosphotransferase
Query Match 79.6%; Score 39; DB 2; Length 592;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 305 MLAGKPPF 312
RESULT 19
A32545
protein kinase C (EC 2.7.1.1) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1999
C:Accession: A32545
R:Rosenthal, A.; Rhee, L.; Yadegari, R.; Paro, R.; Ullrich, A.; Goeddel, D.V.
EMBO J. 6, 433-441, 1987
A:Title: Structure and nucleotide sequence of a Drosophila melanogaster protein kinase
A:Reference number: A32545; MUID:87218499; PMID:3107983
A:Accession: A32545
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-639 <ROS>
A:Cross-references: GB:X05076; NID:g8352; PIDN:CAA28736.1; PID:g8353; GB:Y00042
C:Genetics:
A:Gene: FlyBase:Pkcs3E
A:Cross-references: FlyBase:FBgn0003091
C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:46-95/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:111-160/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:161-273/Domain: protein kinase C C2 region homology <K2>
 F:339-539/Domain: protein kinase homology <KIN>
 F:347-355/Region: protein kinase ATP-binding motif

Query Match 79.6%; Score 39; DB 2; Length 633;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 |||||
 DB 533 MLVGQPPFD 541

RESULT 20
 B55748
 protein kinase (EC 2.7.1.37) Sak.b - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Dec-1997
 C:Accession: B55748
 R:Code: C.; Motif: B.; Yousefi, S.; Heffernan, M.; Dennis, J.W.
 Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
 A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosophila
 A:Reference number: A55748; MUID:94294757; PMID:802279;
 A:Accession: B55748
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-465 <FOD>
 A:Cross-references: B55748C
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
 C:Keywords: ATP; phosphotransferase
 F:10-265/Domain: protein kinase homology <KIN>
 F:18-26/Region: protein kinase ATP-binding motif

Query Match 77.6%; Score 38; DB 2; Length 465;
 Best Local Similarity 55.6%; Pred. No. 20;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 |||||
 DB 204 LLIGRPPFD 212

RESULT 21
 D8864C
 protein P55A8.2 (imported) Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 17-May-2002
 C:Accession: D8864C
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A:Reference number: A75000; MUID:99069613; PMID:985192
 A:Note: see websites genome.wustl.edu/qsc/c_elegans/ and www.sanger.ac.uk/Projects/C_ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: D8864C
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-521 <STO>
 A:Cross-references: GB:chr_IV; PIDN:AAC191861; PID:G3193148; GSPDB:GN00022; CESP:F55A8.
 C:Genetics:
 A:Gene: F55A8.2
 A:Map position: 4
 C:Superfamily: cGMP-dependent protein kinase, cAMP receptor protein cyclic nucleotide-bi

Query Match 77.6%; Score 38; DB 2; Length 521;
 Best Local Similarity 55.6%; Pred. No. 22;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 |||||
 DB 401 LMJGRPPFQ 409

RESULT 22
 S45884
 probable serine/threonine-specific protein kinase (EC 2.7.1.1-) YBR028C - yeast (Sacci
 N:Alternate names: protein YBR0312
 C:Species: Saccharomyces cerevisiae
 C:Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
 C:Accession: S45884; S46558
 R:Grivell, L.A.; de Haan, M.; Maat, M.C.; Smits, P.H.M.
 submitted to the Protein Sequence Database, August 1994
 A:Reference number: S45875
 A:Accession: S45884
 A:Molecule type: DNA
 A:Residues: 1-525 <GR1>
 A:Cross-references: EMBL:Z35897; NID:G536370; PIDN:CAA84970.1; PID:G536371; MIPS:YBR
 A:Experimental source: strain S288C
 R:Smits, P.H.M.; de Haan, M.; Maat, C.; Grivell, L.A.
 Yeast 10 (Suppl.A), S75-S80, 1994
 A:Title: The complete sequence of a 33 kb fragment on the right arm of chromosome II
 ly identified genes and a homologue of the SCO1 gene.
 A:Reference number: S46551; MUID:94378725; PMID:8091864
 A:Accession: S46558
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-525 <SM1>
 A:Cross-references: EMBL:X76078; NID:G498748; PIDN:CAA53684.1; PID:G498756
 A:Experimental source: strain S288C
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 199
 C:Genetics:
 A:Cross-references: SGD:S0000232
 A:Map position: 2R
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:126-423/Domain: protein kinase homology <KIN>
 F:134-142/Region: protein kinase ATP-binding motif
 F:277/Active site: Asp #status predicted

Query Match 77.6%; Score 38; DB 2; Length 525;
 Best Local Similarity 75.0%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 |||||
 DB 355 MLVGKPPY 362

RESULT 23
 S44841
 K06H7.1 protein - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar 2001
 C:Accession: S44841
 R:Favella, A.D.
 submitted to the EMBL Data Library, May 1993
 A:Description: Sequence of the C. elegans cosmid K06H7.
 A:Reference number: S44620
 A:Accession: S44841
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-547 <FAV>
 A:Cross-references: EMBL:L15314; NID:G289690; PIDN:AAA28084.1; PID:G28969;
 C:Genetics:
 A:Introns: 25/3; 36/3; 80/3; 149/3; 186/2; 229/3; 311/3
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
 C:Keywords: ATP; serine/threonine-specific protein kinase
 F:265-518/Domain: protein kinase homology <KIN>

Query Match 77.6%; Score 38; DB 2; Length 547;
 Best Local Similarity 66.7%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9

Db 457 LLEGQPPFE 465
 :|:|:|:|

RESULT 24
 T22856
 hypothetical protein F57F5.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Jun-2002
 C:Accession: T22856
 R:Harris, B.
 submitted to the EMBL Data Library, July 1996
 A:Reference number: Z19627
 A:Accession: T22856
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-547 <WIL>
 A:Cross-references: EMBL:Z75953; PIDN:CAE00101.1; GSPOS:GN00023; CESP:F57F5.5
 A:Experimental source: clone F57F5
 C:Genetics:
 A:Gene: CESP:F57F5.5
 A:Map position: 5
 A:Introns: 43/1; 129/2; 165/3; 187/1; 289/3; 341/2; 450/3; 499/3
 F:11 60/Domain: protein kinase C zinc-binding repeat homology <KZN1>
 F:89-139/Domain: protein kinase C zinc-binding repeat homology <KZN2>

Query Match 77.6%; Score 38; DB 2; Length 547;
 Best Local Similarity 66.7%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 :|:|:|:|
 Db 410 MMAGQPPFE 418

RESULT 25
 B32392
 protein kinase C (EC 2.7.1.1) epsilon-related - fruit fly (Drosophila melanogaster)
 N:Alternate names: protein kinase C 98F
 C:Species: Drosophila melanogaster
 C:Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 11-Jun-1999
 C:Accession: B32392
 R:Schaeffer, E.; Smith, D.; Mardon, G.; Quinn, W.; Zuker, C.
 Cell 57, 403-412, 1989
 A:Title: Isolation and characterization of two new Drosophila protein kinase C genes, in
 A:Reference number: A32392; MUID:89249301; PMID:2720775
 A:Accession: B32392
 A:Molecule type: mRNA
 A:Residues: 1-634 <SCH>
 A:Cross-references: GB:J04848; NID:g158128; PIDN:AAA28618.1; PID:g158129
 C:Genetics:
 A:Gene: FlyBase:Pk98E
 A:Cross-references: FlyBase:FBgn0003033
 C:Function:

A:Description: catalyzes the formation of peptidyl-serine phosphate or peptidyl-threonin
 A:Note: activity is calcium-independent; phospholipid-dependent, and activated by diacyl
 C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; pr
 C:Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransf
 F:58-63/Region: pseudophosphorylation motif
 F:72-121/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:147-196/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:301-560/Domain: protein kinase homology <KIN>
 F:309-317/Region: protein kinase ATP-binding motif
 F:72,102,105,121/Binding site: zinc (His, Cys, Cys, Cys)
 F:85,88,110,113/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:147,177,180,196/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:160,163,185,198/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:332,351,427,429/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 77.6%; Score 38; DB 1; Length 634;
 Best Local Similarity 66.7%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 :|:|:|:|
 Db 495 MMAGQPPFE 503

RESULT 26
 T43337
 polo-like kinase-1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 01-Dec-2000
 C:Accession: T43337; S44761
 R:Chase, D.; Serafinas, C.; Ashcroft, N.; Kosinski, M.; Longo, D.; Ferris, D.K.; Gold
 submitted to the EMBL Data Library, July 1998
 A:Description: The polo-like kinase PLK-1 is required for nuclear envelope breakdown
 A:Reference number: Z22438
 A:Accession: T43337
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-648 <CHA>
 A:Cross-references: EMBL:AF080581; PIDN:AAC34661.1
 R:Favella, A.D.
 submitted to the EMBL Data Library, May 1993
 A:Description: Sequence of the C. elegans cosmid C14B9.
 A:Reference number: S44617
 A:Accession: S44761
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 'MKT', 282-648 <FAV>
 A:Cross-references: EMBL:L15188; NID:g289640; PID:g289648
 C:Genetics:
 A:Gene: pik-1
 A:Map position: 3
 A:Introns: 391/3; 540/3; 578/3
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match 77.6%; Score 38; DB 2; Length 648;
 Best Local Similarity 66.7%; Pred. No. 28;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 :|:|:|:|
 Db 228 LLEGQPPFE 236

RESULT 27
 A53530
 protein kinase C (EC 2.7.1.1) epsilon-related - Caenorhabditis elegans
 N:Alternate names: protein kinase C PKC1B, neuronal
 C:Species: Caenorhabditis elegans
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jun-1999
 C:Accession: A53530
 R:Land, M.; Islas-Trejo, A.; Freedman, J.H.; Rubin, C.S.
 J. Biol. Chem. 269, 9234-9244, 1994
 A:Title: Structure and expression of a novel, neuronal protein kinase C (PKC1B) from
 1 signals.
 A:Reference number: A53530; MUID:94179345; PMID:8132661
 A:Accession: A53530
 A:Molecule type: mRNA
 A:Residues: 1-707 <LAN>
 A:Cross-references: GB:U00181; NID:g484065; PIDN:AAA18259.1; PID:g392435
 C:Genetics:
 A:Gene: Kin-13
 A:Map position: V
 A:Note: located near myo-3, col-1, and CPROT/2 genes
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threc
 A:Note: activity is calcium-independent; phospholipid-dependent, and activated by dia
 C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology;
 C:Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotra
 F:157-162/Region: pseudophosphorylation motif
 F:171-220/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:249-298/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:376-638/Domain: protein kinase homology <KIN>

F;384-392/Region: protein kinase ATP-binding motif
 F;171,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F;184,187,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F;249,279,282,298/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F;262,265,287,290/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F;407,426,502,504/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 77.6%; Score 38; DB 1; Length 707;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 MLLGKPPFE 9
 : : : : :
 Db 570 MMAGQPPFE 579

RESULT 28
 KIRBCE
 protein kinase C (EC 2.7.1.1) epsilon - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
 C;Accession: A29880
 R;Ohno, S.; Akita, Y.; Konno, Y.; Imaizumi, S.; Suzuki, K.
 Cell 53, 731-741, 1988
 A;Title: A novel phorbol ester receptor/protein kinase, nPKC, distantly related to the P
 A;Reference number: A29880; MUID:88223367; PMID:3370672
 A;Accession: A29880
 A;Molecule type: mRNA
 A;Residues: 1-736 <CHN>
 A;Cross-references: GB:M20014
 C;Function:
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
 C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; p
 C;Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid b
 F;156-161/Region: pseudophosphorylation motif
 F;170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
 F;243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
 F;406-667/Domain: protein kinase ATP-binding motif
 F;413-421/Region: protein kinase ATP-binding motif
 F;170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F;183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F;243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F;436,456,531,533/Active site: Lys, Glu, Asp, Lys #status predicted
 F;702,709/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match 77.6%; Score 38; DB 1; Length 579;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 MLLGKPPFE 9
 : : : : :
 Db 599 MMAGQPPFE 597

RESULT 29
 S28942
 protein kinase C (EC 2.7.1.1) epsilon - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999
 C;Accession: S28942
 R;Basta, P.; Strickland, M.B.; Holmes, W.; Loomis, C.R.; Ballas, L.M.; Burns, D.J.
 Biochim. Biophys. Acta 1132, 154-160, 1992
 A;Title: Sequence and expression of human protein kinase C-epsilon.
 A;Reference number: S28942; MUID:93003318; PMID:1382605
 A;Accession: S28942
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-737 <BAS>
 A;Cross-references: EMBL:X65293; NID:G35494; PIDN:CAA46188.1; PID:G35495
 C;Comment: This is a calcium-independent, phospholipid-dependent, serine- and threonine-
 of inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester

C;Genetics:
 A;Gene: GDB:PRKCE
 A;Cross-references: GDB:128039; OMIM:176975
 A;Map position: 3pter-3qter
 C;Function:
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-thre
 A;Note: activity is calcium-independent, phospholipid-dependent, and activated by di
 C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology;
 C;Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotri
 F;156-161/Region: pseudophosphorylation motif
 F;170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
 F;243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
 F;406-668/Domain: protein kinase ATP-binding motif
 F;414-422/Region: protein kinase ATP-binding motif
 F;170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F;183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F;243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F;437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 77.6%; Score 38; DB 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 MLLGKPPFE 9
 : : : : :
 Db 600 MMAGQPPFE 608

RESULT 30
 KIRTCF
 protein kinase C (EC 2.7.1.1) epsilon - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C;Accession: B28163; B26408; S00216
 R;Ono, Y.; Fujii, T.; Ogita, K.; Kikkawa, U.; Igarashi, K.; Nishizuka, Y.
 J. Biol. Chem. 263, 6927-6932, 1988
 A;Title: The structure, expression, and properties of additional members of the prot
 A;Reference number: A92717; MUID:88198270; PMID:2834397
 A;Accession: B28163
 A;Molecule type: DNA
 A;Residues: 1-737 <ONC>
 A;Cross-references: GB:M18331; NID:G206182; PIDN:AAA41872.1; PID:G206183
 R;Housey, G.M.; O'Brian, C.A.; Johnson, M.D.; Kirschmeier, P.; Weinstein, I.B.
 Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987
 A;Title: Isolation of cDNA clones encoding protein kinase C: evidence for a protein
 A;Reference number: A94145; MUID:87147193; PMID:3469647
 A;Accession: B26408
 A;Molecule type: mRNA
 A;Residues: 397-447; GORGLHDDREDFGSGAET', 467, 'LSNPITLLLPDQGPPLLRQ', 487-545, 'C', 547-
 A;Cross-references: GB:M15523; NID:G206192; PIDN:AAA41877.1; PID:G206193
 C;Comment: Protein kinase C epsilon and epsilon' appear to be encoded by the same ge
 C;Function:
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-thre
 A;Note: activity is calcium-independent, phospholipid-dependent, and activated by di
 C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology
 C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; phorbol est

Query Match 77.6%; Score 38; DB 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
| : |||||
DB 600 MMAGQPPPE 608

RESULT 31

KIMSCE
protein kinase C (EC 2.7.11.-) epsilon - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
C:Accession: S02270
R:Schaap, D.; Parker, P.J.; Bristol, A.; Kriz, R.; Knopf, J.
FEBS Lett. 243, 351-357, 1989
A:Title: Unique substrate specificity and regulatory properties of PKC-epsilon: a rational
A:Reference number: S02270; MUID:89137541; PMID:2917656
A:Accession: S02270
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-737 <SCH>
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; p
C:Keywords: ATP; autophosphorylation; duplication; phospholipid binding; phospholipid B
F:156-161/Region: pseudophosphorylation motif
F:170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F:243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F:406-668/Domain: protein kinase homology <KIN>
F:414-422/Region: protein kinase ATP-binding motif
F:170,201,204,220/Binding site: zinc (His, Cys, Cys) #status predicted
F:183,166,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:243,273,276,292/Binding site: zinc (Cys, Cys, Cys, Cys) #status predicted
F:256,259,281,294/Binding site: zinc (His, Cys, His, Cys) #status predicted
F:437,456,532,534/Active site: Cys, Glu, Asp, Lys #status predicted
F:703,710/Binding site: phosphate (Thr) (covalent) #By autophosphorylation) #status pred

Query Match 77.6%; Score 38; DB 1; Length 737;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
| : |||||
DB 600 MMAGQPPPE 608

RESULT 32

A55748
protein kinase (EC 2.7.1.37) Sak-a - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Sep-1999
C:Accession: A55748
R:Fode, C.; Notro, B.; Yousefi, S.; Heflein, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosophila
A:Reference number: A55748; MUID:94294387; PMID:8022793
A:Accession: A55748
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-925 <FOD>
A:Cross-references: GB:L29479; NID:G487869; PIDN:AAC37648.1; PID:G487870
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
C:Keywords: ATP; phosphotransferase
F:10-265/Domain: protein kinase homology <KIN>
F:18-26/Region: protein kinase ATP-binding motif

Query Match 77.6%; Score 38; DB 2; Length 925;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
| : |||||
DB 204 LL:GRPPFD 212

RESULT 33

S51899
probable protein kinase HRC1081 (EC 2.7.11.-) - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein O0784; protein Y0L100W
C:Species: Saccharomyces cerevisiae
C:Date: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 19-Apr-2002
C:Accession: S51899; S59175; S66796
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, January 1995
A:Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV includ
and a Delta.
A:Reference number: S51848
A:Accession: S51899
A:Molecule type: DNA
A:Residues: 1-1081 <VAN>
A:Cross-references: EMBL:Z48149; NID:G663234; PIDN:CAA88162.1; PID:G663254
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995
A:Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including t
a delta element.
A:Reference number: S59156; MUID:96076631; PMID:7502582
A:Accession: S59175
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1081 <VAW>
A:Cross-references: EMBL:Z48149; NID:G663234; PIDN:CAA88162.1; PID:G663254
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R:Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66791
A:Accession: S66796
A:Molecule type: DNA
A:Residues: 1-1081 <DUR>
A:Cross-references: EMBL:Z74842; NID:G1419951; PIDN:CAA99113.1; PID:e251892; PID:G141
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:PKH2
A:Cross-references: SGD:S0005460
A:Map position: 15L
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; phosphotransferase
F:177-443/Domain: protein kinase homology <KIN>
F:185-193/Region: protein kinase ATP-binding motif

Query Match 77.6%; Score 38; DB 2; Length 1081;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
| : |||||
DB 382 MIAGKPPPK 390

RESULT 34

T29223
hypothetical protein F55G1.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T29223
R:Murray, J.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid F55G1.
A:Reference number: Z20591
A:Accession: T29223
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-615 <MUR>
A:Cross-references: EMBL:U58750; PIDN:AAB00642.1; GSPDB:GN00022; CESP:F55G1.8
A:Experimental source: strain Bristol N2; clone F55G1
C:Genetics:
A:Gene: CESP:F55G1.8

A:Map position: 4
 A:Introns: 103/3; 201/1; 238/3; 372/3; 413/3; 525/3
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 75.5%; Score 37; DB 2; Length 616;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY : MLLGKPPFE 9
 |||
 Db 225 LLFGSPPE 233

RESULT 35

G89894

protein kinase [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: G89894

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, K.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:12418146

A:Accession: G89894

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-664 <KUR>

A:Cross-references: GB:BA000018; PID:31701020; PIDN:BA842315.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA1063

Query Match 75.5%; Score 37; DB 2; Length 664;
 Best Local Similarity 75.0%; Pred. No. 44;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY : MLLGKPPF 8
 |||
 Db 202 MLVGPPE 209

RESULT 36

KIMUCA

protein kinase C (EC 2.7.11.-) alpha - human

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999

C:Accession: S09496

R:Finkenzeller, G.; Marme, D.; Hug, H.

Nucleic Acids Res. 18, 2183, 1990

A:Title: Sequence of human protein kinase C alpha.

A:Reference number: S09496; MUID:90245676; PMID:2316401

A:Accession: S09496

A:Molecule type: mRNA

A:Residues: 1-672 <FIN>

A:Cross-references: EMBL:X52479; NID:g35482; PIDN:CAA30718.1; PID:g35483

C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters.
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
 C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.

C:Genetics:

A:Gene: GDB:PRKCA

A:Cross-references: GDB:128015; OMIM:176940

A:Map position: 17q22-17q23.2

C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase

C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding

F:19-29/Region: phospholipid binding #status experimental

F:22-27/Region: pseudophosphorylation motif

F:37-86/Domain: protein kinase C zinc-binding repeat homology <KZ1>

F:102-151/Domain: protein kinase C zinc binding repeat homology <KZ2>

F:152-264/Domain: protein kinase C C2 region homology <KC2>

F:337-597/Domain: protein kinase homology <KIN>

F:345-353/Region: protein kinase ATP-binding motif
 F:37,67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:50,53,75,78/Binding site: zinc (Cys, His, Cys, His, Cys) #status predicted
 F:102,132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:368/Active site: Lys #status predicted
 F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 75.5%; Score 37; DB 1; Length 672;
 Best Local Similarity 66.7%; Pred. No. 45;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY : MLLGKPPFE 9
 |||
 Db 531 MLAGQPPFD 539

RESULT 37

KIRTC

protein kinase C (EC 2.7.11.-) alpha - rat

N:Alternate names: protein kinase C type III

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999

C:Accession: S02248; S02620

R:Ono, Y.; Fujii, T.; Igarashi, K.; Kikkawa, U.; Ogita, K.; Nishizuka, Y.

Nucleic Acids Res. 16, 5199-5200, 1988

A:Title: Nucleotide sequences of cDNAs for alpha and gamma subspecies of rat brain p,

A:Reference number: S02129; MUID:88262515; PMID:3387228

A:Accession: S02248

A:Molecule type: mRNA

A:Residues: 1-672 <ONO>

A:Cross-references: EMBL:X07286; NID:g56913; PIDN:CAA30266.1; PID:g56914

C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
 C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.

C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein

C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding

F:19-29/Region: phospholipid binding #status experimental

F:22-27/Region: pseudophosphorylation motif

F:37-86/Domain: protein kinase C zinc-binding repeat homology <KZ1>

F:102-151/Domain: protein kinase C zinc-binding repeat homology <KZ2>

F:152-264/Domain: protein kinase C C2 region homology <KC2>

F:337-597/Domain: protein kinase homology <KIN>

F:345-353/Region: protein kinase ATP-binding motif

F:368/Active site: Lys #status predicted

F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 75.5%; Score 37; DB 1; Length 672;
 Best Local Similarity 66.7%; Pred. No. 45;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY : MLLGKPPFE 9
 |||
 Db 531 MLAGQPPFD 539

RESULT 38

KIMSCA

protein kinase C (EC 2.7.11.-) alpha - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999

C:Accession: S07104; JS0078

R:Megidish, T.; Mazurek, N.

Nature 342, 807-811, 1989

A:Title: A mutant protein kinase C that can transform fibroblasts.

A:Reference number: S07104; MUID:90098082; PMID:2601739

A:Accession: S07104

A:Molecule type: mRNA

A:Residues: 1-672 <MEG>

A:Cross-references: GB:X52685; GB:X51603; NID:g49938; PIDN:CAA36908.1; PID:g49939

A:Experimental source: strain Balb/c

R:Rose-John, S.; Dietrich, A.; Marks, F.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

QM protein - protein search, using sw model

Run on: November 14, 2003, 12:56:44 ; Search time 6.6871 Seconds
(without alignments)
63.305 Million cell updates/sec

Title: US-09-736-076 17
Perfect score: 49
Sequence: 1 MLLGKPPFE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Fred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	46	93.9	682	1 SNK_MOUSE	P53351 mus musculus
2	46	93.9	682	1 SNK_RAT	Q95C12 rattus norv
3	46	93.9	685	1 SNK_HUMAN	Q9NYV3 homo sapien
4	43	97.8	282	1 STK5_MOUSE	C88445 mus musculus
5	43	87.8	603	1 PLK1_HUMAN	P53350 homo sapien
6	43	87.8	603	1 PLK1_MOUSE	Q27832 mus musculus
7	43	87.8	603	1 PLK1_RAT	Q52673 rattus norv
8	41	83.7	403	1 STK6_HUMAN	Q14965 homo sapien
9	41	83.7	407	1 STK6_XENLA	Q15820 xenopus lae
10	41	83.7	408	1 ST6L_XENLA	Q91819 xenopus lae
11	41	83.7	683	1 PLO1_SCHPO	P50528 schizosacch
12	41	83.7	705	1 CDC5_YEAST	P32562 saccharomyc
13	39	79.6	465	1 KPK1_ARATH	P42818 arabidopsis
14	39	79.6	471	1 KPL9_ARATH	Q19030 arabidopsis
15	39	79.6	576	1 POLO_DROME	P52304 drosophila
16	39	79.6	679	1 KPC1_DROME	P05130 drosophila
17	38	77.6	156	1 STKC_FIG	Q97CX0 sus scrofa
18	38	77.6	344	1 STKC_HUMAN	Q96gd4 homo sapien
19	38	77.6	525	1 KBN8_YEAST	P38070 saccharomyc
20	38	77.6	634	1 KPC3_DROME	P13678 drosophila
21	38	77.6	646	1 PKN1_CORGL	Q8RU98 corynebacte
22	38	77.6	649	1 PLK1_CAEEL	P34331 caenorhabdi
23	38	77.6	707	1 KPC2_CAEEL	P34895 caenorhabdi
24	38	77.6	736	1 KPCE_RABIT	P10830 oryctolagus
25	38	77.6	737	1 KPCE_HUMAN	Q2156 homo sapien
26	38	77.6	737	1 KPCE_MOUSE	P16054 mus musculus
27	38	77.6	737	1 KPCE_RAT	P09216 rattus norv
28	38	77.6	743	1 KPC2_AFLCA	Q16975 aplysia cal
29	38	77.6	1081	1 KOK3_YEAST	Q12236 saccharomyc
30	37	75.5	615	1 PLK3_CAEEL	Q20845 caenorhabdi
31	37	75.5	649	1 KPC1_AFLCA	Q16974 aplysia cal
32	37	75.5	658	1 KPC1_LYTP1	Q25378 lytechinus
33	37	75.5	672	1 KPCA_BOVIN	P04409 bos taurus

34	37	75.5	672	1 KPCA_HUMAN	P17252 homo sapien
35	37	75.5	672	1 KPCA_MOUSE	P20444 mus musculus
36	37	75.5	672	1 KPCA_RABIT	P10102 oryctolagus
37	37	75.5	672	1 KPCA_RAT	P05696 rattus norv
38	37	75.5	682	1 KPCG_BOVIN	P05128 bos taurus
39	37	75.5	697	1 KPCG_HUMAN	P05129 homo sapien
40	37	75.5	697	1 KPCG_MOUSE	P05697 mus musculus
41	37	75.5	697	1 KPCG_RABIT	P10829 oryctolagus
42	36	73.5	217	1 NU2M_MYTED	Q00229 mytilus edu
43	36	73.5	309	1 STKD_HUMAN	Q9UQB9 homo sapien
44	36	73.5	343	1 STKC_RAT	O55099 rattus norv
45	36	73.5	345	1 STKC_MOUSE	O70126 mus musculus

ALIGNMENTS

RESULT 1

SNK_MOUSE

ID SNK_MOUSE STANDARD; PRT; 682 AA.

AC P53351;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Serine/threonine-protein kinase SNK (EC 2.7.1.-) (Serum inducible kinase)

GN SNK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92375085; PubMed=1508211;

RA Simmons D.L., Neel B.G., Stevens R., Evett G., Erikson R.L.;

RT "Identification of an early-growth-response gene encoding a novel

putative protein kinase.";

RL Mol. Cell. Biol. 12:4164-4169(1992).

CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL

TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS,

WOUND HEALING OR NEOPLASIA.

-!- TISSUE SPECIFICITY: BRAIN, LUNG AND HEART.

-!- INDUCTION: BY SERUM AND PHORBOL ESTER.

-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CDG5/POLO SUBFAMILY.

-!- SIMILARITY: Contains 2 POLO box domains.

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EMBL; M96163; -; NOT ANNOTATED_CDS.

PIR; A44493; A44493.

MGI; MGI:1099790; Snk.

InterPro; IPR000959; POLO_box.

InterPro; IPR000719; Prot_kinase.

InterPro; IPR002290; Ser_thr_kinase.

Pfam; PF00069; pkinase; 1.

Pfam; PF00659; POLO_box; 2.

ProDom; PD000001; Prot_kinase; 1.

SMART; SM00220; S_TKc; 1.

PROSITE; PS00078; POLO_BOX; 2.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

XW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.

FT DOMAIN 54 59 POLY-HIS.

FT DOMAIN 79 93 PROTEIN KINASE.

FT NP_BIND 85 93 ATP (BY SIMILARITY).

FT BINDING 108 108 ATP (BY SIMILARITY).
 FT ACT_SITE 202 202 BY SIMILARITY.
 FT DOMAIN 507 570 POLO BOX 1.
 FT DOMAIN 603 674 POLO BOX 2.
 SQ SEQUENCE 682 AA; 77811 MW; 586DEA9FD72C8A9D CRC64;
 Query Match 93.9%; Score 46; DB 1; Length 682;
 Best Local Similarity 88.9%; Pred. No. 0.35;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPFE 9
 DB 270 MLLGKPPFE 278
 RESULT 2
 SNK_RAT STANDARD; PRT; 682 AA.
 AC Q9R012;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine-protein kinase SNK (EC 2.7.1.-) (Serum inducible kinase).
 GN SNK.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99452760; PubMed=10523297;
 RA Kausermann G., Weiler M., Wulff P., Jessberger S., Konietzko U., Scafield J., Staubli U., Bererter-Hahn J., Streibhardt K., Kuhl D.;
 RT "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and integrin-binding protein and are regulated dynamically with synaptic plasticity";
 RT EMBO J. 18:5528-5539(1999).
 CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC5/POLO SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 POLO box domains.
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 DR EMBL: AF136583; AAF08366.1;
 DR InterPro: IPR000959; POLO box.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PFC0659; POLO_box; 2.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PSS00078; POLO_BOX; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
 FT DOMAIN 54 59 POLY-HIS
 FT DOMAIN 79 331 PROTEIN_KINASE
 FT NP_BIND 85 93 ATP (BY SIMILARITY).
 FT BINDING 108 108 ATP (BY SIMILARITY).
 FT ACT_SITE 202 202 BY SIMILARITY.
 FT DOMAIN 507 570 POLO BOX 1.
 FT DOMAIN 603 674 POLO BOX 2.

SQ SEQUENCE 682 AA; 77919 MW; 58C50DEBDE83D5F3 CRC64;
 Query Match 93.9%; Score 46; DB 1; Length 682;
 Best Local Similarity 88.9%; Pred. No. 0.35;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPFE 9
 DB 270 MLLGKPPFE 278
 RESULT 3
 SNK_HUMAN STANDARD; PRT; 685 AA.
 AC Q9NY3; O60679; Q96CV7; Q9UE61;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Serine/threonine-protein kinase SNK (EC 2.7.1.-) (Serum inducible kinase).
 GN SNK.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Ouyang B., Dai W.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Anderson K.M., Nerurkar S.S., Hansbury M.J., Fornwald J., Scott G., Bouzyk M., Mui P., Imbruglia C.S., Carlson K., Marshall L.A., Roshak A.K.;
 RT "Identification and characterization of human serum-inducible kinase (SNK), a novel member of the polo-kinase family of cell cycle regulators: potential implication for regulation of vascular smooth muscle proliferation";
 RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Sodergren E.J., Lu X., Gibbs R.A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (4)
 RP SEQUENCE OF 110-408 FROM N.A.
 RA Fidler C., Boulwood J., Wang Jabs E., Wainscoat J.S.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC5/POLO SUBFAMILY.


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CC -!- SIMILARITY: Contains 2 POLO box domains.
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CC -----
CC EMBL: AF059617; AAC14573.1; -
CC EMBL: AF223574; AAF62897.1; -
CC EMBL: U85755; AAD00575.1; -
CC EMBL: BC013879; AAH13879.1; -
CC MIM: 607023; -
CC InterPro: IPR000959; POLO_box.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF00659; POLO_box; 2.
CC ProDom: PD000003; Prot_kinase; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS00078; POLO_BOX; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP binding; Repeat.
KW DOMAIN 57 64 POLY-HIS.
FT DOMAIN 57 64 POLY-HIS.
FT NP_BIND 82 334 PROTEIN_KINASE.
FT BINDING 88 96 ATP (BY SIMILARITY).
FT BINDING 111 111 ATP (BY SIMILARITY).
FT ACT_SITE 205 205 BY SIMILARITY.
FT DOMAIN 510 573 POLO_BOX_1.
FT DOMAIN 606 677 POLO_BOX_2.
FT CONFLICT 28 28 A -> G (IN REF. 1).
SQ SEQUENCE 685 AA; 78236 MW; 642956EFD830B33 CRC64;

Query Match 93.9%; Score 46; DB 1; Length 685;
Best Local Similarity 88.9%; Pred. No. 0.35;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
   |||||
DB 273 MLLGKPPFE 281

RESULT 4
STKC_MOUSE
ID STKC_MOUSE STANDARD; PRT; 281 AA
AC O8945; Q9JLC2;
DT 28-FEB-2003 (Rel. 41, Created);
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Serine/threonine protein kinase 13 (EC 2.7.1.37) (Aurora/Ipl1/Eg2
protein 1) (Aurora-C).
GN STK13 OR AIE1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1]
RE SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=99025616; PubMed=9809744;
RA Tseng T.C., Chen S.H., Hsu Y.P., Tang T.K.
RT "Protein kinase profile of sperm and eggs: cloning and
characterization of two novel testis-specific protein kinases (AIE1,
AIE2) related to yeast and fly chromosome segregation regulators."
RD CNA Cell Biol. 17:823-833(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=20551164; PubMed=11048210;
```

```
RA Hu H.M., Chuang C.K., Lee M.J., Tseng T.C., Tang T.K.;
RT "Genomic organization, expression, and chromosome localization of a
third aurora-related kinase gene, Aie1."
RD DNA Cell Biol. 19:679-688(2000).
CC -!- FUNCTION: May play a part in organizing microtubules in relation
CC to the function of the centrosome/spindle pole during mitosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to spindle pole from anaphase to
CC cytokinesis (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed only in testis.
CC -!- DEVELOPMENTAL STAGE: Expressed on day 14 dpc in prepubertal
CC testis, expression reached its plateau on day 21 dpc and remained
CC at a high level in adult.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF054620; AAC25954.1; -
CC EMBL: AF195272; AAF25838.1; -
CC HSSP: Q63450; 1A06.
CC MGD: MGI:1321119; Stk13.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC InterPro: IPR001245; Tyr_kinase.
CC Pfam: PF00069; pkinase; 1.
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000003; Prot_kinase; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW Cell cycle; Transferrase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 16 266 PROTEIN_KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT CONFLICT 74 74 R -> P (IN REF. 2).
SQ SEQUENCE 282 AA; 32907 MW; 7CB8AEC4984B7883 CRC64;

Query Match 87.8%; Score 43; DB 1; Length 282;
Best Local Similarity 77.8%; Pred. No. 0.54;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
   |||||
DB 205 LLVGKPPFE 213

RESULT 5
PLK1_HUMAN
ID PLK1_HUMAN STANDARD; PRT; 603 AA.
AC P53350;
DT 01-OCT-1996 (Rel. 34, Created);
DT 01-OCT-1996 (Rel. 34, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Serine/threonine-protein kinase PLK (EC 2.7.1.-) (PLK-1) (Serine-
threonine protein kinase 13) (STPK13).
GN PLK OR PLK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94289253; PubMed=8016357;
```


RC STRAIN=C57BL/6; TISSUE=Bone marrow;
RX MEDLINE=93281660; PubMed=8099445;
RA Clay F.J., McEwen S.J., Bertonecello I., Wilks A.F., Dunn A.R.;
RT "Identification and cloning of a protein kinase-encoding mouse gene,
RT Plk, related to the polo gene of Drosophila";
RJ Proc. Natl. Acad. Sci. U.S.A. 90:4882-4886(1993).
RN (2);
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=94289293; PubMed=8018557;
RA Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.B.,
RA Ferris D.K.;
RT "Cloning and characterization of human and murine homologues of the
RT Drosophila polo serine-threonine kinase";
RL Cell Growth Differ. 5:249-257(1994).
RV [3];
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=94067140; PubMed=7902533;
RA Lake R.J., Jelinek W.R.;
RT "Cell cycle- and terminal differentiation-associated regulation of
RT the mouse mRNA encoding a conserved mitotic protein kinase";
RL Mol. Cell. Biol. 13:7793-7801(1993).
CC -!- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: NEWBORN AND ADULT SPLEEN, FETAL AND NEWBORN
CC KIDNEY, LIVER, BRAIN, THYMUS AND ADULT BONE MARROW, THYMUS,
CC OVARY AND TESTES.
CC -!- DEVELOPMENTAL STAGE: IN THE THYMUS, LEVELS INCREASED DURING FETAL
CC DEVELOPMENT, WERE HIGHEST IN NEWBORN ANIMALS AND DECREASED IN THE
CC ADULT. IN THE TESTES, THE PLK LEVELS WERE HIGHER IN THE ADULT THAN
CC IN PREPUBESCENT MICE WHILE IN THE OVARY, THE LEVELS WERE HIGHER IN
CC THE PREPUBESCENT MICE. ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
CC DURING S PHASE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L06144; AAA39948.1; -;
DR EMBL: U01063; AAA56635.1; -;
DR EMBL: L19558; AAA16071.1; -;
DR PIR: A47545; A47545;
DR PIR: A54596; A54596;
DR MGI: 97621; Plk.
DR InterPro: IPR000959; POLO box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00659; pkinase; 1.
DR Pfam: PF00659; POLO box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00078; POLO BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR TRANSFERASE: Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Nuclear protein.
KW DOMAIN 53 305 PROTEIN KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 450 POLO BOX 1.
FT DOMAIN 417 450

FT DOMAIN 515 584 POLO BOX 2.
FT CONFLICT 4 4 A -> V (IN REF. 1).
FT CONFLICT 15 15 A -> T (IN REF. 1).
FT CONFLICT 23 23 P -> L (IN REF. 1).
FT CONFLICT 27 27 V -> A (IN REF. 1).
FT CONFLICT 29 29 G -> S (IN REF. 1).
FT CONFLICT 41 41 P -> L (IN REF. 1).
FT CONFLICT 54 54 V -> I (IN REF. 1).
FT CONFLICT 495 495 A -> R (IN REF. 1).
SQ SEQUENCE 603 AA; 68300 MW; 1B980646366EFA10 CRC64;
Query Match 87.8%; Score 43; DB 1; Length 603;
Best Local Similarity 77.8%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
DB 244 LLVGKPPFE 252
RESULT 7
PLK1_RAT
ID PLK1_RAT STANDARD; PRT; 603 AA.
AC Q62673;
DT 16-OCT-2001 (Rel. 40, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update);
DT 16-OCT-2001 (Rel. 40, Last annotation update);
DE Serine/threonine-protein kinase PLK (EC 2.7.1.-) (PLK-1).
GN PLK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Amstrup J., Hansen J.A., Hxirlis Nielsen J.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U01088; AAA18885.1; -;
DR InterPro: IPR000959; POLO box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00659; pkinase; 1.
DR Pfam: PF00659; POLO box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00078; POLO BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR TRANSFERASE: Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Nuclear protein.
KW DOMAIN 53 305 PROTEIN KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 480 POLO BOX 1.
FT DOMAIN 515 584 POLO BOX 2.

SQ SEQUENCE 603 AA; 68313 MW; 107AFFB3B7EDCC02 CRC64;

Query Match 87.8%; Score 43; DB 1; Length 603;

Best local Similarity 77.8%; Pred. No. 1.2;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9

DB 244 LLVGKPPFE 252

RESULT 8

STK6_HUMAN STANDARD; PRT; 403 AA.

AC C14955; O60445; O75873; Q9BQD6; Q9UPG5;

DT 28-FEB-2003 (Rel. 41, Created;

DT 28-FEB-2003 (Rel. 41, Last sequence update);

DT 15-SEP-2003 (Rel. 42, Last annotation update);

DE Serine/threonine kinase 6 (EC 2.7.1.37) (Serine/threonine kinase 15)

DE (Aurora/TPK2-related kinase 1) (Aurora-related kinase 1) (BARK1)

DE (Aurora-A) (Breast-tumor-amplified kinase).

GN STK6 OR STK15 OR AIK OR ARK1 OR AURA OR BTK.

OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=97298083; PubMed=9153231;

RA Kimura M., Kotani S., Hattori T., Sumi N., Yoshioka T., Todokoro K.,

RA Okano Y.;

PT "Cell cycle-dependent expression and spindle pole localization of a

PT novel human protein kinase, Aik, related to Aurora of Drosophila and

RT yeast tpk1.";

RL J. Biol. Chem. 272:13766-13771(1997);

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98183439; PubMed=9514916.

RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,

RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;

RT "cDNA cloning, expression, subcellular localization, and chromosomal

RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)

RT 1 and 2.";

RL Biochem. Biophys. Res. Commun. 244:1026-1032(1998);

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Breast;

RX MEDLINE=98442657; PubMed=9771714;

RA Zhou H., Kuang J., Zhong L., Kuo W. L., Gray J.W., Sahin A.,

RA Brinkley B.R., Sen S.;

RT "Tumor amplified kinase STK15/BTK induces centrosome amplification,

RT aneuploidy and transformation.";

RL Nat. Genet. 20:189-193(1998);

RN [4]

RP SEQUENCE FROM N.A.

RA Wang L., Thibodeau S.N.;

RT "Mutational analysis of the STK15 gene in human tumors.";

RL Submitted (OCT-1999) to the EMBL/GenBank/CCDB databases.

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=21638749; PubMed=11780052;

RA Delidakis P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

RA Beasley C.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,

RA Ellington A.G., Frankland J.A., Fraser A., French P., Garner P.,

RA Grainger D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Levaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McJay K., McMurray A.A.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,

RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RA Rogers J.;

RT "The DNA sequence and comparative analysis of human chromosome 20.";

RL Nature 414:865-871(2001).

RN [6]

RP SEQUENCE FROM N.A.

RC TISSUE=Cervix, Colon, Kidney, and Muscle;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bontado M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Shevchenko Y., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Sodergren E.J., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [7]

RP CELL-CYCLE REGULATION

RX MEDLINE=21895866; PubMed=11790771;

RA Tanaka M., Ueda A., Kanamori H., Ideguchi H., Yang J., Kitajima S.,

RA Ishigatsubo Y.;

RT "Cell-cycle-dependent regulation of human aurora A transcription is

RT mediated by periodic repression of E4TF1.";

RL J. Biol. Chem. 277:10719-10726(2002).

RN [8]

RP REVIEW

RX MEDLINE=21306577; PubMed=11413462;

RA Nigg E.A.;

RT "Mitotic kinases as regulators of cell division and its checkpoints.";

RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).

CC -!- FUNCTION: May play a role in cell cycle regulation during anaphase

CC and/or telophase, in relation to the function of the

CC centrosome/spindle pole region during chromosome segregation.

CC Maybe involved in microtubule formation and/or stabilization. May

CC play a key role during tumor development and progression.

CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -!- SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells

CC and at each spindle pole in mitosis.

CC -!- TISSUE SPECIFICITY: Highly expressed in testis and weakly in

CC skeletal muscle, thymus and spleen. Also highly expressed in

CC colon, ovarian, prostate, neuroblastoma, breast and cervical

CC cancer cell lines. Expression is cell-cycle regulated, low in

CC G1/S, accumulates during G2/M, and decreases rapidly after.

CC -!- PTM: Phosphorylated.

CC -!- DISEASE: Defects in STK6 are responsible for numerical centrosome

CC aberrations including aneuploidy.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC AUROA SUBFAMILY.

CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts

CC in positions 105, 125, 129, 235 and 241.
 CC -!- CAUTION: Although authors have considered STK6 and STK15 as two
 CC different proteins, it is clear that they are the same protein.
 CC -----
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 CC -----
 CC EMBL: D84212; SAA2352.1; ALT_FRAME
 CC EMBL: AF038551; AAC12708.1; -
 CC EMBL: AF011467; AAC23448.1; -
 CC EMBL: AF011468; AAC63902.1; -
 CC EMBL: AF195947; AAF29508.1; -
 CC EMBL: AF195942; AAF29508.1; JOINED.
 CC EMBL: AF195943; AAF29508.1; JOINED.
 CC EMBL: AF195944; AAF29508.1; JOINED.
 CC EMBL: AF195945; AAF29508.1; JOINED.
 CC EMBL: AF195946; AAF29508.1; JOINED.
 CC EMBL: AL121914; CAC12717.1; -
 CC EMBL: BC001280; AAH01280.1; -
 CC EMBL: BC002499; AAH02499.1; -
 CC EMBL: BC006423; AAH06423.1; -
 CC EMBL: BC027464; AAH27464.1; -
 CC GK: C14965; -
 CC MIM: 602687; -
 CC MIM: 603072; -
 CC HSSP: P24941; 1BUH.
 CC Genew: HGNC:11409; STK6.
 CC Genew: HGNC:11393; STK15.
 CC GO: GO:0005634; C:nucleus; TAS.
 CC GO: GO:0005819; C:spindle; TAS.
 CC GO: GO:0007067; P:mitosis; TAS.
 CC GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_kinase.
 CC InterPro: IPR01245; Tyr_kinase.
 CC Pfam: PF00069; pkinase; 1.
 CC ProDom: PD000001; Prot_kinase; 1.
 CC SMART: SMC0220; S_TKC; 1.
 CC SMART: SMC0219; TyrKC; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00103; PROTEIN_KINASE_ST; 1.
 CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 CC Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
 CC Phosphorylation.
 CC DOMAIN 133 383 PROTEIN KINASE.
 CC NP_BIND 139 147 ATP (BY SIMILARITY).
 CC BINDING 162 162 ATP (BY SIMILARITY).
 CC ACT_SITE 256 256 BY SIMILARITY.
 CC CONFLICT 31 31 F -> I (IN REF. 2).
 CC CONFLICT 57 57 V -> I (IN REF. 2).
 CC SEQUENCE 403 AA; 45809 MW; 125F1594834C0157 CRC64;
 CC -----
 CC Query Match 83.7%; Score 41; DB 1; Length 403;
 CC Best Local Similarity 87.5%; Pred. No. 1.9;
 CC Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 2 LLGKPPFE 9
 CC Db 323 LVGKPPFE 330
 CC :|||
 CC -----
 CC RESULT 9
 CC STK6_XENLA STANDARD; PRT; 407 AA.
 CC AC Q91820;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serine/threonine protein kinase Eg2 (EC 2.7.1.37) (pEg2) (p46Eg265).
 GN EG2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Egg;
 RX MEDLINE=98122855; PubMed=9454730;
 RA Roghi C., Giet R., Uzbekov R., Morin N., Chartrain I., Le Guellec R.,
 RA Couturier A., Doree M., Philippe M., Prigent C.;
 RT "The Xenopus protein kinase pEg2 associates with the centrosome in a
 RT cell cycle-dependent manner, binds to the spindle microtubules and is
 RT involved in bipolar mitotic spindle assembly.";
 RL J. Cell Sci. 111:557-572(1998).
 CC -!- FUNCTION: Associates with the centrosome in a cell-cycle dependent
 CC manner and invades the microtubules at the poles of the spindle
 CC during mitosis suggesting that it may be involved in the correct
 CC formation of bipolar mitotic spindles.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
 CC especially from prophase through anaphase. Partially colocalised
 CC with gamma tubulin in the centrosome, from S to M phase.
 CC -!- TISSUE SPECIFICITY: Highly expressed in ovary and testis.
 CC -!- PTM: Phosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC AURORA SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: Z17207; CAA78915.1; -
 CC PIR: S52243; S52243.
 CC HSSP: P24941; 1AQ1.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_kinase.
 CC Pfam: PF00069; pkinase; 1.
 CC ProDom: PD000001; Prot_kinase; 1.
 CC SMART: SMC0220; S_TKC; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
 CC Phosphorylation.
 CC DOMAIN 140 390 PROTEIN KINASE.
 CC NP_BIND 146 154 ATP (BY SIMILARITY).
 CC BINDING 169 169 ATP (BY SIMILARITY).
 CC ACT_SITE 263 263 BY SIMILARITY.
 CC SEQUENCE 407 AA; 46372 MW; DE1628A2C6D11277 CRC64;
 CC -----
 CC Query Match 83.7%; Score 41; DB 1; Length 407;
 CC Best Local Similarity 87.5%; Pred. No. 1.9;
 CC Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 2 LLGKPPFE 9
 CC Db 330 LVGKPPFE 337
 CC :|||
 CC -----
 CC RESULT 10
 CC ST6L_XENLA STANDARD; PRT; 408 AA.
 CC ID ST6L_XENLA
 CC AC Q91819;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serine/threonine protein kinase Eg2 like (EC 2.7.1.37) (p46X:Eg22).
OS Xenopus laevis (African clawed frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
CC Xeropodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RA Roghi C., Le Guellec R., Paris C., Couturier A., Philippe M.,
RT "Eg2, selected by differential screening encodes a new Xenopus protein
RT kinase family.";
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
CC especially from prophase through anaphase. Partially colocalised
CC with gamma tubulin in the centrosome, from S to M phase (By
CC similarity).
CC -!- PTM: Phosphorylated (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC
DR EMBL: Z17206; CAA78914.1; ALT_INIT.
DR HSSP: P24941; IAQ1.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00369; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00223; S_TKc; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Cell cycle; Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 143 390 PROTEIN_KINASE.
FT NP_BIND 146 154 ATP_BIND_SIMILARITY.
FT BINDING 169 169 ATP_BIND_SIMILARITY.
FT ACT_SITE 263 263 HY_SIMILARITY.
SQ SEQUENCE 408 AA; 4646; MW: 91656.60735; pI: 5.464.

Query Match 83.7%; Score 41; DB: Length 408;
Best Local Similarity 87.5%; Pred. No. 109;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LUGKPPFE 9
|:|:|:|
DB 330 LUGKPPFE 337

RESULT 11
PLOC_SCHPO
ID PLOC_SCHPO STANDARD; PRT; 683 AA.
AC PS0528;
DT 01-OCT-1996 (Rel. 34, Created;
DT 01-OCT-1996 (Rel. 34, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Serine/threonine-protein kinase ploc (EC 2.7.1.37).
GN PLOC; OR SPAC23C11.16.
OS Schizosaccharomyces pombe (Fission yeast).
CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC Schizosaccharomycetes; Schizosaccharomycetaceae;
CC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=95262899; PubMed=7744248;
RA Ohkura H., Hagan J.M., Glover D.M.;
RT "The conserved Schizosaccharomyces pombe kinase ploc, required to
RT form a bipolar spindle, the actin ring, and septum, can drive septum
RT formation in G1 and G2 cells";
RL Genes Dev. 9:1059-1073(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Gobie A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borczyk K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Senito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: REQUIRED TO FORM A BIPOLAR SPINDLE, THE ACTIN RING AND
CC SEPTUM. FUNCTIONS UPSTREAM OF THE WHOLE SEPTUM FORMATION PATHWAY,
CC INCLUDING ACTIN RING FORMATION (REGULATED BY LATE SEPTATION GENES)
CC AND SEPTAL MATERIAL DEPOSITION (REGULATED BY EARLY SEPTATION
CC GENES). BEHAVES AS A "SEPTUM-PROMOTING FACTOR", AND COULD ALSO BE
CC INVOLVED IN INDUCING OTHER LATE EVENTS OF CELL DIVISION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
DR EMBL: X85758; CAA59766.1; -;
DR EMBL: Z98559; CAB11167.1; -;
DR PIR: T38254; T38254.
DR HSSP: Q63450; IA06.
DR GeneDB Spombe; SPAC23C11.16; -;
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00369; pkinase; 1.
DR Pfam: PF00659; POLO_box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS50078; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.


```
RL Nature 408:820-822(2000).
KN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Theologis A., Ecker J., Davis R.W.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shirozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFus) sequenced by the
RI SSP Consortium (Salk/Stanford/PGECC)";
RL Submitted (JUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY BE INVOLVED IN ADAPTATION OF PLANT TO COLD OR HIGH-
CC SALT CONDITIONS.
CC -!- PTM: UNDERGOES SERINE-SPECIFIC AUTOPHOSPHORYLATION (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC S6 KINASE SUBFAMILY.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to a
CC frameshift in position 391.
CC -----
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CC -----
DR EMBL: D42061; BAA07661.1;
DR EMBL: AC012562; AAG51345.1;
DR EMBL: AF325094; AAK17162.1;
DR EMBL: AY050826; AAK92761.1; ALT_FRAME.
DR F01: S68463; S68463.
DR HSSP: PC5132; ICTP.
DR InterPro: IPR000396; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00433; pkinase_C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; STK_X; 1.
DR SMART: SM00220; STK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
RW Phosphorylation.
FT DOMAIN 140 395 PROTEIN KINASE.
FT NP_BIND 146 154 ATP (BY SIMILARITY).
FT BINDING 169 169 ATP (BY SIMILARITY).
FT ACT_SITE 263 263 BY SIMILARITY.
FT CONFLICT 250 250 A -> V (IN REF. 1).
FT CONFLICT 359 360 LS -> VF (IN REF. 1).
SQ SEQUENCE 471 AA; 53037 MW; 95FC07B44B58CFB5 CRC64;

Query Match 79.6%; Score 39; DB 1; Length 471;
Best Local Similarity 87.5%; Pred.No. 5.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
   | | | | |
DB 330 YLTGKPPF 337

RESULT 15
POLO DROME
ID "POLO DROME STANDARD; PRT; 576 AA.
AC P52304; Q9VWB2;
DT 01-OCT-1996 (Rel. 34, Created)
ET 16-OCT-2001 (Rel. 40, Last sequence update);
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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase polo (EC 2.7.1.-).
GN POLO OR CG12306.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=92084090; PubMed=1660828;
RA Llamazares S., Moreira A., Tavares A., Girdham C., Spruce B.A.,
RA Gonzalez C., Kares R.E., Glover D.M., Sunkel C.E.;
RT "Polo encodes a protein kinase homolog required for mitosis in
RT Drosophila.";
RL Genes Dev. 5:2153-2165(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gortell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: MAY PLAY A ROLE IN REGULATING BOTH NUCLEAR AND
CC CYTOPLASMIC ASPECTS OF THE MITOTIC CYCLE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: LARVAL DISCS, BRAIN AND TESTIS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC -----
CC EMBL: X63361; CAA44963.1; -
CC EMBL: AE003514; AAF49036.1; -
CC PIR: S22127; S22127.
CC RSSP: Q63450; 1A06.
CC FlyBase; FBgn003124; polo.
CC GC: GO:0005813; C:centrosome; IDA.
CC GC: GO:0005819; C:spindle; IDA.
CC GC: GO:0004674; F:protein serine/threonine kinase activity; IDA.
CC GC: GO:0007140; P:male meiosis; IMP.
CC GC: GO:0007067; P:mitosis; IMP.
CC InterPro; IPR000959; POLO_box.
CC InterPro; IPR00719; Prot_kinase.
CC InterPro; IPR02290; Ser_thr_kinase.
CC Pfam; PFC0069; pkinase; 1.
CC Pfam; PFC0659; POLO_box; 2.
CC ProDom; PDC000031; Prot_kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS50078; POLO_BOX; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00138; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 25 277 PROTEIN_KINASE.
FT NP_BIND 31 39 ATP (BY SIMILARITY).
FT BINDING 54 54 ATP (BY SIMILARITY).
FT ACT_SITE 148 148 BY SIMILARITY.
FT DOMAIN 398 461 POLO_BOX_1.
FT DOMAIN 496 564 POLO_BOX_2.
FT CONFLICT 187 187 P -> A (IN REF 1).
SQ SEQUENCE 576 AA; 66973 MW; 5022B9AC0E809FAD CRC64;

Query Match 79.6%; Score 19; DP 1; Length 576;
Best Local Similarity 56.7%; Pred. No. 6.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGQPFPE 9
DB 216 MLLGQPFPE 224

RESULT 16
KPC1 DROME STANDARD; SRT; 19 AA.
AC P05130; G9V7V6; G9V7V7.
CT 13-AUG-1987 (Ref. 35, Created:
CT 28-FEB-2003 (Ref. 41, Last sequence update
CT 28-FEB-2003 (Ref. 41, Last annotation update
DE Protein kinase C, brain isozyme (EC 2.7.1.37) (PKC) (DPC053E1BR1).
GN PKC53E OR PKC1 OR CG6622.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
CX NCB: TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=Canton-S, and Oregon-R;
RX MEDLINE=87218499; PubMed=3107983;
RA Rosenthal A., Rhee L., Yadegari R., Faro R., Willich A., Goeddel D.V.;
RT "Structure and nucleotide sequence of a Drosophila melanogaster
RT protein kinase C gene.";
RJ ENDO J. 6:433-441(1987);
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731152;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Araratides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blake J.G., Champetier N., Pfeiffer B.D.,

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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster.";
RA Science 287:2185-2195(2000);
RL [3]
RN SEQUENCE FROM N.A. (ISOFORM LONG).
RP STRAIN=Berkeley; TISSUE=Ovary;
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Kronmiller B., Li P.W., Liac G.,
RA Miranda A., Murgail C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.E.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P05130-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P05130-2; Sequence=VSP_004743;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: HEAD NEURAL TISSUE.
CC -!- MISCELLANEOUS: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-
CC DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF OREGON-R.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. PKC
CC SUBFAMILY.
CC -----
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CC -----
CC EMBL: X05076; CAA28736.1; -
CC EMBL: X05279; CAA28890.2; -

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DR EMBL; X05280; CAA28890.2; JOINED.
DR EMBL; X05281; CAA28890.2; JOINED.
DR EMBL; X05282; CAA28890.2; JOINED.
DR EMBL; X05283; CAA28890.2; JOINED.
DR EMBL; AE033805; AAF57932.1; .
DR EMBL; AE033805; AAF57933.1; .
DR EMBL; AY095003; AAM11331.1; .
DR HSSP; P05697; ITBN.
DR FlyBase; FBgn0003032; Pkc53E.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR GO; GO:000468; P:protein amino acid phosphorylation; IDA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00168; C2_1; 1.
DR Pfam; PF00433; pkinase C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Multicene family; Zinc;
KW Phorbol-ester binding; Alternative splicing.
FT DOMAIN 46 104 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 120 169 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 191 278 C2 DOMAIN.
FT DOMAIN 350 608 PROTEIN KINASE.
FT NP_BIND 356 364 ATP (BY SIMILARITY).
FT BINDING 379 379 ATP (BY SIMILARITY).
FT ACT_SITE 474 474 BY SIMILARITY.
FT VARSPLOT 67 77 CGYCGGYAWMA -> W; (in isoform Short).
FT /FTID=VSP_004743.
FT M -> I.
FT VARIANT 437 437 F -> S (IN REF. 1).
FT CONFLICT 608 608 DVSNFDKQKTFSEKD -> NQITLTSSSHQKQT (IN
FT CONFLICT 634 648 REF. 1).
FT CONFLICT 649 679 MISSING (IN REF. 1).
FT SEQUENCE 679 AA; 77695 MW; 3069AD31E3687DC CRC64;
Query Match 79.6%; Score 39; DB 1; Length 679;
Best Local Similarity 66.7%; Pred. No. 718;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 1 MLLGKPPPE 9
DB 542 MLVGQPPPD 550
RESULT 17
STKC_PIG
ID STKC_PIG STANDARD; PRT; 156 AA.
AC Q9NCX0;
DT 28-FEB-2003 (Rel. 41, Created);
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora-B)
(Fragment).

GN STK12.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=2223238; PubMed=12270407;
RA Braun F., Hosseini S.M., Lorf T., Laabs S., Ringe B.;
RT "Differential gene expression during intestinal ischemia-reperfusion
injury";
RL Transplant. Proc. 34:2301-2302(2002).
CC -!- FUNCTION: Maybe directly involved in regulating the cleavage of
CC polar spindle microtubules and is a key regulator for the onset of
CC cytokinesis during mitosis (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
CC in late anaphase and concentrated into the midbody in telophase
CC and cytokinesis. Colocalized with gamma tubulin in the mid-body
CC (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC -----
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CC -----
DR EMBL; AF244364; AAF61735.1; .
DR InterPro; IPR002052; N6_Mtase.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP binding.
FT NON_TER 1 1
FT DOMAIN < >156 PROTEIN KINASE.
FT ACT_SITE 51 51 BY SIMILARITY.
FT NON_TER 156 156
FT SEQUENCE 156 AA; 17867 MW; CD23040EDB633FCS CRC64;
Query Match 77.6%; Score 38; DB 1; Length 156;
Best Local Similarity 66.7%; Pred. No. 2.7;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 MLLGKPPPE 9
DB 117 LLVGNPPPE 125
RESULT 18
STKC_HUMAN
ID STKC_HUMAN STANDARD; PRT; 344 AA.
AC Q96GD4; O14630; O60446; O95083; Q96DV5; Q9U046;
DT 28-FEB-2003 (Rel. 41, Created);
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora- and Ipl1-
DE like midbody-associated protein 1) (AIM-1) (Aurora/IPL1-related kinase
DE 2) (Aurora-related kinase 2) (STK-1) (Aurora-B).
GN STK12 OR AIM1 OR ARK2 OR AIK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;


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DT 01 OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16 OCT-2001 (Rel. 40, Last annotation update)
DE Probable serine/threonine-protein kinase YBR028C (EC 2.7.1.1).
GN YBR028C OR YBR0312.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycus.
OX NCBI_TaxID=4932;
RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94378725; PubMed=8091864;
RA Smits P.H.M., de Haan M., Maat C., Graveli L.A.;
RT "The complete sequence of a 33 kb fragment on the right arm of
RT chromosome II from Saccharomyces cerevisiae reveals 16 open reading
RT frames, including ten new open reading frames, five previously
RT identified genes and a homologue of the SGO1 gene."
RL Yeast 10:575-580(1994).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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CC -----
DR EMBL: X76078; CAA53684.1; .
DR EMBL: Z35897; CAA84970.1; .
DR PIR: S45684; S45894.
DR HSSP: P05132; ICTP.
DR SGL: SC000232; YBR028C.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00433; pkinase_C; 1.
DR ProDom: PDC0001; Prot_kinase; 1.
DR SMART: SM00123; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding.
FT DOMAIN 128 424 PROTEIN_KINASE
FT NP_BIND 134 142 ATP (BY SIMILARITY)
FT BINDING 157 157 ATP (BY SIMILARITY)
FT ACT_SITE 277 277 HY SIMILARITY
SC SEQUENCE 525 AA; 59591 MW; B8FFFAA44067677 CD; 4;

Query Match 77.6%; Score 38; E-1; Length 525;
Best local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLUGKPPF 8
EY 355 MLVGKPPY 362
.....

RESULT 20
KPC3_DROME
ID KPC3_DROME STANDARD: PRT: 614 AA.
AC P13678; Q9VAC6;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase C (EC 2.7.1.1) (PKC) (AKC098F).
GN PKC98E OR PKC3 OR CG1954.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

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OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89249302; PubMed=2720775;
RA Schaeffer E., Smith D., Mardon G., Quinn W., Zuker C.;
RT "Isolation and characterization of two new Drosophila protein kinase
RT C genes, including one specifically expressed in photoreceptor
RT cells."
RL Cell 57:403-412(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Prankkoch C., Baldwin D.,
RA Balliew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Shandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.H., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiaros Z., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stاپleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS.
CC -!- MISCELLANEOUS: THIS IS A CALCIUM-ACTIVATED,
CC PHOSPHOLIPID-DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL: J04848; AAA28818.1; .
DR EMBL: AE003768; AAP56946.1; ALT_INIT.

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DR FIR; B32392; B32392.
 DR HSP; P28867; IPTQ.
 DR FlyBase; FBgn030303; PKC98E.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00130; DAG_PE-bind; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM0133; S_TK_X; 1.
 DR SMART; SM0220; S_TK; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
 DR PROSITE; PS0081; DAG_PE_BIND_DOM_2; 2.
 DR PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Calcium-binding; Repeat; ATP-binding; Transferase;
 KW Serine/threonine-protein kinase; Multigene family; Zinc;
 KW Phorbol-ester binding.
 FT DOMAIN 72 121 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 147 196 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 303 560 PROTEIN KINASE.
 FT NP_BIND 309 317 ATP (BY SIMILARITY).
 FT BINDING 322 332 ATP (BY SIMILARITY).
 FT ACT_SITE 427 427 BY SIMILARITY.
 SQ SEQUENCE 634 AA; 71156 MW; 3AE2A3D6B2A276BA CRC64;

Query Match 77.6%; Score 38; DB 1; Length 634;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
 : : : : :
 DB 495 MMAGQPPPE 503

RESULT 2:

PKNI_CORGL STANDARD; PRT; 646 AA.
 AC Q8N338; 15-SEP-2003 (Rel. 42, Created);
 DT 15-SEP-2003 (Rel. 42, Last sequence update);
 DT 15-SEP-2003 (Rel. 42, Last annotation update);
 DE Probable serine/threonine protein kinase [Eukaryota] [EC 2.7.1.37].
 GN CGL3341.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriidae; Corynebacterium.
 OX NCBI_TaxID=1719;
 RN (1);
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RU Submitted (MAY-2002) to the EMBL/GenBank/CCBJ databases.
 CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -|- SIMILARITY: Contains 3 PASTA domains.
 CC
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 CC
 CC EMBL; AF005274; BAB97434.1;
 DR InterPro; IPR005543; PASTA.

DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF03793; PASTA; 3.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
 KW ATP-binding; Repeat; Complete proteome.
 FT DOMAIN 9 278 PROTEIN KINASE.
 FT DOMAIN 365 431 PASTA 1.
 FT DOMAIN 432 500 PASTA 2.
 FT DOMAIN 501 565 PASTA 3.
 FT NP_BIND 15 23 ATP (BY SIMILARITY).
 FT BINDING 38 38 ATP (BY SIMILARITY).
 FT ACT_SITE 136 136 BY SIMILARITY.
 SQ SEQUENCE 646 AA; 68237 MW; 0F3B4980ECF738FB CRC64;
 Query Match 77.6%; Score 38; DB 1; Length 646;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGKPPPE 9
 : : : : :
 DB 207 LVTKGPPPE 215
 RESULT 22
 PLK1_CAEEL STANDARD; PRT; 649 AA.
 AC P34331; G61662; O76763;
 DT 01-FEB-1994 (Rel. 28, Created);
 DT 28-FEB-2003 (Rel. 41, Last sequence update);
 DT 28-FEB-2003 (Rel. 41, Last annotation update);
 DE Serine/threonine-protein kinase pik-1 (EC 2.7.1.1-) (Polo-like
 DE kinase-1).
 GN PLK-1 OR PLC1 OR C14B9.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN (1);
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RX MEDLINE=99304501; PubMed=10376213;
 RA Ouyang B., Wang Y., Dai W.;
 RT "Caenorhabditis elegans contains structural homologs of human prk and
 RT pik-1.";
 RL DNA Seq. 10:109-113(1999).
 RN (2);
 RP SEQUENCE FROM N.A. (ISOFORM A), FUNCTION, AND SUBCELLULAR LOCATION.
 RC STRAIN=Bristol N2;
 RX MEDLINE=20190108; PubMed=10660671;
 RA Chase D., Serafinas C., Ashcroft N., Kosinski M., Longo D.,
 RA Ferris D.K., Golden A.;
 RT "The polo-like kinase PLK-1 is required for nuclear envelope breakdown
 RT and the completion of meiosis in Caenorhabditis elegans.";
 RL Genesis 26:26-41(2000).
 RN (3);
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
 RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Wohldman P.;


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DR SMART; SMO0239; C2; 1.
DR SMART; SMO0133; S_TK_X; 1.
DR SMART; SMO0220; S_TK; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM 1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM 2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
DR Transferase; Serine/threonine-protein kinase; ATP binding; Zinc;
KW Phorbol ester binding; Repeat; Membrane; Cytoskeleton.
FT DOMAIN 1 98 C2 DOMAIN.
FT DOMAIN 171 221 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 249 298 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 378 638 PROTEIN KINASE.
FT NP_BIND 384 392 ATP (BY SIMILARITY).
FT BINDING 407 407 ATP (BY SIMILARITY).
FT ACT_SITE 502 502 BY SIMILARITY.
SQ SEQUENCE 707 AA; 80122 MW; 3DC762C8A7A7BA64 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 707;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
DB 570 MMAGQPPFE 578

RESULT 24
KPCE_RABBIT
ID KPCE_RABBIT STANDARD; PRT; 736 AA.
AC P10830;
RT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.1) (nPKC-epsilon).
GN PRKCE
OS Cryocolagus cuniculus (Rabbit).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Caprimulgidae;
CC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86223367; PubMed=33705672;
RA Chno S., Akita Y., Konno Y., Imazon S., Suzuki K.,
RT "A novel phorbol ester receptor/protein kinase, nPKC, distantly
RT related to the protein kinase C family".
RL Cell 53:731-741(1988).
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SURFAMILY.
CC -----
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CC -----
DR EMBL; M20014; AAA31426.1; -
DR HSSP; P28867; IPTQ.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
```

```
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0109; C1; 2.
DR SMART; SMO0239; C2; 1.
DR SMART; SMO0133; S_TK_X; 1.
DR SMART; SMO0220; S_TK; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM 1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM 2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
KW Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 1 99 C2 DOMAIN.
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 407 667 PROTEIN KINASE.
FT NP_BIND 413 421 ATP (BY SIMILARITY).
FT BINDING 436 436 ATP (BY SIMILARITY).
FT ACT_SITE 531 531 BY SIMILARITY.
FT MOD_RES 702 702 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 709 709 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 736 AA; 83515 MW; 261C4FE9595BFEB CRC64;

Query Match 77.6%; Score 38; DB 1; Length 736;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
DB 599 MMAGQPPFE 607

RESULT 25
KPCE_HUMAN
ID KPCE_HUMAN STANDARD; PRT; 737 AA.
AC Q02156; Q9JUE8;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.1) (nPKC-epsilon).
GN PRKCE OR PKCE.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93003318; PubMed=1382605;
RA Basta P., Strickland M.B., Holmes W., Loomis C.R., Ballas L.M.,
RA Burns D.J.;
RT "Sequence and expression of human protein kinase C-epsilon.";
RL Biochim. Biophys. Acta 1132:154-160(1992).
RN [2]
RP SEQUENCE OF 1-116 FROM N.A.
RA Waterston R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
```



```
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL; X55293; CAA446388.1; -
DR EMBL; U51244; AAC08855.1; -
DR PIR; S28942; S28942.
DR HSSP; P28867; IPTQ.
DR Genew; HGNC:9401; PRKCE.
DR MIM; 176975; -.
DR GO; GO:0035624; C:membrane fraction; TAS.
DR GO; GO:0004697; F:protein kinase C activity; TAS.
DR GO; GO:0004871; F:signal transducer activity; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 1 99 C2 DOMAIN.
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 247 292 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 408 668 PROTEIN KINASE.
FT NP_BIND 414 422 ATP (BY SIMILARITY).
FT BINDING 437 437 ATP (BY SIMILARITY).
FT ACT_SITE 532 532 BY SIMILARITY.
FT MOD_RES 703 703 PHOSPHORYLATION (AUTOCATALYTIC) (POTENTIAL).
FT MOD_RES 710 710 PHOSPHORYLATION (AUTOCATALYTIC) (POTENTIAL).
SQ SEQUENCE 737 AA; 83673 MW; 8503200A091A1F7F CR;64;
Query Match 77.6%; Score 35; CH 1; length 737;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
Db 600 MWAGQPPFE 608
RESULT 26
KPCE_WCUSE
ID_KPCE_MOUSE STANDARD; PR7 737 AA.
AC P16054;
DT 01-APR-1990 (Rel. 14, Created);
ET 01-APR-1990 (Rel. 14, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Protein kinase C, epsilon type (EC 2.7.11.1) (PKC-epsilon,
CA PRKCE OR PKCE OR PKCEA).
```

```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10390;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89137541; PubMed=29176567;
RA Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
RT "Unique substrate specificity and regulatory properties of
RT PKC-epsilon: a rationale for diversity.";
RL FEBS Lett. 243:351-357(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98127436; PubMed=9467942;
RA Wang Q.J., Acs P., Goodnight J., Blumberg P.M., Mischak H.,
RA Mushinski J.F.;
RT "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and -
RT epsilon chimeras, is responsible for conferring tumorigenicity to
RT NIH3T3 cells, whereas both regulatory and catalytic domains of
RT PKC-epsilon contribute to in vitro transformation.";
RL Oncogene 16:53-60(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Wheeler D.L.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL; AF028009; AAB84189.1; -
DR EMBL; AF325507; AAG53692.1; -
DR PIR; S02270; KIMSCE.
DR HSSP; P28867; IPTQ.
DR MGD; MGI:97599; prkce.
DR GO; GO:0004699; F:calcium independent protein kinase C activity; IDA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
```

KW Repeat; ATP binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
FT DOMAIN 1 99 C2 DOMAIN
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1;
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2;
FT DOMAIN 408 668 PROTEIN KINASE
FT NP BIND 414 422 ATP (BY SIMILARITY);
FT BINDING 437 437 ATP (BY SIMILARITY);
FT ACT SITE 532 532 BY SIMILARITY;
FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL);
FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL);
SQ SEQUENCE 737 AA; 83560 MW; 7AERB9CC10C99F57 (P0364)

Query Match 77.6%; Score 36; DB 1; Length 737;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLCKPPPE 9
DB 600 MMAGQPPPE 608

RESULT 27
KPC2 RAT
ID KPC2 RAT STANDARD; PRT; 737 AA.
AC P09216;
DT 01-MAR-1989 (Rel. 10, Created;
DT 01-MAR-1989 (Rel. 10, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.1) (PKC-epsilon).
GN PKCE OR PKCE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Rattus.
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
PC TISSUE-Brain;
RX MEDLINE=88198270; PubMed=28343397;
RA Cho Y., Fujii T., Ogita K., Kikkawa U., Igarashi F., Nishizuka Y.,
RT "The structure, expression, and properties of additional members of
the protein kinase C family".
RL J. Biol. Chem. 263:6927-6932(1988).
RN [2]
RP SEQUENCE OF 135-297 FROM N.A.
RX MEDLINE=88283621; PubMed=3691411;
RA Cho Y., Fujii T., Ogita K., Kikkawa U., Igarashi F., Nishizuka Y.,
RT "Identification of three additional members of the protein kinase C
family: delta-, epsilon-, and zeta-subtypes".
RL FEBS Lett. 226:125-128(1987).
CC -!- FUNCTION: THIS IS CALCIUM INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS (PKC ALSO SERVES AS
THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS).
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; M18331; AAA41872.1;
DR PIR; B28163; KIRTCF.
DR PDB; 1GM1; 25-OCT-01.
DR InterPro; IPR000008; C2.

DR InterPro; IPR002219; DAG-PE-bind.
DR InterPro; IPR000961; PKinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00133; DAG-PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF03433; pkinase_C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00169; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50004; C2 DOMAIN 2; 1.
DR PROSITE; PS00479; DAG-PE_BIND_DOM_1; 2.
DR PROSITE; PS00479; DAG-PE_BIND_DOM_2; 2.
DR PROSITE; PS00081; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW 3D-structure.
FT DOMAIN 1 99 C2 DOMAIN.
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1;
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2;
FT DOMAIN 408 668 PROTEIN KINASE
FT NP BIND 414 422 ATP (BY SIMILARITY).
FT BINDING 437 437 ATP (BY SIMILARITY).
FT ACT SITE 532 532 BY SIMILARITY.
FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 737 AA; 83478 MW; 6AD6999FDD2659F CRC64;

Query Match 77.6%; Score 38; DB 1; Length 737;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLCKPPPE 9
DB 600 MMAGQPPPE 608

RESULT 28
KPC2 AFLCA
ID KPC2 AFLCA STANDARD; PRT; 743 AA.
AC Q16975;
DT 15-JUL-1999 (Rel. 38, Created;
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calcium-independent protein kinase C (EC 2.7.1.1-) (APL II).
GN PKC2.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspiidea;
OC Aplysioidae; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91332620; PubMed=1869917;
RA Kruger K.E., Sossin W.S., Sacktor T.C., Bergold P.J., Beushausen S.,
RA Schwartz J.H.;
RT "Cloning and characterization of Ca(2+)-dependent and Ca(2+)-
independent PKCs expressed in Aplysia sensory cells".
RL J. Neurosci. 11:2303-2313(1991).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=93194877; PubMed=8449941;
RA Sossin W.S., Diaz-Arrastia R., Schwartz J.H.;
RT "Characterization of two isoforms of protein kinase C in the nervous
system of Aplysia californica".
RL J. Biol. Chem. 268:5763-5769(1993).
RN [3]

RP DOMAIN C2.
RX MEDLINE=93348616; PubMed=8346555;
RA Sossin W.S., Schwartz J.H.;
RT "Ca(2+)-independent protein kinase Cs contain an amino-terminal domain
RT similar to the C2 consensus sequence";
RL Trends Biochem. Sci. 18:207-208(1993).
RN [4].
RP CHARACTERIZATION.
RX MEDLINE=98334636; PubMed=9666085;
RA Pepio A.M., Fan X., Sossin W.S.;
RT "The role of C2 domains in Ca2+ activated and Ca2+-independent protein
RT kinase Cs in aplasia";
RL J. Biol. Chem. 273:19040-19048(1998).
RN [5].
RP ERRATUM.
RA Pepio A.M., Fan X., Sossin W.S.;
RL J. Biol. Chem. 273:22856-22856(1998).
RN [6].
RP CHARACTERIZATION.
RX MEDLINE=98138438; PubMed=9477951;
RA Pepio A.M., Sossin W.S.;
RT "The C2 domain of the Ca(2+)-independent protein kinase C Apl II
RT inhibits phorbol ester binding to the C1 domain in a phosphatidic
RT acid-sensitive manner";
RL Biochemistry 32:1256-1263(1993).
RN [7].
CC FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
CC SIMILARITY).
CC ENZYME REGULATION: REQUIRES HIGH LEVELS OF PHOSPHATIDYL-SERINE TO
CC BE ACTIVATED. THE PRESENCE OF THE C2 DOMAIN LOWERS THE AFFINITY OF
CC PROTEIN KINASE C ACTIVATORS FOR THE C1 DOMAINS AND THIS INHIBITION
CC CAN BE REMOVED BY PHOSPHATIDYL-SERINE. PHOSPHATIDIC ACID, HOWEVER,
CC IS MUCH MORE POTENT THAN PHOSPHATIDYL-SERINE IN REDUCING C2 DOMAIN-
CC MEDIATED INHIBITION, SUGGESTING THAT PHOSPHATIDIC ACID MAY BE A
CC REQUIRED COFACTOR FOR THE ACTIVATION OF APL II.
CC SUBCELLULAR LOCATION: Membrane-associated.
CC TISSUE SPECIFICITY: EXPRESSED IN NERVOUS TISSUES, OVOTESTIS AND
CC GUT.
CC SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC SIMILARITY: Contains 1 C2 domain.
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M94894; AAA27771.1; -;
CC HSSP; P28867; IPTQ.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000961; Pkinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_pkinase
CC Pfam; PFC0168; C2; 1.
CC Pfam; PFC0130; DAG_PE-bind; 2.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PFC0433; pkinase_C; 1.
CC PRINTS; PR00008; DAGPEDOMAIN.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00109; C1; 2.
CC SMART; SM00239; C2; 1.
CC SMART; SM00133; S_TK_X; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00499; C2_DOMAIN_1; FALSE_NEG.

DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Transferase; Serine/threonine-protein kinase;
KW Phorbol-ester binding; Zinc; Repeat.
FT DOMAIN 1 108 C2 DOMAIN.
FT DOMAIN 177 226 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 248 297 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 403 663 PROTEIN KINASE.
FT NP_BIND 409 417 ATP (BY SIMILARITY).
FT BINDING 432 432 ATP (BY SIMILARITY).
FT ACT_SITE 527 527 BY SIMILARITY.
SQ SEQUENCE 743 AA; 84413 MW; 4C982C563CA2B659 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 743;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLJGKPPFE 9
Db 595 MMAGQPPFE 603
|:|:|:|
|:|:|:|

RESULT 29
KOKO_YEAST
ID KOKO_YEAST STANDARD; PRT; 1081 AA.
AC Q12236;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable serine/threonine-protein kinase YOL100W (EC 2.7.1.1).
GN YOL100W OR HRC1081.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96076631; PubMed=7502582;
RA Vandenbol M., Durand P., Portetelle D., Hilger F.;
RT "Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV
RT including the Ty1-H3 retrotransposon, the sufl(+) frameshift
RT suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-1a and a
RT delta element";
RL Yeast 11:1069-1075(1995).
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z48149; CAA88162.1; -;
CC EMBL; Z74842; CAA99113.1; -;
CC PIR; S51899; S51899.
CC HSSP; Q63450; 1A06.
CC SGD; S0005460; PKH2.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0000196; P:MAPKK cascade (cell wall biogenesis); IGI.
CC GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding. 179 443 PROTEIN_KINASE.
FT NP_BIND 185 193 ATP (BY SIMILARITY).
FT BINDING 208 208 ATP (BY SIMILARITY).
FT ACT_SITE 303 303 BY SIMILARITY.
SQ SEQUENCE 1081 AA; 121660 MW; BECDD9D49AC2B8C3 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 1081;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
Db 382 MIAGKPPFK 390

RESULT 30
PLK3_CAEEL
ID PLK3_CAEEL STANDARD; PRT; 615 AA.
AC Q28845;
DT 28-FEB-2003 (Rel. 41, Created;
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Serine/threonine-protein kinase plk-3 (EC 2.7.1.1) (Polo-like
DE kinase 3);
GN PLK-3 OR PLC2 OR P55G1.8.
OS Caenorhabditis elegans.
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
CC Rhabditidae; Peleoderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=9304501; PubMed=10376213;
RA Cuyang B., Wang Y., Dai W.;
RT "Caenorhabditis elegans contains structural homologs of human plk and
RT plk-3";
RL DNA Seq. 10:109-113(1999).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Murray J., Le T.T.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBRC databases.
CC -!- FUNCTION: May be required for cell division and may have a role
CC during G1 or S phase (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SERINE/THREONINE KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF059024; AAC14425.1; ..
CC EMBL: U58750; AAB00642.1; ..
CC PIR: T29223; T29223.
CC HSSP: Q63450; 1A06.
CC WormPep: F55G1.8; CE07285.
CC GO: GO:0005634; C:nucleus; ISS.
CC GO: GO:0005524; F:ATP binding activity; ISS.
CC GO: GO:0004674; F:protein serine/threonine kinase activity; ISS.
CC GO: GO:0004648; P:protein amino acid phosphorylation; ISS.
CC InterPro: IPR000959; POLO box.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00069; pkinase; 1.

DR Pfam: PF00659; POLO_box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50078; POLO_BOX; 2.
KW ATP-binding; Serine/threonine-protein kinase; Transferase; Repeat;
KW Nuclear protein.
FT DOMAIN 35 286 PROTEIN_KINASE.
FT NP_BIND 41 49 ATP (BY SIMILARITY).
FT BINDING 64 64 ATP (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
FT DOMAIN 402 463 POLO_BOX 1.
FT DOMAIN 505 573 POLO_BOX 2.
SQ SEQUENCE 615 AA; 70436 MW; D510C727329C4B26 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 615;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
Db 225 LLFGSPFFE 233

RESULT 31
KPC1_APLCA
ID KPC1_APLCA STANDARD; PRT; 649 AA.
AC Q16974;
DT 30-MAY-2000 (Rel. 39, Created);
DT 30-MAY-2000 (Rel. 39, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Calcium-dependent protein kinase C (EC 2.7.1.1) (APL I).
GN PRKCI.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysioidea; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=91332620; PubMed=1869917;
RA Kruger K.E., Sossin W.S., Sacktor T.C., Bergold P.J., Reushausen S.,
RA Schwartz C.H.;
RT "Cloning and characterization of Ca(2+)-dependent and Ca(2+)-
RT independent PKCs expressed in Aplysia sensory cells";
RL J. Neurosci. 11:2303-2313(1991).
RN [2];
RP CHARACTERIZATION.
RX MEDLINE=93194877; PubMed=8449941;
RA Sossin W.S., Diaz-Arrastia R., Schwartz J.H.;
RT "Characterization of two isoforms of protein kinase C in the nervous
RT system of Aplysia californica";
RL J. Biol. Chem. 268:5763-5768(1993).
RN [3];
RP CHARACTERIZATION.
RX MEDLINE=98334636; PubMed=9668085;
RA Pepic A.M., Fan X., Sossin W.S.;
RT "The role of C2 domains in Ca2+-activated and Ca2+-independent protein
RT kinase Cs in aplysia";
RL J. Biol. Chem. 273:19040-19048(1998).
RN [4];
RP ERRATUM.
RA Pepic A.M., Fan X., Sossin W.S.;
RL J. Biol. Chem. 273:22856-22856(1998).
CC -!- FUNCTION: THIS IS CALCIUM-DEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME. ACTIVATION OF PKC BY
CC SEROTONIN RESULTS IN PRESYNAPTIC FACILITATION OF DEPRESSED
CC SENSORY-TO-MOTOR NEURON SYNAPSES, WHICH IS THOUGHT TO UNDERLIE
CC BEHAVIORAL DISHABITUATION.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS

CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
CC SIMILARITY).
CC -!- ENZYME REGULATION: ACTIVATED BY PHOSPHATIDYL SERINE.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC; TRANSLOCATED TO NEURONAL
CC MEMBRANES.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL; M94883; AAA27770.2; -.
DR HSSP; P05697; ITBN.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00363; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRODOM; PE000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKG; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00091; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; TYRKINASE.
DR PROSITE; PS00001; Prot_kinase; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Transferase; Serine/threonine-protein kinase;
KW Phorbol-ester binding; Zinc; Repeat.
FT DOMAIN 22 71 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 86 135 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 157 244 C2 DOMAIN
FT DOMAIN 320 578 PROTEIN KINASE
FT NP_BIND 326 334 ATP (BY SIMILARITY).
FT BINDING 349 349 ATP (BY SIMILARITY).
FT ACT_SITE 444 444 BY SIMILARITY.
SQ SEQUENCE 649 AA; 74079 MW; AS3253399284E33C CRC64;

Query Match 75.5%; Score 37; DB 1; Length 649;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 MLLGKPPFE 9
Db 512 MLAGQPPFD 520

RESULT 32
KPC1_LYTPI STANDARD; PRT; 658 AA.
AC Q25378;
DT 15-JUL-1999 (Rel. 38, Created;
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein kinase C (EC 2.7.1.1).
GN PKC1.

OS Lytechinus pictus (Painted sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Lytechinus.
OX NCBI_TaxID=7653;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Rakow T.L., Shen S.S.;
RT "Molecular cloning and characterization of protein kinase C from the
RT sea urchin Lytechinus pictus."
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME (BY SIMILARITY).
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
CC SIMILARITY).
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL; U02967; AAA03447.1; -.
DR HSSP; P05697; ITBN.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PE000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKG; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; TYRKINASE.
KW ATP-binding; Transferase; Serine/threonine-protein kinase;
KW Phorbol-ester binding; Zinc; Repeat.
FT DOMAIN 28 77 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 93 142 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 164 251 C2 DOMAIN.
FT DOMAIN 325 583 PROTEIN KINASE.
FT NP_BIND 331 339 ATP (BY SIMILARITY).
FT BINDING 354 354 ATP (BY SIMILARITY).
FT ACT_SITE 449 449 BY SIMILARITY.
SQ SEQUENCE 658 AA; 74871 MW; 74B5A27A49C835A2 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 658;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;


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QY      1 MLLGKPPFE 9
Db      517 MLAGQPPFD 525

RESULT 33
KPCA_BOVIN STANDARD; PRT; 672 AA.
AC PS4439;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA.
CS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=86289425; PubMed=3755547;
RA Parker P.J., Coussens L., Totty N., Rhee L., Young S., Chen E.,
RA Stabel S., Waterfield M.D., Ullrich A.;
RT "The complete primary structure of protein kinase C - the major
RT phorbol ester receptor.";
RL Science 233:853-859(1986).
RN [2]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
RT for cellular regulation.";
RL Nature 334:661-665(1988).
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
CC serine- and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with PRKCABP (by similarity).
CC -!- SIMILARITY: Contains 2 zinc dependent phorbol ester and DAG
CC binding domains.
CC -!- SIMILARITY: CONTAINS 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- PKC SUBFAMILY.
CC
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CC
CC -----
CC EMRL; M33973; AAA30706.1; --
CC PIR; A03621; KIBOC.
CC HSSP; P05697; ITBN.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002219; DAG_PE_bind.
CC InterPro; IPR000961; Pkinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_pkinase
CC Pfam; PF00168; C2; 1.
CC Pfam; PF00130; DAG_PE_bind; 2.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00433; pkinase_C; 1.
CC PRINTS; PRC0360; C2DOMAIN.
CC PRINTS; PRC0008; DAGPEDOMAIN.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00139; C1; 2.
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DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 672 AA; 76837 MW; 97BF46DB80FCF21A CRC64;

Query Match 75.5%; Score 37; DA 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLLGKPPFE 9
Db      531 MLAGQPPFD 539

RESULT 34
KPCA_HUMAN STANDARD; PRT; 672 AA.
AC P17252; Q15137; Q96RE4;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA OR PKCA OR PRKACA.
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=90245676; PubMed=2336401;
RA Finkenzeller G., Marne D., Hug H.;
RT "Sequence of human protein kinase C alpha.";
RL Nucleic Acids Res. 18:2183-2183(1990).
RN [2]
RP SEQUENCE OF 15-445 FROM N.A.
RX MEDLINE=91332033; PubMed=1714454;
RA McSwine-Kennick R.L., McKeegan E.M., Johnson M.D., Morin M.J.;
RT "Phorbol diester-induced alterations in the expression of protein
RT kinase C isozymes and their mRNAs. Analysis in wild-type and phorbol
RT diester-resistant HL-60 cell clones.";
RL J. Biol. Chem. 266:15135-15143(1991).
RN [3]
RP SEQUENCE OF 1-57 FROM N.A.
RA Haridas V., Hackenbruck J., Glazer R.I.;
RT "Homo sapiens protein kinase C alpha 5-flanking sequence.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
CC serine- and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with PRKCABP (By similarity).
```

```
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL; X52479; CAA36718.1;
DR EMBL; M22199; AAA60098.1;
DR EMBL; AF395329; AAK84184.1;
DR PIR; S09496; KIHJCA.
DR HSSP; F04410; 1A25.
DR Genew; HGNC:9393; PRKCA.
DR MIM; 176960;
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0004697; F:protein kinase C activity; TAS.
DR GO; GO:0008624; P:induction of apoptosis by extracellular signal; TAS.
DR GO; GO:0000374; P:regulation of cell cycle; TAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM03220; S_TK; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00061; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00017; PROTEIN_KINASE_DOM_1; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST_1; 1.
KW Calcium-binding; Repeat; ATP-binding; transferase;
KW Serine/threonine-protein kinase; Phorbol ester binding; Zinc;
KW phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTOCATALYTIC) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTOCATALYTIC) (POTENTIAL).
FT CONFLICT 50 50 C -> S (IN REF 2).
SQ SEQUENCE 672 AA; 76764 MW; 8780050189C12DA CRC64;
Query Match: 75.5% Score 37; E: 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLOKPPFE 9
DC 531 MLAGQPPFD 539
RESULT 15
```

```
KPCA_MOUSE
ID KPCA_MOUSE STANDARD; PRT; 672 AA.
AC P20444;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA OR PKCA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232737; Pubmed=2469625;
RA Rose-John S., Dietrich A., Marks F.;
RT "Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss
RT 3T3 fibroblasts.";
RJ Gene 74:465-471 (1988).
RW [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=Brain;
RX MEDLINE=90098082; Pubmed=2601739;
RA Megidish T., Mazurek N.;
RT "A mutant protein kinase C that can transform fibroblasts.";
RJ Nature 342:807-811 (1989).
RW [3]
RP INTERACTION WITH PRKCABP.
RX MEDLINE=95146534; Pubmed=7844141;
RA Staudinger J., Zhou J., Burgess R., Elledge S.J., Olson E.N.;
RT "PICK1: A perinuclear binding protein and substrate for protein kinase
RT C isolated by the yeast two-hybrid system.";
RJ Cell Biol. 128:263-271 (1995).
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
CC serine- and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with PRKCABP.
CC -!- DISEASE: Expression of the mutant form UV25 causes malignant
CC transformation of cells.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M25811; AAA39934.1; ALT_SEQ.
DR EMBL; X52685; CAA36908.1;
DR PIR; S07104; KIMSCA.
DR HSSP; P04410; 1A25.
DR GO; MGI:97595; Prkca.
DR GO; GO:0004698; F:calcium dependent protein kinase C activity; IDA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
```

DR PRINTS; PR00008; DAGPEDOMAIN.
 DR PRODOM; P0000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S TK X; 1.
 DR SMART; SM00220; S TKC; 1.
 DR PROSITE; PS00499; C2_DOMAIN_1; 1.
 DR PROSITE; PS00004; C2_DOMAIN_2; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Calcium-binding; Repeat; ATP-binding; Transferase.
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
 KW Phosphorylation.
 FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 172 260 C2 DOMAIN.
 FT DOMAIN 339 597 PROTEIN KINASE.
 FT NP_BIND 345 353 ATP (BY SIMILARITY).
 FT BINDING 368 368 ATP (BY SIMILARITY).
 FT ACT_SITE 463 463 BY SIMILARITY.
 FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 636 636 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT VARIANT 106 106 I -> V (IN MUTANT FORM UV25).
 FT VARIANT 111 111 S -> G (IN MUTANT FORM UV25).
 FT VARIANT 240 240 L -> Q (IN MUTANT FORM UV25).
 FT VARIANT 339 339 F -> L (IN MUTANT FORM UV25).
 FT CONFLICT 147 147 C -> V (IN REF. 2).
 FT CONFLICT 218 218 N -> T (IN REF. 2).
 FT CONFLICT 277 278 AH -> SL (IN REF. 2).
 FT CONFLICT 313 313 V -> A (IN REF. 2).
 FT CONFLICT 467 467 N -> G (IN REF. 2).
 FT CONFLICT 472 472 N -> E (IN REF. 2).
 FT CONFLICT 576 576 Q -> H (IN REF. 2).
 SQ SEQUENCE 672 AA; 76852 MW; 3948483952BR6D50 CR664;

Query Match 75.5%; Score 17; DB 1; Length 672;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY : MLLGKPPFE 9
 DB 531 MLAGQPPED 539

RESULT 36
 KPCA RABIT
 ID KPCA RABIT STANDARD; PFI; 1.0.0.0.
 AC P1102;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Protein kinase C, alpha type (EC 2.7.11.37) (PKC-alpha) (PKC-A).
 GN PRKCA.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=87115883; PubMed=3808073;
 RA Ohno S., Kawasaki H., Imajoh S., Sakaki K., Inagaki M., Yokokura H.,
 RA Sakai T., Hidaka H.;
 RT "Tissue-specific expression of three distinct types of rabbit protein
 kinase C."
 RC Nature 325:161-166 (1987).
 RN [2]
 RP REVIEW.
 RX MEDLINE=88318921; PubMed=3045661;
 RA Nishizuka Y.

RT "The molecular heterogeneity of protein kinase C and its implications
 for cellular regulation.";
 RL Nature 334:661-665(1988).
 CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
 CC serine- and threonine-specific enzyme.
 CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
 CC phosphorylates a range of cellular proteins. PKC also serves as
 CC the receptor for phorbol esters, a class of tumor promoters.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: Interacts with PRKCBP (by similarity).
 CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; X04796; CAA28483.1; -;
 DR PIR; C26037; KIRBC.
 DR HSSP; P04410; IAZ5.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000961; pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00130; DAG_PE-bind; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S TK X; 1.
 DR SMART; SM00220; S TKC; 1.
 DR PROSITE; PS00499; C2_DOMAIN_1; 1.
 DR PROSITE; PS00004; C2_DOMAIN_2; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Calcium-binding; Repeat; ATP-binding; Transferase;
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
 KW Phosphorylation.
 FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 172 260 C2 DOMAIN.
 FT DOMAIN 339 597 PROTEIN KINASE.
 FT NP_BIND 345 353 ATP (BY SIMILARITY).
 FT BINDING 368 368 ATP (BY SIMILARITY).
 FT ACT_SITE 463 463 BY SIMILARITY.
 FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 636 636 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 SQ SEQUENCE 672 AA; 76782 MW; 1031136703577A77 CR664;

Query Match 75.5%; Score 37; DB 1; Length 672;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY : MLLGKPPFE 9
 DB 531 MLAGQPPED 539

```
RESULT 37
KPCA_RAT
ID KPCA_RAT STANDARD; PRT; 672 AA.
AC P05696;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC alpha) (PKC-A).
GN PKCA OR PKCA.
CS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RF SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88262515; PubMed=3387228;
RA Ono Y., Fujii T., Igarashi K., Kikkawa U., Ogita K., Nishizuka Y.;
RT "Nucleotide sequences of cDNAs for alpha and gamma subtypes of rat
    brain protein kinase C."
RL Nucleic Acids Res. 16:5199-5200(1988);
RV [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88030055; PubMed=3666147;
RA Kikkawa U., Ogita K., Ono Y., Asaoka Y., Shearman M.S., Fujii T.,
RA Ase K., Sekiguchi K., Igarashi K., Nishizuka Y.;
RT "The common structure and activities of four subtypes of rat brain
    protein kinase C family."
RL FEBS Lett. 223:212-216(1987);
RV [3]
RF REVIEW.
RX MEDLINE=98318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
    for cellular regulation."
RL Nature 334:661-665(1988).
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
    serine- and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
    phosphorylates a range of cellular proteins. PKC also serves as
    the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with PRKCAPP (by similarity).
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
    binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- PKC SUBFAMILY.
-----
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or send an email to license@isb-sib.ch).
-----
EMBL; X07286; CAA30266.1;
PIR; S02248; KIRTC.
PDB; 1DSY; 26-JAN-00.
InterPro; IPR000008; C2.
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_kinase.
Pfam; PF00168; C2; 1.
Pfam; PF00130; DAG_PE-bind; 2.
Pfam; PF00069; pkinase; 1.
Pfam; PF00433; pkinase_C; 1.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00008; DAGPEDOMAIN.
ProDom; PD000001; Prot_kinase; 1.
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DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation; 3D-structure.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 672 AA; 76792 MW; 94889E7339C17719 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
   |||:|:|:
DB 531 MLAGQPPFD 539

RESULT 38
KPCG_BOVIN
ID KPCG_BOVIN STANDARD; PRT; 682 AA.
AC P05128;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma) (Fragment).
GN PRKCG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
CX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86289426; PubMed=3755548;
RA Coussens L., Parker P.J., Rhee L., Yang-Feng T.L., Chen E.,
RA Waterfield M.D., Francke U., Ullrich A.;
RT "Multiple, distinct forms of bovine and human protein kinase C
    suggest diversity in cellular signaling pathways."
RL Science 233:859-866(1986);
RV [2]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
    for cellular regulation."
RL Nature 334:661-665(1988).
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
    SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
    PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
    THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
    binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
```



```
CC PKC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M13976; AAA30704.1;
DR PIR; C24664; KIBOGC.
DR HSSP; P05697; ITBN.
DR InterPro; IPR000308; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00091; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATR; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT NON_TER 1 1
FT DOMAIN 21 70 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 86 135 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 155 245 C2 DOMAIN.
FT DOMAIN 336 599 PROTEIN KINASE
FT NP_BIND 342 350 ATP (P) SIMILARITY.
FT BINDING 365 365 ATP (P) SIMILARITY.
FT ACT_SITE 465 465 BY SIMILARITY
FT MCD_RES 633 633 PHOSPHORYLATION AND (POTENTIAL).
FT MCD_RES 640 640 PHOSPHORYLATION AND (POTENTIAL).
SQ SEQUENCE 682 AA; 77156 MW; 2039201118807310 CP; 664;

Query Match 75.5%; Score 47; 25 1; Length 682;
Best Local Similarity 66.7%; Pred No 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVLGKPPFE 9
| :|||:
Db 533 MLAGQPPFD 541

RESULT 39
KPCG HUMAN
ID KPCG_HUMAN STANDARD; PRT; 697 AA.
AC P05129;
DT 13-AUG-1987 (Rel. 05, Created);
DT 01-FEB-1994 (Rel. 28, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma);
GN PRKCG OR PKCG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cui W.C., Yu L., Chu Y.Y., Wang J., Zheng L.H., Zhou G.J., Zhao S.Y.;
RC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-318 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=86289426; PubMed=3755548;
RA Coussens L., Parker P.J., Rhee L., Yang-Feng T.L., Chen E.,
RA Waterfield M.D., Francke U., Ulrich A.;
RT "Multiple, distinct forms of bovine and human protein kinase C
RT suggest diversity in cellular signaling pathways.";
RL Science 233:859-866(1986).
RN [3]
RP SEQUENCE OF 162-697 FROM N.A.
RC TISSUE=Hippocampus;
RX MEDLINE=93387312; PubMed=8375396;
RA Kochs G., Meyer D., Hug H., Marne D., Sarre T.F.;
RT "Activation and substrate specificity of the human protein kinase C
RT alpha and zeta isoenzymes.";
RL Eur. J. Biochem. 216:597-606(1993).
RN [4]
RP VARIANTS CYS-141; GLN-415; ASP-523 AND SER-659.
RX MEDLINE=98213587; PubMed=9545390;
RA Al-Maghtheh M., Vithana E.N., Inglehearn C.F., Moore T., Bird A.C.,
RA Bhattacharya S.S.;
RT "Segregation of a PKCG mutation in two RP11 families.";
RL Am. J. Hum. Genet. 62:1248-1252(1998).
RN [5]
RP SHOWS THAT THE VARIANTS ARE NOT A CAUSE OF RP11.
RX MEDLINE=99375047; PubMed=10441600;
RA Dryja T.P., McEvoy J., McGee T.L., Berson E.L.;
RT "No mutations in the coding region of the PRKCG gene in three families
RT with retinitis pigmentosa linked to the RP11 locus on chromosome
RT 19q.";
RL Am. J. Hum. Genet. 65:926-928(1999).
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- PKC SUBFAMILY.
CC -!- DATABASE: NAME=Mutations of the PRKCG gene;
CC NOTE=Retina International's Scientific Newsletter;
CC WWW=http://www.retina-international.com/sci-news/prkcgmut.htm.
CC -----
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CC -----
DR EMBL; AF345987; AAK13533.1; --
DR EMBL; M13977; AAA60102.1; ALT_TERM.
DR EMBL; Z15114; CAA78820.1; --
DR PIR; D24664; D24664.
DR HSSP; P05697; ITBN.
DR Genew; HGNC:9402; PRKCG.
DR MIM; 176980; --
DR GO; GO:0004697; F:protein kinase C activity; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
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DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00133; DAG_PE_bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C7; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C2; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DXX; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phospho-ester binding; Zinc;
KW Phosphorylation; Polymorphism.
FT DOMAIN 36 95 PHORBOL-ESTER AND DAG BINDING 1.
FT DOVAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOVAIN 170 260 C2 DOMAIN.
FT DOVAIN 351 614 PROTEIN KINASE.
FT NP_BIND 357 365 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARIANT 141 141 R -> C.
FT VARIANT 415 415 H -> C.
FT VARIANT 523 523 A -> D.
FT VARIANT 659 659 R -> S.
SQ SEQUENCE 697 AA; 78447 MW; 3F911B95EF713C41 CRC64;
Query Match 75.5%; Score 13; E-17; Ident 60%.
Best Local Similarity 66.2%; Ident 49%.
Matches 6; Conservative 2; Mismatches 1; Gaps 0;
QY 1 MLAGKPPPE 9
EE 548 MLAGQPPFD 556
RESULT 40
KPCG_MOUSE STANDARD; PRT; 697 AA.
AC P05657;
DT 01-NOV-1998 (Rel. 09, Created)
DT 01-NOV-1998 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC gamma).
GN PRKCG OR PKCG OR PRKCC OR PKCC.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Rat; TISSUE=Brain;
RX MEDLINE=80262515; PubMed=3387228;
RA Ono Y., Fujii T., Igarashi K., Kikkawa U., Ogita K., Nishizuka Y.;
RT "Nucleotide sequences of cDNAs for alpha and gamma subspecies of rat
brain protein kinase C.";
Nucleic Acids Res. 16:5199-5200(1988).
[2]
RP SEQUENCE FROM N.A.
RC SPECIES=Rat;
RX MEDLINE=86272097; PubMed=3755379;
RA Knopf J.D., Lee M.-H., Sultzman L.A., Kriz R.W., Loomis C.R.,
Hewick R.M., Bell R.M.;
RT "Cloning and expression of multiple protein kinase C cDNAs.";
Cell 46:491-502(1986).
[3]
RP SEQUENCE OF 1-56 FROM N.A.
RC SPECIES=Rat;
RX MEDLINE=91060619; PubMed=2246272;
RA Chen K.H., Widen S.G., Wilson S.H., Huang K.P.;
RT "Characterization of the 5'-flanking region of the rat protein kinase
C gamma gene.";
J. Biol. Chem. 265:19961-19965(1990).
[4]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; TISSUE=Brain;
RX MEDLINE=93154595; PubMed=8428669;
RA Bowers B.J., Parham C.L., Sikela J.M., Wehner J.M.;
RT "Isolation and sequence of a mouse brain cDNA coding for protein
kinase C-gamma isozyme.";
Gene 123:263-265(1993).
[5]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=BALB/c; TISSUE=Brain;
RA Tseng C.P., Verma A.;
RT Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
[6]
RP STRUCTURE BY NMR OF 91-172.
RC SPECIES=Rat;
RX MEDLINE=97419134; PubMed=9271501;
RA Xu R.X., Pawelczyk T., Xia T.-H., Brown S.C.;
RT "NMR structure of a protein kinase C-gamma phorbol-binding domain and
study of protein-lipid micelle interactions.";
Biochemistry 36:10709-10717(1997).
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
PKC SUBFAMILY.
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EMBL; X07287; CAA30267.1; -
EMBL; M13707; AAA41874.1; -
EMBL; M55417; AAA41873.1; -
EMBL; X67129; CAA47608.1; -
EMBL; L28035; AAA39939.1; -
PIR; A05105; KIRTGC.
PIR; GN0548; JN0548.
PDB; 1TBN; 29-APR-98.
PDB; 1TBO; 29-APR-98.
MGD; MGI:97597; Prkcc.
InterPro; IPR000308; C2.
InterPro; IPR002219; DAG_PE_bind.
InterPro; IPR000361; Pkinase_C.
InterPro; IPR000719; Prot_kinase.
```

DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00130; DAG_PE_bind; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00433; pkinase_C; 1.
 DR PRINTS: PR00360; C2DOMAIN.
 DR PRINTS: PR00008; DAGPECOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000301; Prot_kinase; 1.
 DR SMART: SM00109; C1; 2.
 DR SMART: SMC0239; C2; 1.
 DR SMART: SMC0133; S_TK_X; 1.
 DR SMART: SMC0220; S_TKC; 1.
 DR PROSITE: PS00499; C2_DOMAIN_1; 1.
 DR PROSITE: PS00004; C2_DOMAIN_2; 1.
 DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
 DR PROSITE: PS00001; DAG_PE_BIND_DOM_2; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW Calcium-binding; Repeat; ATP-binding; Transferase;
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
 KW Phosphorylation; 3D-structure.
 FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 170 260 C2 DOMAIN.
 FT DOMAIN 351 614 PROTEIN KINASE.
 FT NF_BIND 357 365 ATP (BY SIMILARITY).
 FT BINDING 390 380 ATP (BY SIMILARITY).
 FT ACT_SITE 480 480 BY SIMILARITY.
 FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT STRAND 103 105
 FT STRAND 113 113
 FT STRAND 120 120
 FT TURN 123 124
 FT STRAND 129 131
 FT TURN 132 134
 FT STRAND 137 138
 FT TURN 140 145
 SQ SEQUENCE 697 AA; 78357 MW; E6B2F7A1B91042FF CRC64;

Query Match: 75.5% Score (7) 25 1; Length (97)
 Best Local Similarity 66.7% Pct. Id. 19
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 N1LGRPFK 9
 DB 548 MLAGCPFD 556

Search completed: November 14, 2003, 13:59:08
 Job time : 6.68571 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 13:18:40 ; Search time 27 seconds
(without alignments)
86,018 Million cell updates/sec

Title: US-09-736-076-17

Perfect score: 49

Sequence: 1 MLGKPPFE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 630525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 930525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_protist:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results identified by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Match	Length	DB ID	Description
1	46	93.9	316	Q9BDK4	Q9BDK4 sus scrofa
2	46	93.9	372	Q8N7M6	Q8N7M6 homo sapien
3	46	93.9	666	Q90XS4	Q90XS4 xenopus lae
4	46	93.9	682	Q8K226	Q8K226 mus musculus
5	45	91.8	456	Q8MYF1	Q8MYF1 dictyosteli
6	43	87.8	526	Q9BDP9	Q9BDP9 sus scrofa
7	43	87.8	582	Q9GRB7	Q9GRB7 hemiceutrot
8	43	87.8	598	P70032	P70032 xenopus lae
9	43	87.8	623	Q8IC35	Q8IC35 asterina pe
10	41	83.7	80	Q91891	Q91891 xenopus lae
11	41	83.7	305	Q61427	Q61427 caenorhabdi
12	40	81.6	673	Q62567	Q62567 suberites d
13	40	81.6	677	Q96997	Q96997 geodia cydo
14	40	81.6	766	Q63407	Q63407 saccharomyc
15	40	81.6	769	Q97143	Q97143 drosophila
16	40	81.6	2883	Q9PEX7	Q9PEX7 xanthomonas

17	39	79.6	270	5	Q95ZT2	Q95ZT2 caenorhabdi
18	39	79.6	325	5	Q8MQ39	Q8MQ39 caenorhabdi
19	39	79.6	371	5	Q20541	Q20541 caenorhabdi
20	39	79.6	454	10	Q9M3V7	Q9M3V7 asparagus o
21	39	79.6	465	10	Q8LFC1	Q8LFC1 arabidopsis
22	39	79.6	480	10	Q43380	Q43380 avena sativ
23	39	79.6	592	3	Q12701	Q12701 schizosacch
24	39	79.6	1759	16	Q8F6Y5	Q8F6Y5 leptospira
25	39	79.6	2483	16	Q8XQB2	Q8XQB2 ralstonia s
26	39	79.6	2497	16	Q8XYB9	Q8XYB9 ralstonia s
27	38	77.6	240	11	Q63432	Q63432 rattus norv
28	38	77.6	324	11	C9CVR6	C9CVR6 mus musculu
29	38	77.6	332	16	C9AJZ9	C9AJZ9 streptomyce
30	38	77.6	554	5	Q95T78	Q95T78 drosophila
31	38	77.6	568	5	Q8MXG6	Q8MXG6 caenorhabdi
32	38	77.6	646	16	Q8NU98	Q8NU98 corynebacte
33	38	77.6	661	5	O01669	O01669 hydra atten
34	38	77.6	707	5	Q20953	Q20953 caenorhabdi
35	38	77.6	749	5	Q8MXG7	Q8MXG7 caenorhabdi
36	38	77.6	754	5	Q8MXB6	Q8MXB6 limulus pol
37	38	77.6	780	5	C76360	C76360 caenorhabdi
38	38	77.6	925	11	Q8RC15	Q8RC15 mus musculu
39	38	77.6	925	11	Q64702	Q64702 mus musculu
40	38	77.6	970	4	Q96Q95	Q96Q95 homo sapien
41	38	77.6	970	4	O00444	O00444 homo sapien
42	38	77.6	970	4	Q81YF0	Q81YF0 homo sapien
43	38	77.6	1036	4	C75119	C75119 homo sapien
44	38	77.6	1036	4	Q81YT8	Q81YT8 homo sapien
45	38	77.6	1037	11	Q9WTP4	Q9WTP4 mus musculu

ALIGNMENTS

RESULT 1
Q9BDK4 PRELIMINARY; PRT; 316 AA.
AC Q9BDK4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serum-inducible kinase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Anger M., Kues W.A., Klima J., Motlik J., Carnwath J.W., Niemann H.;
RT "Porcine serum-inducible kinase";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF348424; AAK27154.1; -;
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PSS0378; POLO_BOX; 1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER 1 1
FT NON_TER 316 316
SQ SEQUENCE 316 AA; 35330 MW; F63BBE4A2691D62F CRC64;

Query Match 93.9%; Score 46; DB 6; Length 316;
Best Local Similarity 88.9%; Pred. No. 0.49;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9
| | | | |
DB 25 MLGKPPFE 33

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RESULT 2
Q9N7M6      PRELIMINARY;      PRT;      172 AA.
AC Q9N7M6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein F4C40844.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Trachea;
RA Suzuki C., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA Matsumura Y., Moriya S., Chiba E., Moriyama H., Grogawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,
RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,
RA Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K.,
RA Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
RA Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuko Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project";
RL Submitted (JUL 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK098163; BAC05247.1; -.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 172 AA; 42632 MW; 7E3C33F65020A009 CRC64;

Query Match      93.9%; Score 46; DB 4; Length 172;
Best Local Similarity 88.9%; Pred. No. 1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
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DB 266 MLLGRPPFE 274

RESULT 3
Q90XS4      PRELIMINARY;      PRT;      666 AA.
AC Q90XS4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Polo-like kinase 2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenocephalidae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21481843; PubMed=11597129;
RA Duncan P.I., Pollet N., Niehrs C., Niehrs E.A.;
RT "Cloning and Characterization of Pix2 and Pix3, Two Additional Polo-
RT like Kinases from Xenopus laevis."
RJ Exp. Cell Res. 270:78-87(2001).
CC -!- SIMILARITY: BELONGS TO THE SPK/THR FAMILY OF PROTEIN KINASES.

```

```

DR EMBL; AF357840; AAL30175.1; -.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 666 AA; 76322 MW; AB4D8F8BDFB5D4FC CRC64;

Query Match      93.9%; Score 46; DB 13; Length 666;
Best Local Similarity 88.9%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
   |||:||||
DB 254 MLLGRPPFE 262

RESULT 4
Q8K226      PRELIMINARY;      PRT;      682 AA.
AC Q8K226;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serum-inducible kinase.
GN SNK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034513; AAH34513.1; -.
DR MGD; MG1:1099790; Snk.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 682 AA; 77777 MW; 89BA65C8DFAFFD95 CRC64;

Query Match      93.9%; Score 46; DB 11; Length 682;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
   |||:||||
DB 270 MLLGRPPFE 278

RESULT 5
Q8MYF1      PRELIMINARY;      PRT;      456 AA.
AC Q8MYF1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

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DR 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-YAR-2003 (TREMBlrel. 23, Last annotation update)
 DE RAC family serine/threonine kinase homolog.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
 CX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;

RA Gloeckner G., Eichinger J., Szafranski K., Pachebat J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April C.F., Guigo R., Kumpf K.,
 RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,
 RT "Sequence and Analysis of Chromosome 2 of Dictyostelium";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC117081; AA043765.1; -;
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR022290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00369; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRINTS; PR00139; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM0133; S_TKC_X; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 456 AA; 5154 MW; EB8749EC64C89309 CRC64;

Query Match 91.8%; Score 45; DB 5; Length 456;
 Best Local Similarity 77.8%; Pred. No. 1.1;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9

DB 319 MMIGKPPFE 327

RESULT 6

Q9BDP8 PRELIMINARY; PRT; 526 AA.

DT 01-JUN-2001 (TREMBlrel. 17, Created).
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update).
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update).
 DE Polo-like protein kinase (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 CX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Anger M., Kues W.A., Klima J., Mielenz M., Motlik J., Carnwath J.W.,
 RA Niemann H.,
 RT "Expression of Polo-like Kinase in Cell Cycle Synchronized Porcine
 RT Fetal Fibroblasts";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AF339021; AAK28550.1; -;
 DR HSSP; C63450; 1AG6.
 DR InterPro; IPR000959; POLO_box.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR022290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00659; POLO_box; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50078; POLO_BOX; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER 1
 FT NON_TER 526
 SQ SEQUENCE 526 AA; 60399 MW; 1AFA1E5E09B2CBB3 CRC64;

Query Match 87.8%; Score 43; DB 6; Length 526;
 Best Local Similarity 77.8%; Pred. No. 3.3;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9

DB 199 LLVGKPPFE 207

RESULT 7

Q9GRB7 PRELIMINARY; PRT; 582 AA.

DT 01-MAR-2001 (TREMBlrel. 16, Created).
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update).
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update).
 DE Polo-like kinase.
 GN UPLK.
 OS Hemichentrotus pulcherrimus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinozoa; Echinacea; Echinoida; Strongylocentrotidae;
 OC Hemichentrotus.
 CX NCBI_TaxID=7650;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Yonemura I., Fujimoto H., Mabuchi I.,
 RT "Cloning of sea urchin polo-like kinase";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AB043897; BAB18588.1; -;
 DR InterPro; IPR001395; Aldo/ket_red.
 DR InterPro; IPR000959; POLO_box.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR022290; Ser_thr_pkinase.
 DR Pfam; PF00369; pkinase; 1.
 DR Pfam; PF00659; POLO_box; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00063; ALDO-KETO_REDUCTASE_3; 1.
 DR PROSITE; PS50078; POLO_BOX; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 582 AA; 66429 MW; A3774A0CAACFDESD CRC64;

Query Match 87.8%; Score 43; DB 5; Length 582;
 Best Local Similarity 77.8%; Pred. No. 3.7;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9

DB 218 LLVGKPPFE 226

RESULT 8

P70032 PRELIMINARY; PRT; 598 AA.

DT 01-FEB-1997 (TREMBlrel. 02, Created).
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update).
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update).

DE Plxl1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
CC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96355660; PubMed=8703070;
RA Kumagai A., Dunphy W.G.;
RT "Purification and molecular cloning of Plxl1, a Cdc25-regulatory kinase
from Xenopus egg extracts.";
RJ Science 273:1377-1382(1996).
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U58205; AAC60017.1; --
DR HSSP: Q63450; 1A06.
DR InterPro; IPR0003959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 598 AA; 68211 MW; 2467195911F225E6 CRC64;

Query Match 87.8%; Score 43; DB 13; Length 598;
Best Local Similarity 77.8%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9
Db 235 LLVGKPPFE 243

RESULT 9
Q8IU35 PRELIMINARY; PRT: 623 AA.
AC Q8IU35;
DT 01-MAR-2003 (TrEMBLrel. 23, Created);
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE POLO-like kinase.
GN Plk.
OS Asterina pectinifera (Starfish).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
CC Asterozoa; Valvatacea; Valvatida; Asterinidae; Asterina.
OX NCBI_TaxID=7594;
RN [1]
RP SEQUENCE FROM N.A.
RA Uchida T.C., Tachibana K., Kishimoto T.;
RT "Starfish Plk.";
RJ Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: ABC84465; BAC22692.1; --
KW Kinase.
SQ SEQUENCE 623 AA; 70929 MW; CFC0190C8C2D724A CRC64;

Query Match 87.8%; Score 43; DB 5; Length 623;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9
Db 220 LLVGKPPFE 228

RESULT 10
Q91891 PRELIMINARY; PRT: 80 AA.
ID Q91891

AC Q91891;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Hypothetical 9.4 kDa protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
CC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Bouvet P., Omilli F., ARLOT-BONNEVAIN Y., Legagneux V., Roghi C.,
Bassez T., OSBORNE H.;
RT "Deadenylation conferred by the 3'Untranslated region of a
developmentally controlled mRNA in xenopus embryos is switched to
polyadenylationby deletion of a short sequences element.";
RJ Mol. Cell. Biol. 14:1893-1900(1995).
DR EMBL: Z24453; CAA80826.1; --
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; ATP-binding; Transferase.
FT NON_TER 1
SQ SEQUENCE 80 AA; 9388 MW; 8DFCEDBA14BE14FB CRC64;

Query Match 83.7%; Score 41; DB 13; Length 80;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPFE 9
Db 3 LVGKPPFE 10

RESULT 11
O01427 PRELIMINARY; PRT: 305 AA.
ID O01427
AC O01427;
DT 01-JUL-1997 (TrEMBLrel. 04, Created);
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE C. ELEGANS AURORA/IPL1-related protein KINASE 2 (AIR-2) (GB:AF071207).
DE CONTAINS SIMILARITY TO PFAM domain PF00069 (PKINASE), SCORE=295.1,
DE E-VALUE=2.8E-85, N=1 (AIR-2) (PKINASE).
GN AIR-2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
CC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RJ Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Henkhaus J., Wohldmann P.;
RT "The sequence of C. elegans cosmid B0207.";
RJ Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RJ Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;

RA Waterston R.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDAJ databases.
 RN 5;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDAJ databases.
 RN 6;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDAJ databases.
 RN 7;
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2 BRISTOL;
 RA Schumacher C.M., Golden A., Donovan P.J.;
 RT "AIR-2: An aurora/1p1-related protein kinase associated with
 RT chromosomes and midbody microtubules is required for polar body
 RT extrusion and cytokinesis in C. elegans embryos.";
 RL J. Cell Biol. 0:0-0(1998).
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; U97196; AAB52459.2; -;
 DR EMBL; AF031207; AAC70945.2; -;
 DR HSSP; P24941; 1AQ1.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 105 AA; 34749 MW; 1635EB3602E14011 CRC64;

Query Match 83.7%; Score 41; DB 5; Length 325;
 Best Local Similarity 87.5%; Pred. No. 4.8;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MLGKPPFE 9
 :|||:
 DB 220 LVGKPPFE 227

RESULT 12
 ID 062567 PRELIMINARY; PRT; 677 AA.
 AC 062567;
 DT 01-AUG-1999 (TrEMBLrel. 07, Created)
 DT 01-AUG-1999 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Serine/threonine protein kinase.
 CS Suberites domuncula (Sponge).
 CC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 CC Hadromerida; Suberitidae; Suberites.
 CX NCBI_TaxID=555567;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mueller W.E.G.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DDAJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96394688; PubMed=8798342;
 RA Kruse M., Gamulin V., Cetkovic H., Panzer Z., Mueller I.M.,
 RA Mueller W.E.G.;
 RT "Molecular evolution of the Metazoa protein kinase C multigene
 RT family.";
 RL J. Mol. Evol. 43:374-383(1996).
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC 1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 DR EMBL; Y13099; CAA73553.1; -;
 DR HSSP; P29867; 1PTQ.
 DR InterPro; IPR000008; C2.

DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000961; pkinase C.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00130; DAG_PE-bind; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase C; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR PROSITE; PS00499; C2_DOMAIN_1; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 673 AA; 77344 MW; 86D24E554977C293 CRC64;

Query Match 81.6%; Score 40; DB 5; Length 673;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9
 :|||:
 DB 535 MLVGRPPFD 543

RESULT 13

096997
 ID 096997 PRELIMINARY; PRT; 677 AA.
 AC 096997;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Protein kinase C.
 GN PKC2.
 OS Geodia cydonium (Sponge).
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 CC Astrophorida; Geodiidae; Geodia.
 CX NCBI_TaxID=5047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99147839; PubMed=10023072;
 RA Seack J., Kruse M., Mueller I.M., Mueller W.E.G.;
 RT "Promoter and exon-intron structure of the protein kinase C gene from
 RT the marine sponge Geodia cydonium: Evolutionary considerations and
 RT promoter activity.";
 RL Biochim. Biophys. Acta 1444:241-253(1999).
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC 1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 DR EMBL; Y17882; CAA76911.1; -;
 DR HSSP; P28867; 1PTQ.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000961; pkinase C.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00130; DAG_PE-bind; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase C; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00008; DAGPEDOMAIN.

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DR ProDom: PC000001; Prot_kinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00133; S_TK_X; 1.
DR PROSITE: PS00499; C2_DOMAIN_1; 1.
DR PROSITE: PS00004; C2_DOMAIN_2; 1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 677 AA; 76787 MW; 530025081B129A33 CRC64;

Query Match      81.6%; Score 40; DB 5; Length 677;
Best local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 MLLGKPPPE 9
DB      539 MLVGRPFDF 547

RESULT 14
Q03407      PRELIMINARY;      PRT;      766 AA.
AC Q03407;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE D8035.33P.
GN PKH1 OR D8035.33 OR YDR490C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1];
RP SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Beino A.,
RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunkeler-Smith S., Hyman R., Kemp C., Lashkari D., Lew H., Lin E.,
RA Mosedale D., Nakahara K., Narath A., Gefner P., Oh C., Petel F.X.,
RA Roberts D., Schiarm S., Schroeder M., Sheguren T., Shroff N.,
RA Wabant A., Yelton M., Botstein D., Davis R.W.
RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [2];
RP SEQUENCE FROM N.A.
RA Dietrich F.S.
RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3];
RP SEQUENCE FROM N.A.
RA Jia Y., Cherry J.M.;
RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U33050; AAB64917.1; -
DR HSSP; P28523; 1LR4.
DR SGO; S0002898; PKH1.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PC00001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 766 AA; 86252 MW; 75FD32E6B8EBC367 CRC64;

Query Match      81.6%; Score 40; DB 5; Length 766;
Best local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY      1 MLLGKPPPE 9
DB      330 MLAGKPPPF 338

RESULT 15
Q97143      PRELIMINARY;      PRT;      769 AA.
AC Q97143;
DT 01-MAY-1999 (TrEMBLrel. 10, Created);
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE SAK protein.
GN SAK OR CG7186.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Saxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell C.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey J., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2];
RP SEQUENCE FROM N.A.
RA Hudson J.W., Dennis J.W.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003594; AAF51737.1; -
DR EMBL; AF106952; AAD19607.1; -
DR HSSP; P00518; 1PHK.
DR FlyBase; FBgn0026371; SAK.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.

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DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR PRODOM: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00078; POLO_BOX; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 769 AA; 85886 MW; F0508F60A5094AA4 CRC64;

Query Match 81.6%; Score 40; DB 5; Length 769;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
 :|||:
 Db 206 LLVGRPPPE 214

RESULT 16

Q8PEX7 PRELIMINARY; PRT; 2883 AA.
 AC Q8PEX7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Shikimate kinase.
 GN XAC4213.
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 CC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 RN 1.
 RP SEQUENCE FROM N.A.
 RC STRAIN=3306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach P.C., Farah C.S., Furlan L.R.,
 RA Quadrigio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves J.M.C., do Amaral A.M., Bertolini M.C., Camargo L.R.A.,
 RA Camarotte G., Canavan F., Cardoso G., Chambergo P., Ciapina L.P.,
 RA Ciccarelli R.M.B., Coutinho L.B., Cursino-Santos J.R., El-Derry H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.T.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.F., Lemos E.G.M., Lemos M.V.F.,
 RA Locati B.C., Machado M.A., Madella A.M.B.N., Martinez-Bossi N.M.,
 RA Martins E.C., Melandris C., Menck C.E.M., Miyaki C.Y., Moon S.H.,
 RA Moreira L.N., Novo M.T.M., Okura V.F., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C.A., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.L.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.N., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities."
 RL Nature 417:459-463(2002).
 DR EXBL: AE012073; AAM39048.1;
 DR InterPro: IPR03439; ABC_transporter.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW Kinase; Complete proteome.
 SQ SEQUENCE 2883 AA; 313973 MW; 6AE3D657B4507D3D CRC64;

Query Match 81.6%; Score 40; DB 16; Length 2883;
 Best Local Similarity 66.7%; Pred. No. 75;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
 :|||:
 Db 1966 LLGKPPPYD 1974

RESULT 17

Q95ZT2 PRELIMINARY; PRT; 270 AA.
 AC Q95ZT2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein F47F2.1a.
 GN F47F2.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN 1.
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN 2.
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Bentley D.;
 RT "The sequence of C. elegans cosmid F47F2.";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN 3.
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: U40943; AAK39236.1;
 DR WormPep: F47F2.1a; CE27166.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR00719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00433; pkinase_C; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR PRODOM: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 270 AA; 31346 MW; CEFFB41BC995B6A5 CRC64;

Query Match 79.6%; Score 39; DB 5; Length 270;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 8
 :|||:
 Db 150 MYVGKPPF 157

RESULT 18

Q8MQ39 PRELIMINARY; PRT; 325 AA.
 AC Q8MQ39;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein F47F2.1c.
 GN F47F2.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN 1.
 RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN (2);
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid F47F2.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN (3);
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U40943; AAM69117.1; -;
DR WormPep; F47F2.1c; CE31171.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 325 AA; 37528 MW; 210DFB8A13FC18D7 CRC64;

Query Match 79.6%; Score 39; DB 5; Length 325;
Best Local Similarity 75.0%; Pred.No. 13;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 205 MMVGKPPF 212

RESULT 19
Q20541
ID Q20541 PRELIMINARY; PRT; 371 AA.
AC Q20541;
DT 01-NOV-1996 (TrEMBLrel. 01, Created).
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update).
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update).
DE Cyclic AMP-dependent protein kinase, catalytic subunit (EC 2.7.1.37).
DE (Hypothetical) protein F47F2.1b).
GN F47F2.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN (1);
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RX MEDLINE=99187058; PubMed=10085246;
RA Tabish M., Clegg R.A., Rees H.H., Fisher M.J.;
RT "Organization and alternative splicing of the Caenorhabditis elegans
cyclic AMP-dependent protein kinase (PK-A) catalytic subunit gene
(kin-1).";
RT Biochem. J. 339:209-216(1999).
RN (2);
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;

RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN (3);
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid F47F2.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN (4);
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ012357; CAB41352.1; -;
DR EMBL; U40943; AAK72061.1; -;
DR HSSP; P05132; IATP.
DR WormPep; F47F2.1b; CE04603.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 371 AA; 42486 MW; 0C4973B5F3A45661 CRC64;

Query Match 79.6%; Score 39; DB 5; Length 371;
Best Local Similarity 75.0%; Pred.No. 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 251 MMVGKPPF 258

RESULT 20
Q9M3V7
ID Q9M3V7 PRELIMINARY; PRT; 454 AA.
AC Q9M3V7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created).
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update).
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update).
DE S6 ribosomal protein kinase.
GN PK1.
OS Asparagus officinalis (Garden asparagus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asparagaceae;
OC Asparagaceae.
CX NCBI_TaxID=4686;
RN (1);
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Conovers Colossal;
RA Deacon K., Warner S.A.J., Draper J.;
RT "Characterisation of an Asparagus S6 ribosomal protein cDNA and an S6
ribosomal protein kinase homologue.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ277534; CAB89082.1; -;
DR HSSP; Q63450; iA06.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.


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DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Ribosomal protein;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 454 AA; 50467 MW; 0E4DEC5250997C5 CRC64;

Query Match 79.6%; Score 39; DB 10; Length 454;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 315 MLTGKPPF 322

RESULT 21
Q8LFC1
ID Q8LFC1 PRELIMINARY; PRT; 465 AA.
AC Q8LFC1;
DR 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative ribosomal-protein S6 kinase ATPK6.
CS Arabidopsis thaliana (mouse-ear cress);
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eucosids 1; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Troupkan M., Alexandrov N.,
RA Feldmann K.,
RA "Full-length cDNA from Arabidopsis thaliana";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.
EMBL; AY084935; AAY61496.1;
DR InterPro; IPR000361; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR00245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 465 AA; 52587 MW; D51EA5FF159E823 CRC64;

Query Match 79.6%; Score 39; DB 10; Length 465;
Best Local Similarity 87.5%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 324 MLTGKPPF 331

RESULT 22

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Q43380
ID Q43380 PRELIMINARY; PRT; 480 AA.
AC Q43380;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative pp70 ribosomal protein S6 kinase.
GN ASPK11.
OS Avena sativa (Oat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Aveneae; Avena.
OX NCBI_TaxID=4498;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Rhiannon; Tissue=Aleurone;
RX MEDLINE=95284341; PubMed=766874;
RA Huttly A.K., Phillips A.L.;
RT "gibberellin regulated expression in oat aleurone cells of two kinases
RT that show homology to nap kinase and a ribosomal protein kinase.";
RL Plant Mol. Biol. 27:1043-1052(1995).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; X79992; CAA56313.1;
DR HSSP; P05132; ICTP.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Ribosomal protein;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 480 AA; 53532 MW; 33596A101DBB077D CRC64;

Query Match 79.6%; Score 39; DB 10; Length 480;
Best Local Similarity 87.5%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 341 MLTGKPPF 348

RESULT 23
Q12701
ID Q12701 PRELIMINARY; PRT; 592 AA.
AC Q12701;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein kinase (EC 2.7.1.37).
GN KSG1 OR SPC576.15C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H90;
RA Niederberger C.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

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DR EMBL: X99280; CAA67672.1; -
DR EMBL: AL031798; CAA21194.1; -
DR GeneB Spombe: SPCG576.15C; -
DR InterPro: IPR001849; PH.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00669; pkinase; 1.
DR ProDom: P000001; Prot_kinase; 1.
DR SMART: SM00233; PH; 1.
DR SMART: SM00220; STKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00117; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00138; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 592 AA; 65661 MW; B9A857D1989F2C61 CRC64;

Query Match 79.6%; Score 39; DB 3; Length 592;
Best Local Similarity 87.5%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 305 MLAGKPPF 312

RESULT 24
Q8F6Y5 PRELIMINARY; PRT; 1959 AA.
AC Q8F6Y5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Probable serine/threonine-protein kinase.
GN LA1164.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar ial;
RA Ref. S.;
RJ Submitted (MAR-2002) to the EMBL/GenBank/CCRC databases.
DR EMBL: AE011299; AAN48363.1; -
KW Kinase; Complete proteome.
SQ SEQUENCE 1759 AA; 203646 MW; 5254410941E358H6 CRC64;

Query Match 79.6%; Score 39; DB 16; Length 1759;
Best Local Similarity 87.5%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLLGKPPF 9
DB 205 LTKKPPF 212

RESULT 25
Q8XQB2 PRELIMINARY; PRT; 2483 AA.
AC Q8XQB2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE SKWP protein 2.
GN RSP1374 OR RS02084.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
CC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GX11000;
RX MEDLINE=21681879; PubMed=11823852;

Query Match 79.6%; Score 39; DB 16; Length 2497;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 9
DB 1545 VLLGKPPYD 1553

RESULT 27
Q63432 PRELIMINARY; PRT; 240 AA.
AC Q63432;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rat protein kinase C-family related (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL: AL646084; CAD18525.1; -
KW Plasmid; Complete proteome.
SQ SEQUENCE 2483 AA; 272286 MW; 21E5F0A4EBA83614 CRC64;

Query Match 79.6%; Score 39; DB 16; Length 2483;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 9
DB 1521 VLLGKPPYD 1529

RESULT 26
Q8XYB9 PRELIMINARY; PRT; 2497 AA.
AC Q8XYB9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE SKWP protein 4.
GN RSC1839 OR RS04276.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
CC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GX11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL: AL646067; CAD15541.1; -
KW Complete proteome.
SQ SEQUENCE 2497 AA; 270604 MW; 128F29A75D3C5F99 CRC64;

Query Match 79.6%; Score 39; DB 16; Length 2497;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 9
DB 1545 VLLGKPPYD 1553

RESULT 27
Q63432 PRELIMINARY; PRT; 240 AA.
AC Q63432;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rat protein kinase C-family related (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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Query Match: 77.6%; Score 38; DB 16; Length 332;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
:|||||
DB 262 ILLGPPPE 270

RESULT 30

Q95T78 PRELIMINARY; PRT; 554 AA;
AC Q95T78;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE GH1363P.
GN PKC98E OR CG1954.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungali S.J.,
RA Nanoo J., Pacleb J., Paragas V., Park S., Phouangavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.
ED Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC 1-1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AY060293; AAU25332.1; -
DR FlyBase; FBgn00303093; PKC98E.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR PRINTS; PR00109; C1; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine protein kinase; Transferase.
SQ SEQUENCE 554 AA; 61598 MW; 300FA905993801F4 CRC64;

Query Match: 77.6%; Score 38; DB 5; Length 554;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
:|||||
DB 415 MXAGPPPE 423

RESULT 31

Q8MXG6 PRELIMINARY; PRT; 646 AA;
AC Q8MXG6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fig. 4 protein (corresponding sequence F55A8.2A).

GN F55A8.2 OR EGL-4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Langston Y., Wohldmann P., Ducke's G.;
RT "The sequence of C. elegans cosmid F55A8.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067612; AAM98011.1; -
DR WormPep; F55A8.2d; CE31542.
DR InterPro; IPR002373; CAMP_kin.
DR InterPro; IPR002374; GMP_kin.
DR InterPro; IPR000595; GMP_binding.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00027; GMP_binding; 2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR PRINTS; PR00133; CAMP_KINASE.
DR PRINTS; PR00104; GMP_KINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00100; GMP; 1.
DR SMART; SM00133; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00888; GMP_BINDING_1; 1.
DR PROSITE; PS00889; GMP_BINDING_2; 1.
DR PROSITE; PS00042; GMP_BINDING_3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 568 AA; 65094 MW; 423AB3BD6E52ACF4 CRC64;

Query Match: 77.6%; Score 38; DB 5; Length 568;
Best Local Similarity 55.6%; Pred. No. 36;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
:|||||
DB 448 LMLGRPPPE 456

RESULT 32

Q8NU98 PRELIMINARY; PRT; 646 AA;
AC Q8NU98;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serine/threonine protein kinases (EC 2.7.1.-).
GN CGL004.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacterium.

Query Match 77.6%; Score 38; DB 5; Length 707;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
Db 570 MWAGQPPFE 578

RESULT 35

Q8MXG7 PRELIMINARY; PRT; 749 AA.
AC Q8MXG7
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE EGI-4 protein (corresponding sequence F55A8.2C).
GN F55A8.2 OR EGI-4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Langston Y., Wohlmann P., Duckels G.
RT "The sequence of C. elegans cosmid F55A8."
RJ Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RE [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.
PL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CR EMBL; AF067612; AAM98010.1;
CR WormPep; F55A8.2C; CE31541.
DR InterPro; IPR002373; CAMP_kin.
DR InterPro; IPR002374; GMP_kin.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR000961; pkinase_C.
DR InterPro; IPR007119; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR01245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00069; pkinase; 2.
DR PRINTS; PR00103; CAMPKINASE.
DR ProDom; PDC00001; Prot_kinase; 1.
DR SMART; SM00100; cNMP; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 2.
DR PROSITE; PS00889; cNMP_BINDING_2; 2.
DR PROSITE; PS00042; cNMP_BINDING_3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 749 AA; 84497 MW; ADEG99F6354D9326 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 749;
Best Local Similarity 55.6%; Pred. No. 48;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
Db 629 LMLGRPPFQ 637

RESULT 36

Q8MXB6 PRELIMINARY; PRT; 754 AA.
AC Q8MXB6
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20356442; PubMed=10901270;
RA Wang Y., Cao Z., Reid E.A., Newkirk R.F., Ivy M.T., Townse J.G.
RT "The use of competitive PCR mimic to evaluate a Limulus lambda phage
genomic DNA library."
RL Cell. Mol. Neurobiol. 20:509-520(2000).
CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; AF289084; AAM90321.1; .
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE_bind.
DR InterPro; IPR000961; pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE_bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 754 AA; 85488 MW; BF16A40497E2BB40 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 754;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
Db 607 MWAGQPPFE 615

RESULT 37

O76360 PRELIMINARY; PRT; 780 AA.
ID O76360
AC O76360;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 86.7 kDa protein F55A8.2 in chromosome IV.
GN F55A8.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Langston Y., Wohlmann P., Duckels G.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B, MAY BE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF067612; AAD36954.1; -
DR EMBL: AF067612; AAD36953.1; -
DR HSSP: P05132; 1APM.
DR WormPep; F55A8.2a; CE19897.
DR WormPep; F55A8.2b; CE19898.
DR InterPro; IPR002374; GMP_kin.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00027; cNMP_binding; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PRC0104; GMPKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00100; cNMP; 2.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 2.
DR PROSITE; PS00889; cNMP_BINDING_2; 2.
DR PROSITE; PS00042; cNMP_BINDING_3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Alternative splicing, Kinase;
KW Serine/threonine-protein kinase; Transferase.
FT VARSPLIC 1 52 MSSGRPSGGGGGGGAGGAGGGGAGGGGIRGFFSKL
ET RKPSDPPNGQ -> MKQQRRLY (IN ISOFORM B).
SQ SEQUENCE 790 AA; 86741 MW; 55E036AF50F2E002 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 925;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCGRPPPF 9
DB 660 LMLGRPPPFQ 668

RESULT 18
Q8R015 PRELIMINARY; PRT; 925 AA.
AC Q8R015;
DT 01-JUN-2002 (TrEMBLrel. 21, Created
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 103.9 kDa protein.
GN Stk18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BCC26785; AAH26785.1; -
DR MGD; MGI:101783; Stk18.
DR InterPro; IPR000959; POLO_box.

DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00078; POLO_BOX; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 925 AA; 103861 MW; 844AFF8C9AAC54C1 CRC64;

Query Match 77.6%; Score 38; DB 11; Length 925;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCGRPPPF 9
DB 204 LMLGRPPPF 212

RESULT 39
Q64702 PRELIMINARY; PRT; 925 AA.
AC Q64702;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SMK/PLK-AKIN Kinase (Protein Kinase SMK/PLK-AKIN) (EC 2.7.1.1).
GN STK18 CR SAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JBA/2; TISSUE=Lymphoma;
RX MEDLINE=94294387; PubMed=8022793;
RA Fode C., Motro B., Yousefi S., Heffernan M., Dennis J.W.;
ET "Sak, a murine protein-serine/threonine kinase that is related to the
RT Drosophila polo kinase and involved in cell proliferation.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:6388-6392(1994).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SAK-A (SHOWN HERE) AND SAK-B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
DR EMBL: L29479; AA14448.1;
DR EMBL: L29480; AA14449.1;
DR HSSP; Q80534; 1B18.
DR MGD; MGI:101783; Stk18.
DR InterPro; IPR000959; POLO_BOX.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00078; POLO_BOX; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Alternative splicing; Serine/threonine-protein kinase;
KW Transferase.
FT VARSPLIC 417 464 SSNHCLGKTPFPFADQTPQMEMVQQWFGNLMNAHLGETN
ET EHTVSP -> RYSPTKSNVNVLTSLTKQPIVKOLLKDRI
FT MTEQYKDNLLNLLNKFDR (IN ISOFORM SAK-B).
FT MISSING (IN ISOFORM SAK-B).
SQ SEQUENCE 925 AA; 103685 MW; D868A76BB7343E81 CRC64;

Query Match 77.6%; Score 38; DB 11; Length 925;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCGRPPPF 9

Db 204 MLGRPPFD 212

RESULT 40
Q96Q95 PRELIMINARY; PKT; 970 AA.
AC Q96Q95;
DT 01-DEC-2001 (TREMBLrel. 19, Created;
DT 01-DEC-2001 (TREMBLrel. 19, Last: sequence update;
DT 01-MAR-2003 (TREMBLrel. 23, Last: annotation update;
DE Sak.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=21486437; PubMed=11489907;
RA Yarashita Y., Kajiigaya S., Yoshida K., Ueno S., Ota J., Ohmine K.,
RA Ueda M., Miyazato A., Ohya K., Kitamura T., Ozawa K., Mano H.;
RT "Sak Serine-Threonine Kinase Acts as an Effector of Testosterone
RT Kinase";
RL J. Biol. Chem. 276:39012-39020(2001).
DR EMBL; AR03972; BAB6958.1; .
DR HSSP; P24941; 1BUH.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000729; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PDC00001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00078; POLO_BOX; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; transferase.
SQ SEQUENCE 970 AA; 109084 MW; 1F431FA607A1550A CRC64.

Query Match: 77.6%; Score 18; DB 4; Length 970;
Best Local Similarity 55.6%; Pred. No 60;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRPPFD 9

Db 204 MLGRPPFD 212

Search completed: November 14, 2003, 13:59:07
Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 12:54:54 / Search time 34.7143 Seconds
(without alignment)
41151 Million cell updates/sec

Title: US-09-736-076-18
Perfect score: 49
Sequence: 1 LORPPFETS 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1:07863 seqs, 158726573 residues 1107863
Total number of hits satisfying chosen parameters.

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database	A Geneseq	19Jun03	*
1	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT	*	
2	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	*	
3	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT	*	
4	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT	*	
5	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT	*	
6	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT	*	
7	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT	*	
8	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT	*	
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11	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT	*	
12	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT	*	
13	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT	*	
14	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT	*	
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17	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT	*	
18	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT	*	
19	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT	*	
20	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT	*	
21	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT	*	
22	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT	*	
23	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT	*	
24	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT	*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	20	AAW74162
2	49	100.0	9	23	AAU98318
3	49	100.0	11	20	AAW74163
4	49	100.0	11	23	AAU98319
5	46	93.9	469	22	AAU98319
6	46	93.9	469	22	AAU98319
7	46	93.9	626	21	AAU98319
8	46	93.9	695	20	AAU98319
9	46	93.9	685	20	AAU98319

10	46	93.9	685	23	ABP61474	Human NF KB activa
11	46	93.9	753	23	ABP41992	Human ovarian anti
12	43	87.8	20	20	AAW74173	HJ loop peptide PO
13	43	87.8	20	23	AAU98306	peptide sequence o
14	43	87.8	329	21	AAU56690	Human prostate can
15	43	87.8	531	23	AAU74656	Mammalian polo-like
16	43	87.8	503	16	AAU74620	Human lung tumour
17	43	87.8	603	23	AAU79306	Mouse polo-like ki
18	43	87.8	603	23	AAU79308	Mouse polo-like ki
19	43	87.8	603	23	AAU79309	Mouse polo-like ki
20	43	87.8	603	23	AAU79310	Mouse polo-like ki
21	43	87.8	603	23	AAU79311	Mouse polo-like ki
22	43	87.8	603	23	AAU79312	Mouse polo-like ki
23	43	87.8	603	23	AAU79313	Mouse polo-like ki
24	43	87.8	603	23	AAU79314	Mouse polo-like ki
25	43	87.8	603	23	AAU79315	Mouse polo-like ki
26	43	87.8	603	23	AAU79316	Mouse polo-like ki
27	43	87.8	603	23	AAU79317	Mouse polo-like ki
28	43	87.8	603	23	AAU79318	Mouse polo-like ki
29	43	87.8	603	23	AAU79319	Mouse polo-like ki
30	43	87.8	603	23	AAU79320	Mouse polo-like ki
31	43	87.8	603	24	ABR48196	Human bladder canc
32	42	85.7	769	22	ABR63267	Drosophila melanog
33	40	81.6	9	20	AAW74159	HJ loop peptide J-
34	40	81.6	9	23	AAU98315	Polo kinase serine
35	40	81.6	10	20	AAW74213	HJ loop peptide KO
36	40	81.6	10	23	AAU98357	Polo kinase SNK se
37	40	81.6	416	17	AAU92176	Sak serine-threoni
38	40	81.6	464	17	AAU92214	SAK-b serine-threo
39	40	81.6	925	17	AAU92177	SAK-a serine-threo
40	40	81.6	925	23	ABR57273	Mouse ischaemic co
41	40	81.6	970	22	AAU78833	Human protein SEQ
42	40	81.6	970	22	AAU39244	Human polypeptide
43	40	81.6	980	22	AAU79817	Human protein SEQ
44	40	81.6	980	22	AAU41030	Human polypeptide
45	39	79.6	183	20	AAU36843	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAW74162
ID AAW74162 standard; peptide; 9 AA.

AC AAW74162;
XX
DT 05-MAY-1999 (first entry)
XX
DE HJ loop peptide J 45.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haerorthagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 9 /note= "amidated"
FT
XX

PN WO9853050-A2
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-0510319.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL) CHILDRENS MEDICAL CENT.

XX Ben-Sasson SA;
PI WPI; 1999-070142/06.
XX
XX
PT New peptides for modulating serine/threonine kinase activity
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
XX Claim 14; Fig 4; 70pp; English.
XX
XX This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 49; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LGRPPFFETS 9
Db 3 LGRPPFFETS 11
RESULT 4
AAU98319
ID AAU98319 standard; Peptide; 11 AA.
XX
XX
AC AAU98319;
XX
XX 13-AUG-2002 (first entry)
XX
XX Polo kinase serine-threonine kinase HJ loop peptide J-46.
XX
XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; J-46.
XX
XX Unidentified.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Misc-difference 9
FT Modified-site 1 /note= "Benzyl ester of Glutamic acid"
FT Modified-site 1 /note= "C-terminal amide"
XX
XX US2002049301-A1.
PN
XX 25-APR-2002.
PJ
XX 13 DEC-2000; 2000US-0736076.

XX 21-MAY-1997; 97US-0861338.
PR (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Ben-Sasson SA;
PI WPI; 2002-462787/49.
XX
XX New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX
XX Disclosure; Fig 4; 41pp; English.
XX
XX The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-46. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 49; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LGRPPFFETS 9
Db 3 LGRPPFFETS 11
RESULT 5
AAB94717
ID AAB94717 standard; Protein; 469 AA.
XX
XX
AC AAB94717;
XX
XX 26-JUN-2001 (first entry)
XX
XX Human protein sequence SEQ ID NO:15726.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
XX Homo sapiens.
OS
XX EP1074617-A2.
PN
XX 07-FEB-2001.
PJ
XX 28-JUL-2000; 2000EP-0116126.
XX
XX 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
XX (HELI-) HELIX RES INST.
PA
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI; 2001-318749/34.
DR
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602

PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full length cDNAs -
 XX
 PS Claim 8; SEQ ID 15726; 2537pp - CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5' end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH3166 to AAH3628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 469 AA;

Query Match 93.9%; Score 46; DB 22; Length 469;
 Best Local Similarity 88.9%; Pred. No. 2.5;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
 |||||
 Db 59 LGRPPFFETT 67

RESULT 6
 AAG67426
 ID AAG67426 standard; Protein; 469 AA.

XX AAG67426;
 AC
 XX 26-NOV-2001 (first entry)
 XX
 DE Amino acid sequence of a human protein kinase; protein phosphatase.
 KW Human; protein kinase; protein phosphatase; signal transduction;
 KW intracellular signalling pathway.
 XX
 OS Homo sapiens.
 XX
 PN WO200109345-A1.
 XX
 PD 08 FEB-2001.
 XX
 PF 28-JUL-2000; 2000WO-JP05060.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 18-OCT-1999; 99US-0159590.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 17-FEB-2000; 2000US-0183322.
 PR 02-MAY-2000; 2000JP-0183767.
 XX
 PA (HELI-) HELIX RES INST.
 XX

Cta T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Furahashi S;
 Senoo C, Nezu J;
 XX

DR WPI; 2001-564736/63.
 DR N-PSDB; AAH78069.
 XX
 PT New genes encoding protein kinase and protein phosphatase, useful for
 PT identifying modulators which can be used to treat human or animal
 PT disorders associated with the expression or function of these enzymes -
 XX
 PS Claim 2; Page 136-139; 336pp; Japanese.
 XX
 CC The present sequence represents a human protein kinase/protein
 CC phosphatase. The polypeptides are expected to participate in signal
 CC transduction in cells. The kinase phosphatases are connected with
 CC intracellular signalling pathways. Antisense oligonucleotides and
 CC compounds identified by screening (agonists or antagonists) can be
 CC used to treat human or animal disorders associated with the expression
 CC or function of the protein. In addition, the polypeptides may be used
 CC as target molecules for drug development.
 XX
 SQ Sequence 469 AA;

Query Match 93.9%; Score 46; DB 22; Length 469;
 Best Local Similarity 88.9%; Pred. No. 2.5;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
 |||||
 Db 59 LGRPPFFETT 67

RESULT 7
 AAB35805
 ID AAB35805 standard; Protein; 626 AA.

XX AAB35805;
 AC
 XX 23-FEB-2001 (first entry)
 DT
 XX
 DE Protein involved in cell cycle regulation SEQ ID 46.
 XX
 KW Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
 KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
 KW cotton; rice; barley; millet.
 XX
 OS Zea mays.
 XX
 PN WO2000065040-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 13-APR-2000; 2000WO-US09975.
 XX
 PR 22-APR-1999; 99US-0130849.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Helentjaris TG, Habben JE, Sun Y;
 XX
 DR WPI; 2000-687333/67.
 DR N-PSDB; AAC83112.
 XX
 PT Nucleic acids useful for producing transgenic plants, preferably maize,
 PT with increased cell cycle gene activity, preferably activity of cyclin
 PT and/or cyclin-dependent kinase -
 XX
 PS Claim 16; Page 117-118; 122pp; English.
 XX

CC Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
 CC AAB35806 which are involved in regulating the cell cycle. The protein and
 CC DNA sequences have been isolated from Zea mays (corn), and the invention
 CC also includes oligonucleotides AAC83114 - AAC83139 which are related to
 CC the cell cycle polynucleotides. The cell cycle polynucleotide sequences
 CC are useful for producing transgenic plants such as maize, soybean,
 CC sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and

CC millet with increased levels of cell cycle gene activity, such as
 CC activity of cyclin and cyclin-dependent kinases. The DNA sequences are
 CC also useful as probes for detecting deficiencies in the level of mRNA in
 CC screening for desired transgenic plants, for detecting mutations in the
 CC gene, for monitoring upregulation of expression or changes in enzyme
 CC activity in screening assays of compounds, for detecting any number of
 CC allelic variants, orthologs or paralogues of the gene, and site directed
 CC mutagenesis in eukaryotic cells. The DNA sequences are also useful for
 CC recombinant expression of the encoded polypeptides and as immunogens for
 CC preparing and screening antibodies. A transgenic plant comprising an
 CC expression cassette including a cell cycle regulatory gene is useful for
 CC assaying enzyme agonists and antagonists, and as immunogens or antigens
 CC to obtain antibodies. The antibodies are useful in assaying expression
 CC levels of cell cycle regulatory proteins, for identifying and isolating
 CC nucleic acids from expression libraries, for identifying homologues of
 CC polypeptides from other species, and for purification of the proteins.

XX Sequence 626 AA;

SQ Query Match 93.9%; Score 46; DB 21; Length 626;
 Best Local Similarity 88.9%; Pred. No. 3.4;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
 Db 230 VGRPPFFETS 238

RESULT 8
 AAY00915
 ID AAY00915 standard; Protein: 685 AA.
 XX AC AAY00915;
 XX DT 26-MAY-1999 (first entry);
 XX DE Human serum inducible kinase.

XX KW Serum inducible kinase; SNK protein; human; proliferative disease;
 KW leukemia; solid tumour cancer; metastasis; chronic inflammatory;
 KW psoriasis; rheumatoid arthritis; proliferative cardiovascular disease;
 KW restenosis; ocular disorder; diabetic retinopathy; haemangioma;
 KW benign hyperproliferative disease; diagnosis;
 XX CS Homo sapiens.
 XX PN WO9909146-A1.
 XX PD 25-FEB-1999.
 XX PF 20 AUG-1998; 98WO-US17249.
 XX PR 20-AUG-1997; 97US-0056112.
 XX PA (SMK : SMITHKLINE BEECHAM CORP.
 XX PI Anderson KV, Bouzyk M, Hadsbury MJ, Jackson JR,
 XX PI Nerurkar SS, Roshak AK;
 XX WPI; 1999-181027/15.
 XX DR N-PSDB; AAX27227.

XX PF New serum inducible kinase (SNK) polypeptides and polynucleotides -
 XX useful for treating proliferative diseases
 XX Claim 1; Page 39-40; 41pp; English.
 XX This sequence is a human serum inducible kinase (SNK) of the
 CC invention. The invention relates to diagnostic assays or kits for
 CC detecting diseases associated with inappropriate SNK activity or levels.
 CC Disease states that can be diagnosed include proliferative diseases such
 CC as leukemia, solid tumour cancers and metastases, chronic inflammatory
 CC proliferative diseases such as psoriasis and rheumatoid arthritis.

CC proliferative cardiovascular diseases such as restenosis, proliferative
 CC ocular disorders such as diabetic retinopathy and benign
 CC hyperproliferative diseases such as haemangiomas. The polynucleotides can
 CC be used as hybridisation probes for cDNA and genomic DNA or as primers
 CC for a nucleic acid amplification (PCR) reaction, to isolate full-length
 CC cDNAs and genomic clones encoding polypeptides of this invention and to
 CC isolate cDNA and genomic clones of other genes which have a high sequence
 CC similarity to the SNK coding sequence. The differences between cDNA and
 CC genomic sequences can be observed and therefore mutations detected. Any
 CC mutations may then be attributed to likely causative agents of disease.
 CC The nucleotide sequences are also useful for chromosome identification.

XX Sequence 685 AA;

SQ Query Match 93.9%; Score 46; DB 20; Length 685;
 Best Local Similarity 88.9%; Pred. No. 3.7;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
 Db 275 LGRPPFFET 283

RESULT 9
 AAW88432
 ID AAW88432 standard; Protein: 685 AA.
 XX AC AAW88432;
 XX DT 26-APR-1999 (first entry)
 XX DE Disease associated protein kinase DAPK-1.

XX KW DAPK-1; disease associated protein kinase; human; diagnosis;
 KW therapy; adult respiratory distress syndrome; allergy; asthma;
 KW arteriosclerosis; bronchitis; emphysema; hyper eosinophilia;
 KW myocardial inflammation; pericardial inflammation; anaemia;
 KW rheumatoid arthritis; Addison's disease; AIDS; atherosclerosis;
 KW atopic dermatitis; dermatomyositis; diabetes mellitus;
 KW glomerulonephritis; gout; Grave's disease; lupus erythematosus;
 KW multiple sclerosis; myasthenia gravis; osteoarthritis;
 KW osteoporosis; pancreatitis; polycystic kidney disease;
 KW polymyositis; scleroderma; Sjogren's syndrome;
 KW autoimmune thyroiditis; cancer; infection; trauma;
 KW cell proliferation.

XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Binding-site 89..96
 XX FT Peptide /note= "potential ATP binding site"
 XX FT /note= "presumed regulatory sequence common to
 XX FT polo family protein kinases"

XX PN WO9558052-A2.
 XX PD 23-DEC-1998.
 XX PF 19-JUN-1998; 98WO-US12813.
 XX PR 19-JUN-1997; 97US-0878989.
 XX PA (INCY-) INCYTE PHARM INC.
 XX PI Bardman G, Corley NC, Goli SK, Guegler KJ, Hillman JL;
 XX PI Lal P, Shah P;
 XX WPI; 1999-080952/07.
 XX DR N-PSDB; AAX06831.

XX PF New disease associated protein kinases - used to stimulate cell
 XX proliferation and to treat the immune response and cancer

XX
PS Claim 1; Page 54-56; 93pp; English.
XX
CC This is the amino acid sequence of human disease associated protein
CC kinase DAPK-1, as deduced from a consensus sequence (see AAX06831)
CC of overlapping cDNA clones from libraries which are immortalised
CC or cancerous and show inflammatory or immune responses. DAPK-1
CC shows 53% homology to human proliferation-related protein kinase
CC PRK (GI 1488263). The invention provides DAPK 1 to DAPK 7
CC polypeptides (see AAX08432-38) and cDNA clones encoding them (see
CC AAX06831; 36 and AAX06882), as well as expression vectors, host cells,
CC agonists, antagonists and antibodies. The invention further
CC provides uses of such products in the diagnosis, prevention and
CC treatment of diseases associated with cell proliferation,
CC especially cancer or an immune response (elained). Conditions
CC that may be treated include adult respiratory distress syndrome,
CC allergies, asthma, arteriosclerosis, bronchitis, emphysema,
CC hypereosinophilia, myocardial or pericardial inflammation,
CC rheumatoid arthritis, Addison's disease, AIDS, anaemia,
CC atherosclerosis, various diseases of the digestive system, atopic
CC dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis,
CC gout, Grave's disease, lupus erythematosus, multiple sclerosis,
CC myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis,
CC polycystic kidney disease, polymyositis, scleroderma, Sjorgren's
CC syndrome, autoimmune thyroiditis, complications of cancer,
CC extracorporeal circulation, viral, bacterial, fungal, parasitic,
CC protozoal and helminthic infections, and trauma (disclosed).
XX
SQ Sequence 685 AA;
Query Match 93.9%; Score 46; DB 20; Length 685;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPPFETS 9
Db 275 LGRPPPFET 283
RESULT 1:
ABP41474
ID ABP41474 standard; Protein; 685 AA.
XX
AC ABP41474;
XX
DT 30-SEP-2002 (first entry)
XX
DE Human NF KB activating protein SEQ ID NO 101.
XX
KW Human; NF-kB; nuclear factor kappa B; tumour necrosis inflammatory;
KW immunomodulatory; cycostatic; anti-HIV; autoimmune disease; drug screening;
KW neuroprotective; anti-HIV; autoimmune disease; drug screening;
KW bone disease; AIDS; neurodegenerative disease; immunologic disorder.
XX
OS Homo sapiens.
XX
PN WC2002053737-A1.
XX
PD 11-JUL-2002.
XX
PF 25 DEC-2001; 2001WO-JP11359.
XX
PR 28-DEC-2000; 2000JP-0402288.
XX
PR 26-MAR-2001; 2001JP-0088912.
XX
PR 24-AUG-2001; 2001JP-0254018.
XX
PA (ASAH) ASAH KASEI KOGYO KK.
XX
XX Matsuda A, Honda G, Muramatsu S, Nagano Y;
XX
XX WI; 2002-583617/62.
XX
DR N-PSDB; A5Q91962.
XX

PT NF-approximatelyKB activating gene and expressed protein, applicable in
PT diagnosis and screening inhibitors or promoters to control excessive
PT activation or inhibition for treating e.g. inflammations, autoimmune
PT diseases and cancer.
XX
PS Claim 1; Page 449-451; 841pp; Japanese.
XX
CC The invention relates to a purified protein (I), comprising one of 90
CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
CC the sequences but with some amino acids deleted, substituted or added and
CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
CC encoding gene (ABQ91912-ARQ92001) are useful in diagnosis and screening
CC inhibitors or promoters to control excessive activation or inhibition
CC and for treating e.g. inflammations, autoimmune diseases, cancers,
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
CC disorders.
XX
SQ Sequence 685 AA;
Query Match 93.9%; Score 46; DB 23; Length 685;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPPFETS 9
Db 275 LGRPPPFET 283
RESULT 1:
ABP41992
ID ABP41992 standard; Protein; 753 AA.
XX
AC ABP41992;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen. HACSM08, SEQ ID NO:3124.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW anti-inflammatory; gynaecological; reproductive; chromosome 5.
XX
OS Homo sapiens.
XX
PN WC200200677-A1.
XX
PD 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US18569.
XX
PR 07-JUN-2000; 2000US-209467P.
XX
PA (HUYA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
XX WI; 2002-147878/19.
XX
DR N-PSDB; ABQ55069.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases.
XX
PS Claim 11; SEQ ID NO 3124; 2922pp; English.
XX

CC The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution.
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the peptide sequence of the HJ
CC loop of serine-threonine kinase polo kinase. This sequence is one of the
CC short peptides of the invention that selectively modulate the activity
CC of STK.

XX
SQ Sequence 20 AA;
Query Match 87.8%; Score 43; DB 23; Length 20;
Best Local Similarity 77.8%; Pred. No. 0.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
Db 5 VGKPPFFETS 13
:|:|||||

RESULT 14
AAB5669C
ID AAB56690 standard; Protein; 329 AA.
XX
AC AAB5669C;
XX
CC 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen protein sequence SEQ ID NO:1268.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX
CS Homo sapiens.
XX
PN WO2000055174-A1.
XX
PD 21 SEP-2000.
XX
PF 08 MAR-2000; 2003WO-US05988.
XX
PE 12 MAR 1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (RCSE/) RCSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587513/55.
DR N-PSDB; AAF15893.
XX
PT Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer.
PS
PS Claim 11; Page 1691-1692; 2338pp; English.
XX
CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAF566163 to AAF57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome

CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.

XX
SQ Sequence 329 AA;
Query Match 87.8%; Score 43; DB 21; Length 329;
Best Local Similarity 77.8%; Pred. No. 6.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
Db 262 VGKPPFFETS 270
:|:|||||

RESULT 15
AAU74656
ID AAU74656 standard; Protein; 53; AA.
XX
AC AAU74656;
XX
DT 09-APR-2002 (first entry)
XX
DE Mammalian polo-like kinase (Plk).
XX
KW Polo-like kinase; PLK; polo-box; cytostatic; neoplasm;
KW hyperproliferative disorder; cytokinesis; solid tumour;
KW carcinoma; sarcoma; cancer; small cell carcinoma; adenocarcinoma;
KW Mullerian tumour; squamous cell carcinoma; protein.
XX
OS Mammalia.

XX
FH Key Location/Qualifiers
FT Misc-difference 130 /label= Unknown
FT Misc-difference 131 /label= Unknown
FT Misc-difference 132 /label= Unknown
FT Misc-difference 133 /label= Unknown
FT Misc-difference 134 /label= Unknown
FT Misc-difference 135 /label= Unknown
FT Misc-difference 136 /label= Unknown
FT Misc-difference 137 /label= Unknown
FT Misc-difference 138 /label= Unknown
FT Misc-difference 139 /label= Unknown
FT Misc-difference 140 /label= Unknown
FT Misc-difference 141 /label= Unknown
FT Misc-difference 147 /label= Unknown
FT Misc-difference 347 /label= Unknown
FT Misc-difference 348 /label= Unknown
FT Misc-difference 349 /label= Unknown
FT Misc-difference 350 /label= Unknown
FT Misc-difference 351 /label= Unknown
FT Misc-difference 352 /label= Unknown
FT Misc-difference 352 /label= Unknown

FT Misc difference 353 /label= Unknown
FT Misc-difference 354 /label= Unknown
FT Misc-difference 355 /label= Unknown
FT Misc-difference 356 /label= Unknown
FT Misc-difference 357 /label= Unknown
FT Misc-difference 358 /label= Unknown
FT Misc-difference 359 /label= Unknown
FT Misc-difference 360 /label= Unknown
FT Misc-difference 361 /label= Unknown
FT Misc-difference 362 /label= Unknown
FT Misc-difference 363 /label= Unknown
FT Misc difference 364 /label= Unknown
FT Misc-difference 365 /label= Unknown
FT Region 410..439
FT /label= Polo-box
FT /note= "Core polo-box consensus sequence"
XX
PN WC200190401-A2.
XX 29-NOV-2001.
XX 23-MAY-2002; 2001WO-US16903.
XX 23 MAY-2000; 2000US-206588P.
XX (HARD) HARVARD COLLEGE.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (USSH) US NAT INST OF HEALTH.
XX
XX Lee KS, Song S, Erikson R;
XX WPI: 2002 106210/14.
XX
XX identifying polo-like kinase modulators by contacting eukaryotic cells
XX expressing polo-box peptides with test compounds and evaluating changes
XX in dominant negative cytokinesis-defective growth patterns -
XX
XX Example 2; Fig 5; 57pp; English.
XX
XX The invention describes a novel method of detecting compounds with
XX polo-like kinase (PLK) modulating activity. This comprises contacting
XX eukaryotic cells expressing polo-box or polo-box related peptides,
XX binding peptides comprising 25 contiguous residues from a polo-like
XX kinase C-terminal region, with a test compound. Ectopic expression of a
XX polo-box in a eukaryotic cell causes a severe cytotoxic defect in the
XX cell. These eukaryotic cells can also be tested with the test compound
XX used in the method of the invention. The polo-box related peptides and
XX polo like kinase activity modulatory compounds can be used to inhibit or
XX enhance cellular proliferation and subsequently for treating
XX hyper-proliferative disorders including neoplasm, solid tumours,
XX carcinomas, sarcomas and cancers e.g small cell carcinoma,
XX adenocarcinoma, Mullerian tumours and squamous cell carcinomas. This
XX is the amino acid sequence of a mammalian polo-like kinase (Plk),
XX uncontrolled expression of the Plk family is implicated in the
XX development of human cancers, discussed in the method of the invention.
XX
XX Sequence 531 AA;
XX
XX Query Match: 87.8%; Score 43; DB 23; Length 531;
XX Best Local Similarity 77.8%; Pred. No. 10;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPFETS 9
Db 206 VGKPPFETS 214
RESULT 16
AAR74620
ID AAR74620 standard; Protein; 603 AA.
XX
AC AAR74620;
XX
DT 25-MAR-2003 (updated)
DT 26-OCT-1995 (first entry)
XX
DE Human lung tumour Polo-like kinase.
XX
KW Polo-like kinase; PLK; serine threonine kinase; human; lung tumour;
KW auto-immune disease; lymphocyte activity.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 60..86
FT /label= ATP-binding_motif
FT Region 174..177
FT /note= "motif that is highly conserved in protein
FT kinases"
FT Region 194..196
FT /note= "motif that is highly conserved in protein
FT kinases"
XX
PN DE4329177-A1.
XX
XX 02-MAR-1995.
XX
XX 30-AUG-1993; 93DE-4329177.
XX
XX 30-AUG-1993; 93DE-4329177.
XX
XX (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.
XX
XX Holtrich U, Rubsamen-Waigmann H, Strebhardt K;
XX Ruebsamen-Waigmann H;
XX WPI: 1995-099454/14.
XX N-PSDB; AAQ88155.
XX
XX A polo-like serine threonine kinase-protein - isolated from
XX proliferating human tissue, useful in the determn of lymphocyte
XX activity, eg in auto-immune diseases
XX
XX Claim 1; Page 8-10; lipp; German.
XX
XX A human lung tumour-derived cDNA (AAQ88155) was found to have high
XX homology with sequences from members of the serine/threonine kinase
XX family. Due to the strong homology with the Drosophila polo gene,
XX the protein encoded by the new cDNA (AAR74620) was designated a polo-
XX like kinase (PLK). PLK mRNA is expressed in proliferating cells such
XX as placenta, colon and tumours of the lung, oesophagus, gut and
XX intestine. Resting lymphocytes do not express the PLK gene but after
XX stimulation with phytohaemagglutinin, PLK is expressed and can be
XX used as an indicator of lymphocyte stimulation.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 603 AA;
XX
XX Query Match: 87.8%; Score 43; DB 16; Length 603;
XX Best Local Similarity 77.8%; Pred. No. 12;
XX Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LGRPPFETS 9

XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T210D mutant.
XX
KW Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Thr substituted by Asp"
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPFETS 9
:|||||
Db 246 VGKPPPFETS 254

RESULT 19
AAU79309
ID AAU79309 standard; Peptide; 603 AA.
XX
AC AAU79309;
XX
DT 02-JUL-2002 (first entry)

XX
DE Mouse polo-like kinase (Plk).
XX
KW Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo like kinase; Plk.
XX
OS Mus musculus.
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Column 59-64; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of the polo-like kinase (Plk), a
CC protein from which mitotic protein polo kinase inhibitory peptides are
CC derived.
XX
SQ Sequence 603 AA;

Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPFETS 9
:|||||
Db 246 VGKPPPFETS 254

RESULT 18
AAU79308
ID AAU79308 standard; Peptide; 603 AA.
XX
AC AAU79308;

XX Mouse polo-like kinase (Plk) T210E mutant.
DE
XX
KW Polo box; PBL; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc difference 210 /note= "Wild type Thr substituted by Glu"
FT
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79310 using information
CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGKPPFFETS 9
: : : : :
DB 246 VGRPPFFETS 254
RESULT 20
AAU79310
ID AAU79310 standard; Peptide; 603 AA.
XX
AC AAU79310;
XX
DT 02-JUL 2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) T210V mutant.

XX Polo box; PBL; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc difference 210 /note= "Wild type Thr substituted by Val"
FT
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 1; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGKPPFFETS 9
: : : : :
DB 246 VGRPPFFETS 254
RESULT 21
AAU79311
ID AAU79311 standard; Peptide; 603 AA.
XX
AC AAU79311;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) E206V mutant.
XX
KW Polo box; PBL; cytostatic; fungicide; protozoacide; antihelminthic;

KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; candida; lichen; trichophyton;
KW throat cancer; fungal infection; candida; lichen; trichophyton;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
OS Mus musculus.
OS Synthetic.
XX
XX
OS
OS
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Glu substituted by Val"
FT XX
XX
PN US6358738-B1.
XX
XX
PD 19-MAR-2002.
XX
XX
PF 13-MAY-1999; 99US-0311311.
XX
XX
PR 13-MAY-1999; 98US-085296P.
XX
XX
PA (HARD) HARVARD COLLEGE.
XX
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections
XX
XX
PS Example 1; Page -; 47pp; English.
XX
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPFFETS 9
:|||||
Db 246 VGRPPFFETS 254
RESULT 22
AAU79312
ID AAU79312 standard; Peptide; 603 AA.
XX
AC AAU79312;
XX
XX 02-JUL 2002 (first entry)
XX
DE Mouse polo like kinase (Plk) E206N mutant
XX
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;

KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; candida; lichen; trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Glu substituted by Asn"
FT XX
XX
PN US6358738-B1.
XX
XX
PD 19-MAR-2002.
XX
XX
PF 13-MAY-1999; 99US-0311311.
XX
XX
PR 13-MAY-1998; 98US-085296P.
XX
XX
PA (HARD) HARVARD COLLEGE.
XX
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections
XX
XX
PS Example 1; Page -; 47pp; English.
XX
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPFFETS 9
:|||||
Db 246 VGRPPFFETS 254
RESULT 23
AAU79313
ID AAU79313 standard; Peptide; 603 AA.
XX
AC AAU79313;
XX
XX 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) E206V/T210V mutant.
XX
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;

KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Glu substituted by Val"
FT Misc-difference 213 /note= "Wild type Thr substituted by Val"
FT
XX
XX US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections -
XX
XX Example 1; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Sequence 603 AA;
SQ
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPPFETS 9
Db 246 VGKPPPFETS 254
RESULT 24
AAU79314
ID AAU79314 standard; Peptide; 603 AA.
XX
XX AAU79314;
XX
XX 02-JUL-2002 (first entry)
XX
XX Mouse polo-like kinase (Plk) D:94N mutant.
XX
XX Polo box; Pbl; cytostatic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;

KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 194 /note= "Wild type Asp substituted by Asn"
FT
XX US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections -
XX
XX Example 1; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Sequence 603 AA;
SQ
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPPFETS 9
Db 246 VGKPPPFETS 254
RESULT 25
AAU79315
ID AAU79315 standard; Peptide; 603 AA.
XX
XX AAU79315;
XX
XX 02-JUL-2002 (first entry)
XX
XX Mouse polo-like kinase (Plk) D:194R mutant.
XX
XX Polo box; Pbl; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;

KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 194 /note= "Wild type Asp substituted by Arg"
FT
XX
XX US6358738-B1.
XX
XX 19 MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 1; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Sequence 603 AA;
XX
XX Query Match 87.8%; Score 43; DB 23; Length 603;
XX Best Local Similarity 77.8%; Pred. No. 12;
XX Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LGRPFFETS 9
XX :|||:
XX 246 VGRPPFFETS 254
XX
XX
XX RESULT 26
XX AAU79316
XX ID AAU79316 standard; Peptide; 603 AA.
XX
XX AC AAU79316;
XX
XX DT 02-JUL-2002 (first entry)
XX
XX DE Mouse polo-like kinase (Plk) K28X mutant.
XX
XX Polo box; PBl; cytostatic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
XX

OS Mus musculus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 28 /note= "Wild type Lys substituted by Met"
FT
XX
XX US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US 085296P.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 2; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Sequence 603 AA;
XX
XX Query Match 87.8%; Score 43; DB 23; Length 603;
XX Best Local Similarity 77.8%; Pred. No. 12;
XX Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LGRPFFETS 9
XX :|||:
XX 246 VGRPPFFETS 254
XX
XX
XX RESULT 27
XX AAU79317
XX ID AAU79317 standard; Peptide; 603 AA.
XX
XX AC AAU79317;
XX
XX DT 02-JUL-2002 (first entry)
XX
XX DE Mouse polo-like kinase (Plk) V415A mutant.
XX
XX Polo box; PBl; cytostatic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
XX
XX Mus musculus.
XX Synthetic.
XX

XX	Key	Location/Qualifiers		
PH	Misc-difference	415		
FT	/note= "Wild type Val substituted by Ala"			
XX	US6358738-B1			
PN	19-MAR-2002			
XX	13-MAY-1999	99US-0311311		
PF	13-MAY-1999	99US-085296P		
XX	(HARD) HARVARD COLLEGE			
PA	Erikson RL, Lee KS;			
XX	WPI; 2002-314756/35			
PI	Administering polo kinase inhibitors for the treatment of			
XX	fungal infections			
PS	Example 7; Page 7; 47pp; English			
XX	The invention describes a method of inhibiting growth of			
CC	population of cells by inhibiting a cell polo kinase by a			
CC	polo kinase inhibitor. The inhibitor comprises a sequence			
CC	carboxy terminal domain of the polo kinase which excludes			
CC	kinase catalytic domain. The method is used for the treat			
CC	(e.g. cancer of the lung, the breast, the uterus, the ova			
CC	cervix, the epithelium, the brain, the retina, the prosta			
CC	throat), infection by fungi (e.g. Candida, Lichen, Tricho			
CC	Epidermophyton, and Microsporium), protozoans, helminthes,			
CC	this is the amino acid sequence of a mouse polo-like kina			
CC	mutant, used to determine the residues required for kinas			
CC	Note: This sequence does not appear in the specification			
CC	created from the wild type sequence shown in AAU79306 usi			
CC	given in the invention.			
XX	Sequence	603 AA;		
SQ				
Query Match				
Best Local Similarity 87.8%; Score 43; DB 23; Length 63				
Matches 7; Conservative 2; Mismatches 0; Indels				
QY	: LGRPPFFETS 9			
DB	246 VGRPPFFETS 254			
RESULT 28				
AAU79308				
XX	ID	AAU79318 standard; Peptide; 603 AA		
AC	AAU79319;			
XX	02-JUL-2002 (first entry)			
XX	Mouse polo-like kinase (Plk) L427A mutant			
KW	Polo box; PBI; cytostatic; fungicide; protozoacide; antin			
KW	arthropodicide; Mitotic protein polo kinase; polo kinase			
KW	polo kinase catalytic domain; cancer, lung cancer; breast			
KW	cancer of the uterus; ovarian cancer, cervical cancer;			
KW	epithelial cancer; brain cancer; retina cancer; prostate			
KW	throat cancer; fungal infection; Candida; Lichen; Trichoph			
KW	Epidermophyton; Microsporium; protozoan infection; helmin			
KW	arthropod infection; mouse; polo-like kinase; Plk; mutant			
XX	Mus musculus			
CS	Synthetic			
XX				
PH	Key	Location/Qualifiers		

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FT Misc-difference 427
FT /note= "Wild type Lys substituted by Ala"
XX
PN US6358738-B1.
XX
PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections -
XX
PS Example 7; Page -; 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0

QY 1 LGRPPPFETS 9
   :|:|:|:|:|
DB 246 VGKPPPFETS 254

RESULT 29
AAU79319
ID AAU79319 standard; Peptide; 603 AA.
XX
AC AAU79319;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) N437; mutant.
XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelmintic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 437
FT /note= "Wild type Asn substituted by Ile"

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```
XX US6358738-B1.
XX PN
XX PD
XX 19-MAR-2002.
XX PF
XX 13-MAY-1999; 99US-0311311.
XX PR
XX 13-MAY-1998; 98US-085296P.
XX PA
XX (HARD ) HARVARD COLLEGE.
XX PI
XX Erikson RL, Lee KS;
XX WPI; 2002-314756/35.
XX DR
XX Administering polo kinase inhibitors for the treatment of cancers and
XX PT fungal infections .
XX PS
XX Example 7; Page -; 47pp; English.
XX CC
XX The invention describes a method of inhibiting growth of an isolated
XX CC population of cells by inhibiting a cell polo kinase by administering a
XX CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX CC carboxy terminal domain of the polo kinase which excludes the polo
XX CC kinase catalytic domain. The method is used for the treatment of cancer
XX CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX CC cervix, the epithelium, the brain, the retina, the prostate, and the
XX CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX CC mutant, used to determine the residues required for kinase activity.
XX CC Note: This sequence does not appear in the specification but has been
XX CC created from the wild type sequence shown in AAU79306 using information
XX CC given in the invention.
XX SQ Sequence 603 AA;

Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
DB 246 VGKPPFFETS 254
|||
|||

RESULT 30
AAU79320
ID AAU79320 standard; Peptide; 603 AA.
XX AC
XX AAU79320;
XX DT
XX 03-JUN-2003 (first entry)
XX DE
XX Mouse polo-like kinase (Plk) W414F/T114D mutant.
KW Polo box; PS1; cytostatic; fungicidal; protozoacidal; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retinal cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
XX XX
CS Mus musculus.
CS Synthetic.
XX PH
XX Key Location/Qualifiers
FT Misc-difference 414 /note= "Wild type T11 substituted by P48"
FT FT
FT Misc-difference 210 /note= "Wild type T11 substituted by Asp"
```

```
XX US6358738-B1.
XX PN
XX PD
XX 19-MAR-2002.
XX PF
XX 13-MAY-1999; 99US-0311311.
XX PR
XX 13-MAY-1998; 98US-085296P.
XX PA
XX (HARD ) HARVARD COLLEGE.
XX PI
XX Erikson RL, Lee KS;
XX WPI; 2002-314756/35.
XX DR
XX Administering polo kinase inhibitors for the treatment of cancers and
XX PT fungal infections .
XX PS
XX Example 10; Page -; 47pp; English.
XX CC
XX The invention describes a method of inhibiting growth of an isolated
XX CC population of cells by inhibiting a cell polo kinase by administering a
XX CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX CC carboxy terminal domain of the polo kinase which excludes the polo
XX CC kinase catalytic domain. The method is used for the treatment of cancer
XX CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX CC cervix, the epithelium, the brain, the retina, the prostate, and the
XX CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX CC mutant, used to determine the residues required for kinase activity.
XX CC Note: This sequence does not appear in the specification but has been
XX CC created from the wild type sequence shown in AAU79306 using information
XX CC given in the invention.
XX SQ Sequence 603 AA;

Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
DB 246 VGKPPFFETS 254
|||
|||

RESULT 31
ABR48196
ID ABR48196 standard; Protein; 603 AA.
XX AC
XX ABR48196;
XX DT
XX 12-JUN-2003 (first entry)
XX DE
XX Human bladder cancer associated protein sequence SEQ ID NO:110.
KW Human; bladder cancer; cytostatic; Gene therapy; vaccine.
XX OS
XX Homo sapiens.
XX PN
XX WO2003003906-A2.
XX PD
XX 16-JAN-2003.
XX PF
XX 03-JUL-2002; 2002WO-US21338.
XX PR
XX 03-JUL-2001; 2001US-302814P.
XX PR
XX 03-AUG-2001; 2001US-310099P.
XX PR
XX 08-NOV-2001; 2001US-343705P.
XX PR
XX 13-NOV-2001; 2001US-350666P.
XX PR
XX 12-APR-2002; 2002US-372246P.
XX PA
XX (ECSB-) EOS BIOTECHNOLOGY INC.
```

XX Mack DH, Aziz N;
PI
XX
DR WPI: 2003-201532/19.
DR N-PSDB; ACC51009.
XX
XX Detecting a bladder cancer-associated transcript in a cell from a
PI patient, comprises contacting a biological sample from the patient with
PT a bladder cancer-associated polynucleotide or antibody -
PT
XX
XX Claim 10; Page 269; 307pp; English.
XX
XX The present invention describes a method for detecting a bladder cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from a patient with a polynucleotide
CC that selectively hybridizes to a sequence that is not identical to a
CC table of sequences (see ACC50951 to ACC51059; ACC50951 to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
CC ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer-associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications.
XX
SQ Sequence 603 AA;

Query Match 87.8%; Score 41; DB 24; Length 603;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPFETS 9
Db 246 VGRPPPFETS 254

RESULT 32
ABE63067
ID ABE63067 standard; Protein; 769 AA.
XX
AC ABE63067;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 1599.
XX
XX Drosophila developmental biology; cell signaling insecticides;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX
XX WC200171042-A2.
PN
XX
XX 27-SEP-2001.
PC
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PE
XX
XX 11-JUL-2000; 2000US-0614150.
PR
XX
XX (PERE) PE CORP NY.
PA
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
XX WPI: 2001 656860/75.
DR
XX
XX N-PSDB; ABL07170.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions -
PT

XX
PS Disclosure; SEQ ID NO 15993; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 769 AA;

Query Match 85.7%; Score 42; DB 22; Length 769;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPFET 8
Db 208 VGRPPPFET 215

RESULT 33
AAW74159
ID AAW74159 standard; peptide; 9 AA.
XX
AC AAW74159;
XX
XX 05-MAY-1999 (first entry)
DT
XX
XX HJ loop peptide J-42.
DE
XX
XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site ;
FT Modified-site 9 /note= "acetylated"
FT Modified-site 9 /note= "amidated"
FT Modified-site 9 /note= "benzyl ester of Glu"
XX
XX WC0853050-A2.
PN
XX
XX 26-NOV-1998.
PD
XX
XX 20-MAY-1998; 98WO-US10319.
PF
XX
XX 21-MAY-1997; 97US-0861338.
PR
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX
XX Ben-Sasson SA;
PI
XX
XX WPI; 1999-070142/06.
DR
XX
XX New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
XX Claim 14; Fig 4; 70pp; English.
PS
XX

CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.

XX Sequence 9 AA;
SQ Query Match 81.6%; Score 40; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFE 7
Db 3 LGRPPFE 9

RESULT 34
AAU98315
ID AAU98315 standard; Peptide; 9 AA.
XX
AC AAU98315;
XX
DT 11-AUG-2002 (first entry)
XX
DE Polo kinase serine-threonine kinase HJ loop peptide J-42.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; J 42.

XX Unidentified.
CS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 9 /note= "N-terminal entry"
FT Modified-site 9 /note= "Benzyl ester of Glutamic acid"
FT Modified-site 9 /note= "C-terminal amide"

XX US2002049301-A1.
XX
XX 25-APR-2002.
PD
XX 13-DEC-2000; 2000US-0736076.
PF
XX 21-MAY-1997; 97US-0861338.
PR
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA Ben Sasson SA;
XX WPI; 2002-462787/49.

XX New peptide from the HJ loop of serine threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies.
PT
XX Disclosure; Fig 4; 41pp; English.

XX The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory, and for
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-42. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.

XX Sequence 9 AA;
SQ Query Match 81.6%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFE 7
Db 3 LGRPPFE 9

RESULT 35
AAW74213
ID AAW74213 standard; peptide; 10 AA.
XX
AC AAW74213;
XX
DT 05-MAY-1999 (first entry)
XX
DE HJ loop peptide K038H101.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.

XX Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "myristylated"
FT Modified-site 10
FT Modified-site 10 /note= "amidated"

XX WC9853050-A2.
XX 26-NOV-1998.
PD
XX 20-MAY-1998; 98WO-US10319.
PF
XX 21-MAY-1997; 97US-0861338.
PR
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX Ben Sasson SA;
XX WPI; 1999-070142/06.

XX New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
PT
XX Disclosure; Fig 6; 70pp; English.
PS This sequence represents a peptide of the invention, and is a derivative
XX of the HJ loop of a serine/threonine kinase (STK). The peptides can be

used for the treatment of disorders caused by overactivity or underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis, arteriosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and hypertension), immunosuppressive and inflammatory disorders (e.g. asthma, psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression of organ transplant rejection, multiple sclerosis, inflammatory bowel disease and AIDS), central nervous system diseases (e.g. Alzheimer's disease, stroke and trauma), septic shock, Parkinson's disease or hypertension. The peptides can also be used to produce antibodies which can be used to identify cells expressing the STK and to study the intracellular distribution of the STK. In addition, the peptides can be used to identify and quantitate ligands which bind the HJ loop of the STK from which the peptide was derived.

Sequence 10 AA;
Query Match 81.6%; Score 40; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFE 7
Db 4 LGRPPFE 10

RESULT 36
AAU98357
ID AAC98357 standard; Peptide; 10 AA.

AC AAU98357;
XX 13-AUG-2002 (first entry)
DE Polo kinase SNK serine-threonine kinase HJ loop peptide K038H101.
XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
KW modulating STK activity; polo kinase; SNK; K038H101.

OS Unidentified.
OS Synthetic.

PH Key Location/Qualifiers
FT Modified site 1 /note= "N-terminal 'tylstyl'"
FT Modified site 1C /note= "Benzyl Ester of Glutamic Acid, C-terminal amide"

XX US2002049301A1.

PN 25-APR-2002.

XX 13 DEC-2000; 2000US-0736076.

PR 21-MAY-1997; 97US-0861338.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Ben Sasson SA;

XX WPI; 2002-462787/49.

XX New peptide from the HJ loop of serine threonine kinase, useful for treating e.g. cancer and for producing diagnostic antibodies

PS Disclosure; Fig 6; 41pp; English.

XX The present invention relates to new peptides derived from the HJ loop of a serine/threonine kinase (STK). The peptides of the invention are

used to modulate STK activity, especially for treating cancer, diabetes, obesity or a wide variety of central nervous system, inflammatory, autoimmune or cardiovascular disorders, also haemorrhagic shock, and for regulating lipid metabolism. The peptides are also used to generate antibodies that bind specifically to the parent STK, used e.g. for identifying STK-expressing cells and to study intracellular distribution of STK, and to identify or quantify ligands that bind to the HJ loop. The present amino acid sequence represents the polo kinase SNK serine-threonine kinase HJ loop peptide K038H101. This sequence is one of the short peptides of the invention that selectively modulate the activity of STK.

Sequence 10 AA;
Query Match 81.6%; Score 40; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFE 7
Db 4 LGRPPFE 10

RESULT 37
AAR92176
ID AAR92176 standard; Protein; 416 AA.

XX AAR92176;
AC AAR92176;
XX 25-MAY-1996 (first entry)
XX Sak serine-threonine kinase N-terminus.
DE Sak; serine-threonine kinase; STK; agonist; antagonist;
KW proliferative disease; cancer; tumour; antisense; transgenic animal; therapy.

XX Mus musculus.

XX CA2150789-A.

XX 03-DEC-1995.

XX 01-JUN-1995; 95CA-2150789.

XX 02-JUN-1994; 94US-0252995.

XX (MOUN) MOUNT SINAI HOSPITAL CORP.

PI Dennis JW, Fode C, Heffernan M;

XX WPI; 1996-129817/14.

XX N-PSDB; AAT08710.

PT Nucleic acid encoding Sak serine-threonine kinase - useful for identifying modulators potentially useful in treatment or prevention of proliferative disease.

PS Claim 3; Page 46-48; 73pp; English.

XX 2 Isoforms, sak-a and sak-b, of a novel serine/threonine kinase have an identical N-terminal sequence (AAR92176) that contains the kinase domain and that shows significant homology to the polo subfamily. The C-terminal sequences (each contg. 3 PEST regions) of the 2 isoforms differ (see AAR92177 and AAR92214). Sak-a and Sak-b are associated with mitotic and meiotic cell division, and may be involved in cell proliferation. They can be obtd. in recombinant form by expression of encoding sequences (see AAT08710-12) and used to test for inhibitory or stimulatory cpds. that may be useful in the treatment/diagnosis of proliferative disorders, such as cancer and viral (esp. HIV) infection.

XX Sequence 416 AA;

Query Match 81.6%; Score 40; DB 17; Length 416;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
:|||||:
Db 206 IGRPPFDT 213

RESULT 38
AAR92214
ID AAR92214 standard; Protein: 464 AA.
XX
AC AAR92214;
XX
DT 25-MAY-1996 (first entry)
XX
DE SAK-b serine-threonine kinase.
XX
KW SAK b; serine-threonine kinase; STK; agonist; antagonist;
KW proliferative disease; cancer; tumour; antisense; transgenic animal;
KW therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Domain 1..416
FT /label= N-terminal domain
FT /note= "contains the kinase domain"
FT 417..464
FT /label= C-terminal domain
FT /note= "contains 3 PEST regions"
XX
PN CA2150789-A.
XX
PD 03-DEC-1995.
XX
PE 01-JUN-1995; 95CA-2150789.
XX
PR 02-JUN-1994; 94US-0252995.
XX
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
XX
PI Dennis JW, Fode C, Heffernan M;
XX
DR WPI; 1996-129817/14.
DR N-PSDB; AAT08712.
XX
PT Nucleic acid encoding Sak serine-threonine kinase - useful for
PT identifying modulators potentially useful in treatment or prevention
PT of proliferative disease.
XX
PS Claim 6; Page 58-61; 73pp; English.
XX
CC 2 Isoforms, SAK-a (AAR92177) and SAK-b (AAR92214), of a novel
CC serine/threonine kinase are associated with mitotic and meiotic cell
CC division and are characterized by having a kinase domain at the
CC N-terminus and 3 PEST sequences (rich in Pro, Ser, Thr, Asp, Glu) at
CC the C-terminus. The N-terminal regions of the 2 isoforms are
CC identical (see AAR92176). SAK-a and SAK-b can be obtd. in recombinant
CC form by expression of encoding sequences (see AAT08711-12), and used
CC to test for inhibitory or stimulatory cpds. useful in the
CC treatment/diagnosis of proliferative disorders such as cancer and
CC and viral (esp. HIV) infection, or used to raise antibodies.
XX
SQ Sequence 464 AA;

Query Match 81.6%; Score 40; DB 17; Length 464;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
:|||||:
Db 206 IGRPPFDT 213

RESULT 40
ABB57273

Db 206 IGRPPFDT 213
:|||||:
RESULT 39
AAR92177
ID AAR92177 standard; Protein: 925 AA.
XX
AC AAR92177;
XX
DT 25-MAY-1996 (first entry)
XX
DE SAK-a serine-threonine kinase.
XX
KW SAK-a; serine-threonine kinase; STK; agonist; antagonist;
KW proliferative disease; cancer; tumour; antisense; transgenic animal;
KW therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Domain 1..416
FT /label= N-terminal domain
FT /note= "contains the kinase domain"
FT 417..925
FT /label= C-terminal domain
FT /note= "contains 3 PEST regions"
XX
PN CA2150789-A.
XX
PD 03-DEC-1995.
XX
PE 01-JUN-1995; 95CA-2150789.
XX
PR 02-JUN-1994; 94US-0252995.
XX
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
XX
PI Dennis JW, Fode C, Heffernan M;
XX
DR WPI; 1996-129817/14.
DR N-PSDB; AAT08711.
XX
PT Nucleic acid encoding Sak serine-threonine kinase - useful for
PT identifying modulators potentially useful in treatment or prevention
PT of proliferative disease.
XX
PS Claim 5; Page 50-55; 73pp; English.
XX
CC 2 Isoforms, SAK-a (AAR92177) and SAK-b (AAR92214), of a novel
CC serine/threonine kinase are associated with mitotic and meiotic cell
CC division and are characterized by having a kinase domain at the
CC N-terminus and 3 PEST sequences (rich in Pro, Ser, Thr, Asp, Glu) at
CC the C-terminus. The N-terminal regions of the 2 isoforms are
CC identical (see AAR92176). SAK-a and SAK-b can be obtd. in recombinant
CC form by expression of encoding sequences (see AAT08711-12), and used
CC to test for inhibitory or stimulatory cpds. useful in the
CC treatment/diagnosis of proliferative disorders such as cancer and
CC and viral (esp. HIV) infection, or used to raise antibodies.
XX
SQ Sequence 925 AA;

Query Match 81.6%; Score 40; DB 17; Length 925;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
:|||||:
Db 206 IGRPPFDT 213

RESULT 40
ABB57273

ID AB857273 standard; Protein; 925 AA.
XX
AC AB857273;
XX
DT 07 MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related protein sequence SEQ ID NO:766.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
XX
OS Mus musculus.
XX
PN W0200188186-A2.
XX
PD 22 NOV-2001.
XX
PF 18 MAY-2001; 2001WO-JP04192.
XX
PR 18 MAY-2000; 2000JP-0145977.
XX
PA (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
DR WP1: 2002-034733/04.
DR N-PSDB; AB199713.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -
XX
PS Claim 2; Page 1893-1897; 2690pp; English.
XX
CC The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (1) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (1). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (AB199713 to AB199912, encoding
CC the protein sequences in AB857020 to AB857374) or by determining the
CC expression profile of a gene group comprising these genes. The
CC expression levels or expression profiles produced by these genes are
CC used as an indicator when screening for ischaemic condition improving
CC drugs or therapeutics for ischaemic diseases. AB199913 and AB199914
CC represent PCR primers for a mouse ischaemic condition related sequence,
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 325 AA;

Query Match 81.63; Score 4.11E-04; Length 925;
Best Local Similarity 75.03; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Cy 1 LGPPPPET 8
cb 206 LGPPPPDT 213

Search completed: November 14, 2003, 13:25:01
Job time : 34.7143 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 13:23:00 / Search time 11.8286 Seconds
(without alignments)
32.193 Million cell updates/sec

Title: US-09-736-076-18
Perfect score: 49
Sequence: 1 LGRPPFETS 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : issued Patents AA:
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/FCUS_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	3	US-08-861-338-18 Sequence 18, Appl
2	49	100.0	11	3	US-08-861-338-19 Sequence 19, Appl
3	46	93.9	272	1	US-04-252-995D-12 Sequence 12, Appl
4	46	93.9	272	2	US-08-834-108-10 Sequence 12, Appl
5	46	93.9	685	2	US-08-834-108-10 Sequence 1, Appl
6	46	93.9	685	3	US-09-198-122-2 Sequence 2, Appl
7	46	93.9	685	3	US-09-198-122-2 Sequence 6, Appl
8	46	93.9	685	3	US-09-505-244-2 Sequence 2, Appl
9	43	87.8	20	3	US-08-861-338-6 Sequence 6, Appl
10	43	87.8	272	1	US-08-252-995D-14 Sequence 14, Appl
11	43	87.8	272	2	US-08-834-108-14 Sequence 14, Appl
12	43	87.8	603	3	US-09-198-122-2 Sequence 2, Appl
13	43	87.8	603	4	US-09-311-311C-26 Sequence 26, Appl
14	40	81.6	9	3	US-08-861-338-18 Sequence 15, Appl
15	40	81.6	273	1	US-08-252-995D-10 Sequence 10, Appl
16	40	81.6	273	2	US-08-834-108-10 Sequence 10, Appl
17	40	81.6	416	1	US-08-252-995D-2 Sequence 2, Appl
18	40	81.6	416	2	US-08-834-108-2 Sequence 2, Appl
19	40	81.6	464	1	US-08-252-995D-6 Sequence 6, Appl
20	40	81.6	464	2	US-08-834-108-6 Sequence 6, Appl
21	40	81.6	925	1	US-08-252-995D-4 Sequence 4, Appl
22	40	81.6	925	2	US-08-834-108-4 Sequence 4, Appl
23	38	77.6	271	1	US-08-252-995D-11 Sequence 11, Appl
24	38	77.6	271	2	US-08-834-108-11 Sequence 11, Appl
25	37	75.5	9	3	US-08-861-338-19 Sequence 17, Appl
26	36	73.5	220	1	US-08-233-146-2 Sequence 2, Appl
27	36	73.5	220	1	US-08-463-470-2 Sequence 2, Appl

28	36	73.5	607	2	US-08-878-989-15 Sequence 15, Appl
29	36	73.5	607	3	US-09-272-796-15 Sequence 15, Appl
30	35	71.4	182	4	US-09-134-001C-3742 Sequence 3742, Ap
31	35	71.4	403	2	US-08-755-728-4 Sequence 4, Appli
32	35	71.4	403	2	US-08-974-655-4 Sequence 4, Appli
33	35	71.4	403	3	US-09-283-011-4 Sequence 4, Appli
34	34	69.4	226	4	US-09-134-001C-5260 Sequence 5260, Ap
35	34	69.4	254	4	US-09-252-991A-24255 Sequence 24255, A
36	34	69.4	344	2	US-08-755-728-3 Sequence 3, Appli
37	34	69.4	344	2	US-08-974-655-3 Sequence 3, Appli
38	34	69.4	344	3	US-09-283-011-3 Sequence 3, Appli
39	34	69.4	347	2	US-09-016-000-1 Sequence 1, Appli
40	34	69.4	1019	4	US-09-252-991A-24417 Sequence 24417, A
41	34	69.4	1312	4	US-09-345-882-29 Sequence 29, Appl
42	33	67.3	240	4	US-09-107-532A-4655 Sequence 4655, Ap
43	33	67.3	304	1	US-08-569-806-6 Sequence 6, Appli
44	33	67.3	327	1	US-08-420-235B-35 Sequence 35, Appl
45	33	67.3	327	3	US-08-793-624-35 Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-08-861-338-18
Sequence 18, Application US/08861338
Patent No. 6174993
GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,338
FILING DATE: 21-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brock, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC-590
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amio acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "N-Acetyl Leucine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9


```

OTHER INFORMATION: /note= "Serine-NH2"
US-08-861-338-18
Query Match: 100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
Db 1 LGRPPFFETS 9

RESULT 2
US-08-861-338-19
Sequence 19, Application US/08861338
Patent No. 6174993
GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.00
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,338
FILING DATE: 21-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brock, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMC 590
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "N Acetyl Methionine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /note= "Serine-NH2"
US-08-861-338-19
Query Match: 100.0%; Score 49; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
Db 3 LGRPPFFETS 11

```

```

RESULT 3
US-08-252-995D-12
Sequence 12, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-252-995D-12
Query Match: 93.9%; Score 46; DB 1; Length 272;
Best Local Similarity 88.9%; Pred. No. 0.34;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
Db 201 LGRPPFFETS 209

RESULT 4
US-08-834-108-12
Sequence 12, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/834,108
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-08-834-108-12

```

```

Query Match 93.9%; Score 46; DB 2; Length 272;
Best Local Similarity 88.9%; Pred. No. 0.34;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY : LGRPPFFETS 9
    |||||
Db 201 LGRPPFFET 209

```

RESULT 5

```

US-08 878 989-1
; Sequence 1, Application US/08878989
; Patent No. 5885903
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HJVENOB01
; CLONE: 39043
; US-08-878-989-1

```

```

Query Match 93.9%; Score 46; DB 2; Length 685;
Best Local Similarity 88.9%; Pred. No. 0.89;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LGRPPFFETS 9
    |||||
Db 275 LGRPPFFET 283

```

RESULT 6

```

US-09-136-282-2
; Sequence 2, Application US/09136282
; Patent No. 6063609
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, KAREN
; APPLICANT: JACKSON, JEFFREY
; APPLICANT: HANSBURY, MICHAEL
; APPLICANT: NERURKAR, SANDHYA
; APPLICANT: ROSHAK, AMY
; APPLICANT: BOJZYK, MARK
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,282
; FILING DATE: 20-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,112
; FILING DATE: 20-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-136-282-2

```

```

Query Match 93.9%; Score 46; DB 3; Length 685;

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Best Local Similarity 88.9%; Pred. No. 0.89;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
Db 275 LGRPPFFET 283

RESULT 7
US-09-272-796-1
; Sequence 1, Application US/09272796
; Patent No. 620748
; GENERAL INFORMATION:
; APPLICANT: Bardman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Kari G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 2;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ballings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF 0120 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENOB01
; CLONE: 39043
; US-09-272-796-1

Query Match 93.9%; Score 46; DB 3; Length 685;
Best Local Similarity 88.9%; Pred. No. 0.89;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
Db 275 LGRPPFFET 283

RESULT 8
US-09-505-744-2
; Sequence 2, Application US/09505744

; Patent No. 6245544
; GENERAL INFORMATION:
; APPLICANT: Karen M. Anderson
; APPLICANT: Mark M. Bouzyk
; APPLICANT: Michael J. Hansbury
; APPLICANT: Jeffrey R. Jackson
; APPLICANT: Sandhya S. Nerurkar
; APPLICANT: Amy K. Roshak
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; FILE REFERENCE: GH-70231-D1
; CURRENT APPLICATION NUMBER: US/09/505,744
; CURRENT FILING DATE: 2000-02-16
; EARLIER APPLICATION NUMBER: 09/136,282
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/056,112
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 685
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-505-744-2

Query Match 93.9%; Score 46; DB 3; Length 685;
Best Local Similarity 88.9%; Pred. No. 0.89;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
Db 275 LGRPPFFET 283

RESULT 9
US-08-861-338-6
; Sequence 6, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-861-338-6

Query Match 87.8%; Score 43; DB 3; Length 20;
Best Local Similarity 77.8%; Pred. No. 0.083;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LGRPPFFETS 9
Db 5 VGKPPFFETS 13

RESULT 1:
US-08-252-995D-14
; Sequence 14, Application US/08252995C
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995C
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-252-995D-14

Query Match 87.8%; Score 43; DB 3; Length 272;
Best Local Similarity 77.8%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LGRPPFFETS 9
Db 201 VGKPPFFETS 209

RESULT 1:
US-08-834-108-14
; Sequence 14, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-834-108-14

Query Match 87.8%; Score 43; DB 2; Length 272;
Best Local Similarity 77.8%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LGRPPFFETS 9
Db 201 VGKPPFFETS 209

RESULT 12
US-09-198-122-2
; Sequence 2, Application US/09198122
; Patent No. 6180380
; GENERAL INFORMATION:
; APPLICANT: Strebhardt, Klaus; Rubsamen-Waigmann, Helga;
; APPLICANT: Holtrich, Uwe
; TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE-
; TITLE OF INVENTION: THREONINE-KINASE FAMILY
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
; MEDIUM TYPE: storage
; COMPUTER: NEC Powermate SX-20
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/198,122
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/601,014
; FILING DATE: 23-FEB-1996

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; APPLICATION NUMBER: PCT/EP94/02863
; FILING DATE: 30-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4329177
; FILING DATE: 30-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Payer 9514 KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-09 198-122-2

Query Match      87.8%  Score 43. DB 3; Length 603;
Best Local Similarity 77.8%  Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRRPFETS 9
DB      246 VGRPPFETS 254

RESULT 13
US-09-311-311C 26
; Sequence 26, Application US/09211311C
; Patent No. 6358736
; GENERAL INFORMATION:
; APPLICANT: Eriksen, et al.
; TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS,
; TITLE OF INVENTION: METHODS, AND USES THEREFOR
; FILE REFERENCE: 1874/117
; CURRENT APPLICATION NUMBER: US/09/311,311C
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/065,296
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: 11...1603
; OTHER INFORMATION: Plk protein
US-09-311-311C 26

Query Match      87.8%  Score 43. DB 4; Length 603;
Best Local Similarity 77.8%  Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRRPFETS 9
DB      246 VGRPPFETS 254

RESULT 14
US-08-861-338-15
; Sequence 15, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Sen-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; OTHER INFORMATION: Glutamic Acid-NH2"
US-08-861-338-15

Query Match      81.6%  Score 40; DB 3; Length 9;
Best Local Similarity 100.0%  Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPFEE 7
DB      3 LGRPFEE 9

RESULT 15
US-08-252-995D-10
; Sequence 10, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```


APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-252-995D-10

Query Match 81.6%; Score 40; DB 1; Length 273;
Best Local Similarity 75.0%; Pred. No. 4.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
Db 202 IGRPPFET 209

RESULT 16
US-08-834-108-10
Sequence 10, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
City: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-834-108-10

Query Match 81.6%; Score 40; DB 2; Length 273;
Best Local Similarity 75.0%; Pred. No. 4.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
Db 202 IGRPPFET 209

RESULT 17
US-08-252-995D-2
Sequence 2, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
City: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-995D-2

Query Match 81.6%; Score 40; DB 1; Length 416;
Best Local Similarity 75.0%; Pred. No. 7.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
Db 206 IGRPPFET 213

RESULT 18
US-08-834-108-2
Sequence 2, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West

CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153 210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-834-108-2

Query Match 81.6%; Score 40; DB 2; Length 416;
Best Local Similarity 75.0%; Pred. No. 7.1;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
|||
DB 206 IGRPPFET 213
RESULT 19
US-08-252-995D-6
Sequence 6, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-995D-6
Query Match 81.6%; Score 40; DB 1; Length 464;
Best Local Similarity 75.0%; Pred. No. 7.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
|||
DB 206 IGRPPFET 213
RESULT 20
US-08-834-108-6
Sequence 6, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-834-108-6

Query Match 81.6%; Score 40; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 7.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
|||
DB 206 IGRPPFET 213
RESULT 21
US-08-252-995D-4
Sequence 4, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE

```

; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 925 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US 08-252-995D-4

```

```

Query Match      81.6%; Score 40; DB 1; Length 925;
Best Local Similarity 75.0%; Pred. No. 16;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      1 LGPPPFET 8
      :|||||:
DB      206 IGRPPFDT 213

RESULT 22
US-08-834-108-4
; Sequence 4, Application US/08034108
; Patent No. 5876893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311

```

```

; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 925 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-834-108-4

Query Match      81.6%; Score 40; DB 2; Length 925;
Best Local Similarity 75.0%; Pred. No. 16;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

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QY      1 LGPPPFET 8
      :|||||:
DB      206 IGRPPFDT 213

RESULT 23
US-08-252-995D-11
; Sequence 11, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; US-08-252-995D-11

Query Match      77.6%; Score 38; DB 1; Length 271;
Best Local Similarity 75.0%; Pred. No. 11;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

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QY      1 LGPPPFET 8
      :|||||:
DB      200 VQPPFET 207

RESULT 24
US-08-834-108-11

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```

; Sequence 11, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; City: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
US-08 834-108-11

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```

Query Match 77.6%; Score 181 DB 2; Length 271;
Best Local Similarity 75.0%; Pred. No. 117
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LGRPPPEF 8
|:|:|:|
DB 200 VQPPPEF 207

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RESULT 15
US-08-861-338 17
; Sequence 17, Application US/06861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; City: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; OTHER INFORMATION: Glutamine Acid-NH2"
US-08-861-338-17

```

```

Query Match 75.5%; Score 37; DB 3; Length 9;
Best Local Similarity 85.7%; Pred. No. 2.5e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LGRPPPE 7
|:|:|:|
DB 3 LGKPPPE 9

```

```

RESULT 26
US-08-233-146-2
; Sequence 2, Application US/08233146
; Patent No. 5648256
; GENERAL INFORMATION:
; APPLICANT: BEPPU, TERUHIKO
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: NAGASAWA, TORU
; APPLICANT: HORINOUCHI, SUEHARU
; APPLICANT: NISHIYAMA, MAKOTO
; TITLE OF INVENTION: A GENE ENCODING A POLYPEPTIDE HAVING
; TITLE OF INVENTION: NITRILE HYDRATASE ACTIVITY, A TRANSFORMANT CONTAINING THE
; TITLE OF INVENTION: GENE AND A PROCESS FOR THE PRODUCTION OF AMIDES USING THE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; City: NEW YORK
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,146
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/694,746
; FILING DATE: 02-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE

```

REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-024-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Pseudomonas chlororaphis
STRAIN: B23 (FERM BP 187)
US-08-233-146-2

Query Match 73.5%; Score 36; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPE 7
Db 120 GRPPE 125

RESULT 27
US-08-463-470-2
Sequence 2, Application US/08463470
Patent No. 5789211
GENERAL INFORMATION:
APPLICANT: BEPPU, TERUHIKO
APPLICANT: YAMADA, HIDEAKI
APPLICANT: NAGASAWA, TORU
APPLICANT: HORINOUCHI, SUEHARU
APPLICANT: NISHIYAMA, MAKOTO
TITLE OF INVENTION: A GENE ENCODING A POLYPEPTIDE HAVING
TITLE OF INVENTION: NITRILE HYDRATASE ACTIVITY, A TRANSFORMANT CONTAINING THE
TITLE OF INVENTION: GENE AND A PROCESS FOR THE PRODUCTION OF AMIDES USING THE
TITLE OF INVENTION: TRANSFORMANT
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICANS
CITY: NEW YORK
STATE: N.Y.
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,470
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,146
FILING DATE: 22-APR-1994
APPLICATION NUMBER: US 07/694,746
FILING DATE: 02-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005 024 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Pseudomonas chlororaphis
STRAIN: B23 (FERM BP-187)
US-08-463-470-2

Query Match 73.5%; Score 36; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPE 7
Db 120 GRPPE 125

RESULT 28
US-08-878-989-15
Sequence 15, Application US/08878989
Patent No. 5865803
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1827450
US-08-878-989-15

Query Match 73.5%; Score 36; DB 2; Length 607;
Best Local Similarity 75.0%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;


```

QY      2 GRPFETS 9
      | | | | |
Db      217 GSPPFETA 224

RESULT 29
US-09-272-796-15
; Sequence 15, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 607 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1827450
US-09-272-796-15

Query Match      73.5%; Score 36; DB 0; Length 607;
Best Local Similarity 75.0%; Pred. No. 59;
Matches      6; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

QY      2 GRPFETS 9
      | | | | |
Db      217 GSPPFETA 224

RESULT 30
US-09-134-001C-3742
; Sequence 3742, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:

```

```

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-38
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3742
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3742

Query Match      71.4%; Score 35; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. No. 26;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 LGRPPF 6
      | | | | |
Db      177 LGRPPF 182

RESULT 31
US-08-755-728-4
; Sequence 4, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,728
; FILING DATE: No. 5962312ember 25, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI SENSE: NO
US-08-755-728-4

Query Match 71.4%; Score 35; DB 2; Length 403;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9

Db 324 VGKPPFEAN 332

RESULT 32

US-08-974-655-4
Sequence 4, Application US/08974655
Patent No. 5972676
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR 1
TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,655
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/755,728
FILING DATE: No. 5972676ember 25, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-974-655-4

Query Match 71.4%; Score 35; DB 2; Length 403;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9

Db 324 VGKPPFEAN 332

RESULT 33

US-09-283-011-4
Sequence 4, Application US/09283011
Patent No. 6207401
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/283,011
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/012,135
FILING DATE: January 22, 1998
APPLICATION NUMBER: 08/755,728
FILING DATE: No. 6207401ember 25, 1996
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-09-283-011-4

Query Match 71.4%; Score 35; DB 3; Length 403;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9

Db 324 VGKPPFEAN 332

RESULT 34

US-09-134-001C-5260
Sequence 5260, Application US/29134001C
Patent No. 6380370

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; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5260
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5260

Query Match 69.4%; Score 34; DB 4; Length 226;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPPT 8
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DB 54 LGNPPPT 61

RESULT 35
US-09-252-991A-24255
; Sequence 24255, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/374,798
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/394,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24255
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US 09-252-991A-24255

Query Match 69.4%; Score 41; DB 4; Length 254;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPE 7
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DB 34 LARPE 40

RESULT 36
US-08-755 728-3
; Sequence 3, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,728
; FILING DATE: No. 5962312ember 25, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,909
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-755-728-3
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; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,728
; FILING DATE: No. 5962312ember 25, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,909
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-755-728-3

Query Match 69.4%; Score 34; DB 2; Length 344;
Best Local Similarity 55.6%; Pred. No. 77;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
   : |||||
DB 268 VGNPPFESA 276

RESULT 37
US-08-974-655-3
; Sequence 3, Application US/08974655
; Patent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:
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CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/755,728
 FILING DATE: No. 5972676ember 25, 1996
 APPLICATION NUMBER: 60/008,809
 FILING DATE: December 18, 1995
 APPLICATION NUMBER: 60/023,943
 FILING DATE: August 14, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 223/113
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 344 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-974 655-3

Query Match 69.4%; Score 34; DB 2; Length 344;
 Best Local Similarity 55.6%; Pred. No. 77;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LGRPPFFETS 9
 Db 268 VGNPPFESA 276

RESULT 38
 US-08-974 655-3
 Sequence 3, Application US/09283011
 Patent No. 6207401
 GENERAL INFORMATION:
 APPLICANT: Plowman, Gregory
 APPLICANT: Messie, Kevin
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUP
 TITLE OF INVENTION: AND/OR AUP-2 RELATED DISORDERS
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/283,011
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/012,134
 FILING DATE: January 22, 1998
 APPLICATION NUMBER: 08/755,728
 FILING DATE: No. 6207401ember 25, 1996
 APPLICATION NUMBER: 60/023,943
 FILING DATE: August 14, 1996
 APPLICATION NUMBER: 60/008,809
 FILING DATE: December 18, 1996

ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 231/282
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 344 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-09-283-011-3

Query Match 69.4%; Score 34; DB 3; Length 344;
 Best Local Similarity 55.6%; Pred. No. 77;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LGRPPFFETS 9
 Db 268 VGNPPFESA 276

RESULT 39
 US-09-016-000-1
 Sequence 1, Application US/09016000
 Patent No. 5962232
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Lal, Preeti
 APPLICANT: Bandman, Olga
 APPLICANT: Akerbloom, Ingrid E.
 APPLICANT: Shah, Purvi
 APPLICANT: Corley, Neil C.
 APPLICANT: Guegler, Karl G.
 TITLE OF INVENTION: PROTEIN KINASE MOLECULES
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,000
 FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0465 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 347 amino acids
 TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HMC:NOTC1
CLONE: 294C
US-09-016-000-1

Query Match: 69.4%; Score 34; DB 2; Length 247;
Best Local Similarity 55.6%; Pred. No. 77;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY : LGRPPFFETS 9
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DB 271 VGNPPFESA 279

RESULT 40
US-09-252-991A-24417
Sequence 24417, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24417
LENGTH: 1019
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24417

Query Match: 69.4%; Score 34; DB 4; Length 1019;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPFFETS 9
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DB 412 GKPPFFAA 424

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Job time : 11.6286 secs

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OM protein - protein search, using sw model

Run on: November 14, 2003, 13:23:05 ; Search time 22:37:14 Seconds
(without alignments)
#3,443 Million cell updates/sec

Title: US-09-736-076 18

Perfect score: 49

Sequence: 1 LGRPPFFETS 9

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Match	Length	DB	ID	Description
1	49	100.0	9	9	US-09-736-076 18	Sequence 18, Appl
2	49	100.0	11	9	US-09-736-076-19	Sequence 19, Appl
3	46	93.9	400	15	US-10-026-021 5	Sequence 5, Appl
4	46	93.9	469	15	US-10-059-585-14	Sequence 14, Appl
5	46	93.9	685	10	US-09-771-161A 249	Sequence 249, App
6	46	93.9	685	10	US-09-771-161A-250	Sequence 250, App
7	46	93.9	685	10	US-09-771-161A 251	Sequence 251, App
8	46	93.9	685	12	US-10-024-298A-101	Sequence 101, App
9	46	93.9	685	12	US-09-769-970-1	Sequence 1, Appl
10	46	93.9	685	12	US-10-042-211A-101	Sequence 101, App
11	43	87.8	20	9	US-09-736-076-6	Sequence 6, Appl
12	43	87.8	329	10	US-09-925-300-1268	Sequence 1268, Ap
13	43	87.8	367	15	US-10-026-021-6	Sequence 6, Appl
14	43	87.8	516	10	US-09-771-161A-123	Sequence 123, App
15	43	87.8	603	10	US-09-771-161A-214	Sequence 214, App

16	43	87.8	603	15	US-10-171-311-186	Sequence 186, App
17	40	81.6	9	9	US-09-736-076-15	Sequence 15, Appl
18	40	81.6	10	9	US-09-736-076-57	Sequence 57, Appl
19	40	81.6	379	15	US-10-026-021-3	Sequence 3, Appl
20	40	81.6	970	15	US-10-026-021-2	Sequence 2, Appl
21	37	75.5	9	9	US-09-736-076-17	Sequence 17, Appl
22	36	73.5	373	15	US-10-026-021-4	Sequence 4, Appl
23	36	73.5	505	15	US-10-156-761-14310	Sequence 14310, A
24	36	73.5	607	12	US-09-769-970-15	Sequence 15, Appl
25	36	73.5	607	12	US-10-204-041-16	Sequence 16, Appl
26	36	73.5	607	15	US-10-108-580-2	Sequence 2, Appl
27	36	73.5	899	12	US-10-318-906A-48	Sequence 48, Appl
28	36	73.5	899	12	US-10-319-236A-48	Sequence 48, Appl
29	36	73.5	1210	9	US-09-922-217-692	Sequence 692, App
30	36	73.5	1210	10	US-09-833-263-692	Sequence 692, App
31	36	73.5	1210	14	US-10-025-380-692	Sequence 692, App
32	36	73.5	1548	9	US-09-922-217-1095	Sequence 1095, Ap
33	36	73.5	1548	14	US-10-025-380-1095	Sequence 1095, Ap
34	36	73.5	1551	12	US-10-318-906A-46	Sequence 46, Appl
35	36	73.5	1551	12	US-10-319-236A-46	Sequence 46, Appl
36	35	71.4	403	9	US-09-012-135A-4	Sequence 4, Appl
37	35	71.4	403	15	US-10-026-021-7	Sequence 7, Appl
38	35	71.4	403	15	US-10-059-585-33	Sequence 33, Appl
39	35	71.4	403	15	US-10-209-324-2	Sequence 2, Appl
40	35	71.4	633	11	US-09-934-455-186	Sequence 186, App
41	34	69.4	200	12	US-09-882-227-124	Sequence 124, App
42	34	69.4	309	15	US-10-128-714-3051	Sequence 3051, Ap
43	34	69.4	326	10	US-09-925-300-1605	Sequence 1605, Ap
44	34	69.4	344	9	US-09-012-135A-3	Sequence 3, Appl
45	34	69.4	344	15	US-10-059-585-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-736-076-18
; Sequence 18, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(0)
; OTHER INFORMATION: position 7 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (0)...(9)
; OTHER INFORMATION: J45
US-09-736-076-18

Query Match 100.0%; Score 49; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.9e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9

Db 1 LGRPPFFETS 9

RESULT 2

```
US-09-736-076-19
; Sequence 19, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736.076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)..(0)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (0)..(11)
; OTHER INFORMATION: J46
; US-09-736-076 19

Query Match          100.0%; Score 49; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches      9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPFETS 9
      :|||||
Db      3 LGRPPFETS 11

RESULT 3
US-10-026 021-5
; Sequence 5, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/303,000
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(400)
; OTHER INFORMATION: human SNK mitotic kinase domain
US-10-026 021-5

Query Match          93.9%; Score 46; DB 15; Length 400;
Best Local Similarity 88.9%; Pred. No. 2.9;
Matches      8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LGRPPFETS 9
      :|||||
Db      275 LGRPPFETT 283
```

```
RESULT 4
US-10-059-585-14
; Sequence 14, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-059-585-14

Query Match          93.9%; Score 46; DB 15; Length 469;
Best Local Similarity 88.9%; Pred. No. 3.4;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPFETS 9
      :|||||
Db      59 LGRPPFETT 67

RESULT 5
US-09-771-161A-249
; Sequence 249, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 249
; LENGTH: 685
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-249

Query Match: 93.9%; Score 46; DB 10; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : LGRPPFFETS 9
   |||||:
Db 275 LGRPPFFET 283

RESULT 6
US-09-771-161A-250
; Sequence 250, Application US/09771161A
; Patent No. US2002010811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-250

Query Match: 93.9%; Score 46; DB 10; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : LGRPPFFETS 9
   |||||:
Db 275 LGRPPFFET 283

RESULT 7
US-09-771-161A-251
; Sequence 251, Application US/09771161A
; Patent No. US2002010811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 251
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-251

Query Match: 93.9%; Score 46; DB 10; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : LGRPPFFETS 9
   |||||:
Db 275 LGRPPFFET 283

RESULT 8
US-10-024-298A-101
; Sequence 101, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAH; KASE; KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2003-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-101

Query Match: 93.9%; Score 46; DB 12; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : LGRPPFFETS 9
   |||||:
Db 275 LGRPPFFET 283

RESULT 9
US-09-769-970-1
; Sequence 1, Application US/09769970
; Publication No. US20030170219A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Corley, Neil C.
; Guegler, Karl G.
; Lal, Preeti
; Goli, Surya K.
; Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

```

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/769,970
  FILING DATE: 24-Jan-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/272,796
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Billings, Lucy J
  REGISTRATION NUMBER: 36,749
  REFERENCE/DOCKET NUMBER: PP-0321 US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 415-855-0555
  TELEFAX: 415-845-4166
  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 685 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  IMMEDIATE SOURCE:
    LIBRARY: HJVENOB01
    CLONE: 39C43
  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US 09 769 970-1
Query Match      93.9%; Score 46; DB 12; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPFFETS 9
      |||||
Db      275 LGRPPFFET 283

RESULT 10
US-10-042 211A-101
; Sequence 101, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, AKIO et al
; TITLE OF INVENTION: NFKB ACTIVATION GENE
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US 10/041,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-40218P
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001 088911
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-101
Query Match      93.9%; Score 46; DB 12; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/769,970
  FILING DATE: 24-Jan-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/272,796
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Billings, Lucy J
  REGISTRATION NUMBER: 36,749
  REFERENCE/DOCKET NUMBER: PP-0321 US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 415-855-0555
  TELEFAX: 415-845-4166
  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 685 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  IMMEDIATE SOURCE:
    LIBRARY: HJVENOB01
    CLONE: 39C43
  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US 09 769 970-1
Query Match      93.9%; Score 46; DB 12; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPFFETS 9
      |||||
Db      275 LGRPPFFET 283

RESULT 11
US-09-736-076-6
; Sequence 6, Application US/09736076
; Patent No. US2002004931A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Samuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: POLO
US-09-736-076-6
Query Match      87.8%; Score 43; DB 9; Length 20;
Best Local Similarity 77.8%; Pred. No. 0.54;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPFFETS 9
      |||||
Db      5 VGKPPFFETS 13

RESULT 12
US-09-925-300-1268
; Sequence 1268, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (307)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (308)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (314)

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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (317)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (323)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (327)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (329)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1268

```

```

Query Match      87.8%  Score 43;  DB 10;  Length 329;
Best Local Similarity 77.8%  Pred. No. 9.2;
Matches 7;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

QY      1 LGRPPPFETS 9
      :|:|:|:|:|
DB      262 VGKPPPFETS 270

```

```

RESULT 13
US-10-026-021-6
; Sequence 6, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi;
; APPLICANT: Demo, Susan
; APPLICANT: Genkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210CS
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1).....(367)
; OTHER INFORMATION: human PLK1 mitotic kinase kinase domain
US-10-026-021-6

```

```

Query Match      87.8%  Score 43;  DB 10;  Length 367;
Best Local Similarity 77.8%  Pred. No. 9.2;
Matches 7;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

QY      1 LGRPPPFETS 9
      :|:|:|:|:|
DB      246 VGKPPPFETS 254

```

```

RESULT 14
US-09-771-161A-123
; Sequence 123, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A

```

```

; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 123
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-123

```

```

Query Match      87.8%  Score 43;  DB 10;  Length 516;
Best Local Similarity 77.8%  Pred. No. 13;
Matches 7;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

QY      1 LGRPPPFETS 9
      :|:|:|:|:|
DB      159 VGKPPPFETS 167

```

```

RESULT 15
US-09-771-161A-214
; Sequence 214, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 214
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-214

```

```

Query Match      87.8%  Score 43;  DB 10;  Length 603;
Best Local Similarity 77.8%  Pred. No. 15;
Matches 7;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

QY      1 LGRPPPFETS 9
      :|:|:|:|:|
DB      246 VGKPPPFETS 254

```

```

RESULT 16
US-10-171-311-186
; Sequence 186, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhang
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; CURRENT APPLICATION NUMBER: OF CERVICAL CANCER

```



```

FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,945
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 186
LENGTH: 603
TYPE: PRT
ORGANISM: Homo sapiens
US-10-171-311-186

Query Match      87.8%   Score 43;   DB 15;   Length 603;
Best Local Similarity 77.8%   Pred. No. 15;
Matches 7;   Conservative 2;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1 LGRPPPFES 9
DB      246 VGRPPPFES 254

RESULT 17
US-09-736-076-15
Sequence 15, Application US/09736076
Patent No. US20020049301A1
GENERAL INFORMATION:
APPLICANT: Ben-Sasson Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
FILE REFERENCE: 1242.1015-009
CURRENT APPLICATION NUMBER: US/09/736-076
CURRENT FILING DATE: 2003-12-13
PRIOR APPLICATION NUMBER: US 08/861,438
PRIOR FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: ACETYLATION
LOCATION: (1)...(9)
OTHER INFORMATION: position 8 is benzylester
NAME/KEY: AMIDATION
LOCATION: (1)...(9)
OTHER INFORMATION: J42
US-09-736-076-15

Query Match      81.6%   Score 40;   DB 9;   Length 9;
Best Local Similarity 100.0%   Pred. No. 598-039;
Matches 7;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1 LGRPPFE 7
DB      3 LGRPPFE 9

RESULT 18
US-09-736-076-57
Sequence 57, Application US/09736076
Patent No. US20020049301A1
GENERAL INFORMATION:
APPLICANT: Ben-Sasson Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
FILE REFERENCE: 1242.1015-009
CURRENT APPLICATION NUMBER: US/09/736-076

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CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 08/861,338
PRIOR FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MYRISTATE
LOCATION: (1)...(10)
OTHER INFORMATION: position 10 is benzylester
NAME/KEY: AMIDATION
LOCATION: (1)...(10)
OTHER INFORMATION: SNK
US-09-736-076-57

Query Match      91.6%   Score 40;   DB 9;   Length 10;
Best Local Similarity 100.0%   Pred. No. 0.93;
Matches 7;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1 LGRPPFE 7
DB      4 LGRPPFE 10

RESULT 19
US-10-026-021-3
Sequence 3, Application US/10026021
Publication No. US20030027756A1
GENERAL INFORMATION:
APPLICANT: Hitoshi, Yasumichi
APPLICANT: Demo, Susan
APPLICANT: Jenkins, Yonchu
APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
TREATMENT OF CANCER
FILE REFERENCE: 021044-C01210US
CURRENT APPLICATION NUMBER: US/10/026,021
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/309,632
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 379
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)...(379)
OTHER INFORMATION: SAK serine/threonine kinase kinase domain
US-10-026-021-3

Query Match      91.6%   Score 40;   DB 15;   Length 379;
Best Local Similarity 75.0%   Pred. No. 32;
Matches 6;   Conservative 2;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1 LGRPPFET 8
DB      206 IGRPPFET 213

RESULT 20
US-10-026-021-2
Sequence 2, Application US/10026021
Publication No. US20030027756A1
GENERAL INFORMATION:
APPLICANT: Hitoshi, Yasumichi
APPLICANT: Demo, Susan
APPLICANT: Jenkins, Yonchu
APPLICANT: Rigel Pharmaceuticals, Inc.

```

; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 970
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human SAK serine/threonine kinase
US-10-026-021-2

Query Match 81.6%; Score 40; DB 15; Length 970;
Best Local Similarity 75.0%; Pred. No. 78;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPEF 8
Db 206 IGRPPPEF 213

RESULT 21
US-09-736-076-17
; Sequence 17, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (0)...(9)
; OTHER INFORMATION: J43.1
US-09-736-076-17

Query Match 75.5%; Score 37; DB 9; Length 9;
Best Local Similarity 85.7%; Pred. No. 5.9e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPEF 7
Db 3 LGRPPPEF 9

RESULT 22
US-10-026-021-4
; Sequence 4, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for

; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(373)
; OTHER INFORMATION: human FNK mitotic kinase domain
US-10-026-021-4

Query Match 73.5%; Score 36; DB 15; Length 373;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPPEFS 9
Db 256 GSPPPEFA 263

RESULT 23
US-10-156-761-14310
; Sequence 14310, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14310
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14310

Query Match 73.5%; Score 36; DB 15; Length 505;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPPE 7
Db 305 GRPPPE 310

RESULT 24
US-09-769-970-15
; Sequence 15, Application US/09769970
; Publication No. US20030170219A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti

Geli, Surya K.
Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/769,970
FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/272,796
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1827450
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-769-970-15

Query Match 73.5%; Score 36; DB 12; Length 607;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPFFTS 9
| | | | |
Db 217 GSPPFETA 224

RESULT 26
US-10-204-041-16
; Sequence 16, Application US/10204041
; Publication No. US20030176443A1
; GENERAL INFORMATION:
; APPLICANT: STEIN-GERLACH, MATTHIAS
; APPLICANT: SALASSIDIS, KONSTADINOS
; APPLICANT: BACHER, GERALD
; APPLICANT: MULLER, STEFAN
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Pric
; FILE REFERENCE: AXM-007.1P US
; CURRENT APPLICATION NUMBER: US/10/204,041
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: EP 01111654.5
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: PCT/EP02/05420
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 16
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-204-041-16

Query Match 73.5%; Score 36; DB 12; Length 607;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPFFTS 9
| | | | |
Db 217 GSPPFETA 224

RESULT 26
US-10-108-580-2
; Sequence 2, Application US/10108580
; Publication No. US2003007768A1
; GENERAL INFORMATION:
; APPLICANT: Cogswell, John
; TITLE OF INVENTION: PLK3 PROTEIN-PROTEIN INTERACTIONS
; FILE REFERENCE: PU4458
; CURRENT APPLICATION NUMBER: US/10/108,580
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 607
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-108-580-2

Query Match 73.5%; Score 36; DB 15; Length 607;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPFFTS 9
| | | | |
Db 217 GSPPFETA 224

RESULT 27
US-10-318-906A-48
; Sequence 48, Application US/10318906A
; Publication No. US20030157678A1
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: Mitogenic Oxygenases
; FILE REFERENCE: 05501-0221
; CURRENT APPLICATION NUMBER: US/10/318,906A
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/437,568
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 899
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-906A-48

Query Match 73.5%; Score 36; DB 12; Length 899;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPFFE 7
| | | | |
Db 842 GRPPFE 847

RESULT 28
US-10-319-236A-48
; Sequence 48, Application US/10319236A
; Patent No. US20030166198A1
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: Antibodies to Mitogenic Oxygenases
; FILE REFERENCE: 05501-0220 (43150-281176)
; CURRENT APPLICATION NUMBER: US/10319236A
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/437,568
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 899
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-319-236A-48

Query Match 73.5%; Score 36; DB 12; Length 899;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
|:|||||
DB 842 GRPFFE 847

RESULT 29
US-09-922 217-692
; Sequence 692, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922.217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 692
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-217-692

Query Match 73.5%; Score 36; DB 3; Length 1210;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
|:|||||
DB 1153 GRPFFE 1158

RESULT 30
US-09-833-263-692
; Sequence 692, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 692
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-263-692

Query Match 73.5%; Score 36; DB 10; Length 1210;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
|:|||||
DB 1153 GRPFFE 1158

RESULT 31
US-10-025-380-692
; Sequence 692, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 692
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-380-692

Query Match 73.5%; Score 36; DB 14; Length 1210;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
|:|||||
DB 1153 GRPFFE 1158

RESULT 32
US-09-922-217-1095
; Sequence 1095, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Weagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922.217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1095
; LENGTH: 1548
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-217-1095

Query Match 73.5%; Score 36; DB 9; Length 1548;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GRPPE 7
Db 1491 GRPPE 1496

RESULT 33
US-10-025-380-1095
; Sequence 1095, Application US/10025252
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Weagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole E.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025.180
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1095
; LENGTH: 1548
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-025-380-1095

Query Match 73.5%; Score 36; DB 14; Length 1548;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GRPPE 7
Db 1491 GRPPE 1496

RESULT 34
US-10-318-906A-46
; Sequence 46, Application US/10318906A
; Publication No. US20030157678A1
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griending, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: Mitogenic Oxygenases
; FILE REFERENCE: 05501-0221
; CURRENT APPLICATION NUMBER: US/10/318,906A
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/437,568
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-906A-46

Query Match 73.5%; Score 36; DB 12; Length 1551;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GRPPE 7
Db 1494 GRPPE 1499

RESULT 35
US-10-319-236A-46
; Sequence 46, Application US/10319236A
; Publication No. US20030166199A1
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griending, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: Antibodies to Mitogenic Oxygenases
; FILE REFERENCE: 05501-0220 (43150-281176)
; CURRENT APPLICATION NUMBER: US/10/319,236A
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/437,568
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-319-236A-46

Query Match 73.5%; Score 36; DB 12; Length 1551;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GRPPE 7


```

Db          1494 GRPPE 1499
|||||
RESULT 36
US-09-012-135A-4
; Sequence 4, Application US/09012135A
; Patent No. US20020081578A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,268
; FILING DATE: January 9, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. US20020081578A1 October 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-012-135A-4

Query Match          71.4%; Score 35; DB 2; Length 403;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY          : LGRPPFFETS 9
            : |||||
Db          324 VGKPPFEAN 332

RESULT 37
US-10-026-021-7
; Sequence 7, Application US/10026021
; Publication No. US20030027756A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susar
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human ARK mitotic kinase
US-10-026-021-7

Query Match          71.4%; Score 35; DB 15; Length 403;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY          1 LGRPPFFETS 9
            : |||||
Db          324 VGKPPFEAN 332

RESULT 38
US-10-059-585-33
; Sequence 33, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-059 595-33

Query Match 71.4%; Score 35; DB 15; Length 403;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFFTS 9
DB 324 VGKPPFEAN 332

RESULT 39

US-10-209-324-2
Sequence 2, Application US/10209324
Publication No. US20030108910A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF CALIFORNIA SAN FRANCISCO
APPLICANT: TOLAND, Amanda E.
APPLICANT: BALMAIN, Allan
TITLE OF INVENTION: STK15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANCER
FILE REFERENCE: UCSF1120-2
CURRENT APPLICATION NUMBER: US/10/209,324
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/334,146
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/308,911
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (317..431)
OTHER INFORMATION: Xaa is Ile or Phe
US-10-209-324-2

Query Match 71.4%; Score 35; DB 15; Length 403;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFFTS 9
DB 324 VGKPPFEAN 332

RESULT 40

US-09 934 455-186
Sequence 186, Application US/09934455
Publication No. US20030121070A1
GENERAL INFORMATION:
APPLICANT: Adam, Luc
APPLICANT: Creelman, Robert
APPLICANT: Dubeil, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Keddie, James
APPLICANT: Pilgrim, Marsha
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, Lynne
APPLICANT: Riechmann, Jose Luis
APPLICANT: Yu, Guo-Liang
APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227419
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PatentIn version 3.1
SEQ ID NO 186
LENGTH: 633
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-934-455-186

Query Match 71.4%; Score 35; DB 11; Length 633;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPF 6
DB 382 LGRPPPF 387

Search completed: November 14, 2003, 13:43:27
Job time : 22.3714 secs

GenCore version 5.1.6
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OM Protein - protein search, using sw model

Run on: November 14, 2003, 13:20:05 ; Search time 10.8 Seconds
(without alignments)
90.141 Million cell updates/sec

Title: US-09-736-076-18
Perfect score: 49
Sequence: 1 LGRPPFFETS 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 3.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	93.9	682	2 A44493	serum-inducible ki
2	43	87.8	603	2 S34130	serine/threonine-s
3	43	87.8	603	2 A47545	protein kinase (EC
4	43	87.8	603	2 A54596	protein kinase - m
5	41	83.7	521	2 D88640	protein F55A8.2 [i
6	40	81.6	465	2 B55748	protein kinase (EC
7	40	81.6	925	2 A55748	protein kinase (EC
8	39	79.6	153	2 E71526	hypothetical prote
9	39	79.6	389	2 S52242	protein kinase (EC
10	39	79.6	407	2 S52243	p46Eg265 protein -
11	38	77.6	576	2 S22127	protein kinase pol
12	38	77.6	656	2 D96831	hypothetical prote
13	36	73.5	179	2 H81682	conserved hypotet
14	36	73.5	220	1 B42725	nitrile hydratase
15	36	73.5	256	2 A81354	glutamine-binding
16	36	73.5	631	2 A57286	probable serine/th
17	35	71.4	217	2 AD3132	hypothetical prote
18	35	71.4	217	2 H98155	probable permease
19	35	71.4	403	2 JC5974	aurora-related kin
20	35	71.4	445	2 A60488	histidine-rich gly
21	35	71.4	558	2 JC2004	nuclear factor-kap
22	35	71.4	589	2 JG0196	protein kinase DYP
23	35	71.4	629	2 JG0195	protein kinase DYP
24	35	71.4	633	2 C85010	hypothetical prote
25	35	71.4	1044	2 T31072	heterocyst differe
26	35	71.4	1044	2 AB2158	heterocyst differe
27	34	69.4	162	2 T26802	hypothetical prote
28	34	69.4	177	2 D83727	RNA polymerase ECF
29	34	69.4	200	2 B64621	conserved hypotet

30 34 69.4 200 2 A71895 hypothetical prote
31 34 69.4 221 2 A89825 conserved hypotet
32 34 69.4 227 2 H84064 hypothetical prote
33 34 69.4 242 2 AE3528 flagellar m-ring p
34 34 69.4 252 2 E83469 hypothetical prote
35 34 69.4 256 2 F72421 iron(III) ABC tran
36 34 69.4 303 2 G71109 hypothetical prote
37 34 69.4 305 2 T43221 serine/threonine-s
38 34 69.4 320 2 A12393 hypothetical prote
39 34 69.4 329 2 B87790 protein B0207.4 [i
40 34 69.4 359 2 F87524 histidinol-phospha
41 34 69.4 370 2 C75268 carboxypeptidase G
42 34 69.4 426 2 AF2663 hypothetical prote
43 34 69.4 426 2 E97445 nitrate transport
44 34 69.4 1018 2 E83099 probable RND efflu
45 34 69.4 1100 2 T42260 guanylate cyclase

ALIGNMENTS

RESULT 1
A44493
serum-inducible kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 10-Sep-1997
C;Accession: A44493
R;Simmons, D.L.; Neel, B.G.; Stevens, R.; Evett, G.; Erikson, R.L.
Mol. Cell. Biol. 12, 4164-4169, 1992
A;Title: Identification of an early-growth-response gene encoding a novel putative pr
A;Reference number: A44493; MUID:92375085; PMID:1508211
A;Accession: A44493
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-682 <SIM>
A;Experimental source: F-2 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:111721, NCBIP:111722)
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hor
C;Keywords: ATP
F;77-331/Domain: protein kinase homology <KIN>

Query Match 93.9%; Score 46; DB 2; Length 682;
Best Local Similarity 88.9%; Pred. No. 0.79;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
|||
Db 272 LGRPPFFET 280

RESULT 2
S34130
serine/threonine-specific protein kinase PLK (EC 2.7.1.-) - human
N;Alternate names: polo-like protein kinase; protein kinase plk-1
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C;Accession: S34130; I38123; S61543
R;Golsteyn, R.M.; Schultz, S.J.; Bartek, J.; Ziemiecki, A.; Ried, T.; Nigg, E.A.
submitted to the EMBL Data Library, June 1993
A;Description: Cloning and characterization of a novel human protein kinase plk-1 a p
through mitosis.
A;Reference number: S34130
A;Accession: S34130
A;Molecule type: mRNA
A;Residues: 1-603 <GOL>
A;Cross-references: EMBL:X73458; NID:g312997; PIDN:CAA51837.1; PID:g312998
A;Experimental source: nasopharyngeal carcinoma
R;Holtrich, U.; Wolf, G.; Brauning, A.; Karn, T.; Bohme, B.; Rubsamen-Waigmann, H.;
Proc. Natl. Acad. Sci. U.S.A. 91, 1736-1740, 1994
A;Title: Induction and down-regulation of PLK, a human serine/threonine kinase expres
A;Reference number: A53134; MUID:94173904; PMID:8127874
A;Accession: I38123
A;Status: preliminary; nucleic acid sequence not shown

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A;Molecule type: mRNA
A;Residues: 1-140, 'P', 142-226, 'E', 228-603 <RES>
A;Cross-references: EMBL:X75932; NID:G460768; PIDN:CAA53536.1; PID:G460769
A;Experimental source: lung tumor
R;Braeckinger, A.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Oncogene 11, 1793-1803, 1995
A;Title: Identification and functional characterization of the human and murine polo-like
kinase 1.
A;Reference number: S61543; MUID:9606906; PMID:7478607
A;Accession: S61543
A;Molecule type: DNA
A;Residues: 1-122, 'T', 124-136 <BRA>
A;Cross-references: EMBL:X90725; NID:G1061143; PIDN:CAA62260.1; PID:G1061144
A;Experimental source: placenta
A;Note: the authors translated the codon ACG for residue 107 as Met
C;Genetics:
A;Gene: GDB:PLX
A;Cross-references: GDB:331003
A;Map position: 17pter-17p12
C;Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolog
C;Keywords: ATP; phosphotransferase; serine/threonine specific protein kinase
F;51-305/Domain: protein kinase homology <KIN>

Query Match      87.8%; Score 43; DB 2; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPPFETS 9
      :|||:|:|
Db      246 VGKPPPFETS 254

RESULT 3
protein kinase (EC 2.7.1.37) Plk mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: A47545
R;Clay, F.J.; McEwen, S.J.; Bertencelie, I.; Wilks, A.F.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4982-4986, 1993
A;Title: Identification and cloning of a protein kinase encoding mouse gene, Plk, related
to the human and murine polo-like kinase.
A;Reference number: A47545; MUID:93281660; PMID:8099445
A;Accession: A47545
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-603 <CLA>
A;Cross-references: GDB:106144; NID:G106144; PIDN:AAA19948.1; PID:G106144
C;Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolog
C;Keywords: ATP; phosphotransferase
F;51-305/Domain: protein kinase homology <KIN>

Query Match      87.8%; Score 43; DB 2; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPPFETS 9
      :|||:|:|
Db      246 VGKPPPFETS 254

RESULT 4
A54596
protein kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: A54596
R;Lake, R.J.; Jeilnek, W.R.
Mol. Cell. Biol. 13, 7793-7801, 1993
A;Title: Cell cycle- and terminal differentiation-associated regulation of the mouse mRNA
for cyclin B1.
A;Reference number: A54596; MUID:94067140; PMID:7902533
A;Accession: A54596
A;Status: preliminary; translated from GB/EMBL/CCDB
A;Molecule type: mRNA
A;Residues: 1-603 <RES>

A;Cross-references: GB:L19558; NID:G403473; PIDN:AAA16071.1; PID:G403474
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
F;51-305/Domain: protein kinase homology <KIN>

Query Match      87.8%; Score 43; DB 2; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPPFETS 9
      :|||:|:|
Db      246 VGKPPPFETS 254

RESULT 5
D88640
protein F55A8.2 [imported]; - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
C;Accession: D88640
R;anonymus, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
logical processes.
A;Reference number: A75003; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_elegans/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
Science 283, 2103, 1999;
A;Accession: D88640
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-521 <STO>
A;Cross-references: GB:chr_IV; PIDN:AAC19186.1; PID:G3193148; GSPDB:GN00022; CESP:F55
A;Genetics:
A;Gene: F55A8.2
A;Map position: 4
C;Superfamily: cGMP-dependent protein kinase; cAMP receptor protein cyclic nucleotide
phosphodiesterase

Query Match      83.7%; Score 41; DB 2; Length 521;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LGRPPPFETS 9
      :|||:|:|
Db      403 LGRPPPFQAS 412

RESULT 6
B55748
protein kinase (EC 2.7.1.37) Sak-b - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Dec-1997
C;Accession: B55748
R;Fode, C.; Mctro, B.; Yousefi, S.; Heffernan, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
A;Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosophila
homolog of the protein kinase CK2.
A;Reference number: A55748; MUID:94294387; PMID:8022793
A;Accession: B55748
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-465 <FOC>
A;Cross-references: GS:L29480
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP; phosphotransferase
F;10-265/Domain: protein kinase homology <KIN>
F;18-26/Region: protein kinase ATP-binding motif

Query Match      81.6%; Score 40; DB 2; Length 465;
Best Local Similarity 75.0%; Pred. No. 7.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPPFET 8
      :|||:|:|
Db      206 IGRPPPFDT 213

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RESULT 7
A55748
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision: 02 Jun-1995 #text_change 24-Sep-1999
C:Accession: A55748
R:Fode, C.; Mouro, B.; Yousefi, S.; Heffernan, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosophila
A:Reference number: A55748; MUID:9429438v; PMID:8022793
A:Accession: A55748
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-925 <FOD>
A:Cross-references: GB:L29479; NID:9487869; PIDN:AAC37648.1; PID:g487870
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; phosphotransferase
F:10-265/Domain: protein kinase homology <KIN>
F:18-26/Region: protein kinase ATP-binding motif

Query Match      81.6%; Score 40; DB 2; Length 925;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPPFET 8
Db      206 LGRPPPFDT 213

RESULT 8
E71526
Hypothetical protein CT338 - Chlamydia trachomatis (serotype D, strain LW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision: 13-Sep-1998 #text_change 08 Oct-1999
C:Accession: E71526
R:Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genoto sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: E71526
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-153 <ARN>
A:Cross-references: GB:AE001307; GB:AE001203; NID:g3326757; PIDN:AAC67933.1; PID:g332879
A:Experimental source: serotype D, strain LW-3/Cx
C:Genetics:
A:Gene: CT338

Query Match      79.6%; Score 39; DB 2; Length 153;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPPFET 8
Db      11 LGAPPFET 18

RESULT 9
S52242
protein kinase (EC 2.7.1.1) p46X1B22 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-May-1995 #sequence_revision: 21-Jul-1995 #text_change 18-Jun-1999
C:Accession: S52242
R:Roghi, C.; Le Gueliec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening; encodes a new Xenopus protein kin
A:Reference number: S52242
A:Accession: S52242
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-389 <ROG>
A:Cross-references: EMBL:Z17206; NID:g609280; PIDN:CAA8914.1; PID:g609280
C:Superfamily: kinase-related transforming protein kinase homology
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C:Keywords: ATP; phosphotransferase
F:119-371/Domain: protein kinase homology <KIN>
F:127-135/Region: protein kinase ATP-binding motif

Query Match      79.6%; Score 39; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 9.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPPFET 8
Db      312 VGKPPPFET 319

RESULT 10
S52243
p46Eg265 protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-May-1995 #sequence_revision: 03-Aug-1995 #text_change 24-Sep-1999
C:Accession: S52243; S34642; I51695
R:Roghi, C.; Le Gueliec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein
A:Reference number: S52242
A:Accession: S52243
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-407 <ROG>
A:Cross-references: EMBL:Z17207; NID:g609281; PIDN:CAA78915.1; PID:g609282
R:Bouvet, P.; Omilli, F.; Arlot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Basset, T.;
submitted to the EMBL Data Library, June 1993
A:Description: Targetted deadenylation of specific mRNAs in Xenopus embryos by a mech
A:Reference number: S34642
A:Accession: S34642
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 328-407 <BOJ>
A:Cross-references: EMBL:Z24453; NID:g394756; PIDN:CAA80826.1; PID:g394757
R:Bouvet, P.; Omilli, F.; Arlot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Bassez, T.,
Mol. Cell. Biol. 14, 1893-1900, 1994
A:Title: The deadenylation conferred by the 3' untranslated region of a developmental
A:Reference number: I51695; MUID:94158861; PMID:8114721
A:Accession: I51695
A:Status: preliminary; translated from GB/EMBL/DCBJ
A:Molecule type: mRNA
A:Residues: 328-407 <BO2>
A:Cross-references: EMBL:Z24453; NID:g394756; PIDN:CAA80826.1; PID:g394757
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; phosphotransferase; protein kinase
F:138-390/Domain: protein kinase homology <KIN>
F:146-154/Region: protein kinase ATP-binding motif

Query Match      79.6%; Score 39; DB 2; Length 407;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPPFET 8
Db      331 VGKPPPFET 338

RESULT 11
S22127
protein kinase polo (EC 2.7.1.1) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Feb-1995 #sequence_revision: 20-Feb-1995 #text_change 24-Sep-1999
C:Accession: S22127
R:Sunkei, C.E.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22127
A:Accession: S22127
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-576 <SUN>
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A/Cross references: EMBL:X63361; NID:98355; PIDN:CAA44963.1; PID:q9356
C/Genetics:
A/Gene: FlyBase:fc01c
A/Cross references: FlyBase:FBgn0003124
C/Superfamily: Unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C/Keywords: ATP; phosphotransferase
F/23-272/Domain: protein kinase homology <Kin>

Query Match 77.6%; Score 38; DB 2; Length 506;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPFET 8
DB 218 VGPPPFET 225

RESULT 12
E96831
Hypothetical protein F18B13.8 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02 Mar-2001 #text_change 31-Mar-2001
C/Accession: D96831
R/Theologis, A.; Ecker, C.R.; Palm, C.C.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, G.L.; Jenkins, J.; Johnson Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
Chen, J.; Hsu, J.; Jin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Mauch, R.; Marziani,
Pizzo, V.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.P.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11150712
A/Accession: D96831
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-656 <STC>
A/Cross references: GB:AE005173; NID:95902379; PIEN:AAL5548.1.1; GSPDB:GN00141
C/Genetics:
A/Gene: F18B13.8
A/Map position: 1

Query Match 77.6%; Score 38; DB 2; Length 506;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGPPPFETS 9
DB 271 LGPPPFETA 279

RESULT 13
H81682
conserved hypothetical protein frameshift TC0615 [imported] - Chlamydia muridarum (strain
C/Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C/Accession: H91682
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gild, S.R.; Hovielberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A/Reference number: A81500; MUID:20150255; PMID:10684919
A/Accession: H81682
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-179 <TET>
A/Cross references: GB:AE002330; GB:AE002140; NID:9719049; PIDN:AAF39446.1; PID:G719365
A/Experimental source: strain Nigg (MoPn)
C/Genetics:
A/Gene: TC0615

Query Match 73.5%; Score 19; DB 2; Length 109;

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Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGPPPFETS 9
DB 37 VGAPPFKTS 45

RESULT 14
B42725
nitrile hydratase (EC 4.2.1.84) beta chain - Pseudomonas chlororaphis (strain B23)
C/Species: Pseudomonas chlororaphis
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C/Accession: B42725
R/Nishiyama, M.; Horinouchi, S.; Kobayashi, M.; Nagasawa, T.; Yamada, H.; Beppu, T.
J. Bacteriol. 173, 2465-2472, 1991
A/Title: Cloning and characterization of genes responsible for metabolism of nitrile
A/Reference number: A42725; MUID:91193202; PMID:2013568
A/Accession: B42725
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-220 <NIS>
A/Cross references: GB:U902216; NID:9216850; PIDN:BAA14246.1; PID:G216853
C/Superfamily: nitrile hydratase beta chain
C/Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 73.5%; Score 36; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPFE 7
DB 120 GRPPFE 125

RESULT 15
A81354
glutamine-binding periplasmic protein Cj0817 [imported] - Campylobacter jejuni (stra
C/Species: Campylobacter jejuni
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C/Accession: A81354
R/Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chi
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba
Nature 403, 665-669, 2000
A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A/Reference number: A81250; MUID:20150912; PMID:10686204
A/Accession: A81354
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-256 <PAR>
A/Cross references: GB:AL139076; GB:AL111168; NID:96968128; PIDN:CAB73082.1; PID:G69
A/Experimental source: serotype O2, strain NCTC 11168
C/Genetics:
A/Gene: glrH; Cj0817
C/Superfamily: lysine-arginine-ornithine-binding protein

Query Match 73.5%; Score 36; DB 2; Length 256;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGPPPFETS 9
DB 27 LGYPPFEMS 35

RESULT 16
A57286
probable serine/threonine protein kinase (EC 2.7.1.-) fnk - mouse
C/Species: Mus musculus (house mouse)
C/Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 10-Sep-1997
C/Accession: A57286
R/Donohue, P.J.; Alberts, G.F.; Guo, Y.; Winkles, J.A.
J. Biol. Chem. 270, 10351-10357, 1995

```

A;Title: Identification by targeted differential display of an immediate early gene encod
A;Reference number: A57286; MUID:95247749; PMID:7730342
A;Accession: A57286
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-631 <DON>
A;Cross-references: GB:U21192; GB:U22434
C;Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolo
C;Keywords: ATP; phosphotransferase
F;61-315/Domain: protein kinase homology <KIN>

Query Match 73.5%; Score 16; DB 2; Length 631;
Best Local Similarity 75.0%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPPFETS 9
Db 257 GSPPFETA 264
I |||||

RESULT 17
AD3132
hypothetical protein Atu4680 (imported) - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11 Jan-2002 #text_change 18-Nov-2002
C;Accession: AD3132
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Yanks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD3132
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <KJR>
A;Cross-references: GB:AE008689; PIDN:AA045474.1; PID:gi17743180; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4680
A;Map position: linear chromosome
C;Superfamily: histidine permease protein X

Query Match 71.4%; Score 35; DB 2; Length 217;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPFETS 9
Db 82 LGWPPFTTS 90
I |||||

RESULT 18
H98155
probable permease of ABC transporter PA1257 (imported) - Agrobacterium tumefaciens (stra
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22 Oct 2001 #text_change 18-Nov-2002
C;Accession: H98155
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Woliam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: H98155
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <KJR>
A;Cross-references: GB:AE007870; PIDN:AAK88770.1; PID:gi15158516; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L_403
A;Map position: linear chromosome

C;Superfamily: histidine permease protein M

Query Match 71.4%; Score 35; DB 2; Length 217;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPPFETS 9
Db 82 LGWPPFTTS 90
I |||||

RESULT 19
JC5974
aurora-related kinase 1 (EC 2.7.1.1) - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jan-2000
C;Accession: JC5974
R;Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara, M.; Gilbert, D.J.; J
Biochem. Biophys. Res. Commun. 244, 285-292, 1998
A;Title: cDNA cloning, expression, subcellular localization, and chromosomal assignm
A;Reference number: JC5974; MUID:98183439; PMID:9514916
A;Accession: JC5974
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-403 <SHI>
A;Cross-references: GB:AF008551
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C;Keywords: phosphotransferase
F;131-383/Domain: protein kinase homology <KIN>

Query Match 71.4%; Score 35; DB 2; Length 403;
Best Local Similarity 55.6%; Pred. No. 57;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPPFETS 9
Db 324 VGKPPFEAN 332
I |||||

RESULT 20
A60488
histidine-rich glycoprotein - bovine (fragments)
N;Alternate names: autorosette inhibition factor
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1993 #sequence_revision 23-Mar-1995 #text_change 07-Jul-1995
C;Accession: S35687; JC2196; A60488
R;Sorensen, C.B.; Krogh-Pedersen, H.; Petersen, T.E.
FEBS Lett. 328, 285-290, 1993
A;Title: Determination of the disulphide bridge arrangement of bovine histidine-rich
A;Reference number: S35687; MUID:93351678; PMID:8348977
A;Accession: S35687
A;Molecule type: protein
A;Residues: 1-25;26-52;57-75;82-88;95-119;146-173;175-206;210-309;313-445 <SOR>
A;Note: 355-Gln and 368-Tyr were also found
R;Halkier, T.; Andersen, H.; Vestergaard, A.; Magnusson, S.
Biochem. Biophys. Res. Commun. 200, 78-82, 1994
A;Title: Bovine histidine-rich glycoprotein is a substrate for bovine plasma factor X
A;Reference number: JC2196; MUID:94220160; PMID:7909439
A;Accession: JC2196
A;Molecule type: protein
A;Residues: 1-23;35-54;VK',57-101,'R','TVGEYTEG',116,'N',118,'R',120-136;137-145;150
A;Experimental source: plasma
R;Vestergaard, A.B.; Andersen, H.F.; Magnusson, S.; Halkier, T.
Thromb. Res. 60, 385-396, 1990
A;Title: Histidine-rich glycoprotein inhibits contact activation of blood coagulation
A;Reference number: A60488; MUID:91196010; PMID:2084959
A;Accession: A60488
A;Molecule type: protein
A;Residues: 1-6,'X',8-15 <VES>
C;Comment: This protein is a single-chained plasma protein which participates in tran
C;Superfamily: histidine-rich glycoprotein; cystatin homology
C;Keywords: glycoprotein; plasma
F;2-113/Domain: cystatin homology <CY>

```
F:122-207/Domain: cystatin homology (fragments) <CY2>
F:7-424,60-71,87-108,165-346,180-203,258-288/Disulfide bonds: #status experimental
F:74,107,164,266/Binding site: carbohydrate (Asn) (covalent): #status experimental

Query Match          71.4%; Score 35; DB 2; Length 445;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 GRPPPFETS 9
      |||||
DB      235 GRPPPKPS 242

RESULT 21
JC2004
nuclear factor kappa B p65 chain - chicken
C:Species: Gallus gallus (chicken)
C>Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C:Accession: JC2004
Gene 133, 237-242, 1993
A:Title: Isolation of the chicken NF-kappaB p65 subunit-encoding cDNA and characterization
A:Reference number: JC2004; MUID:94040817; PMID:7916720
A:Accession: JC2004
A:Molecule type: mRNA
A:Residues: 1-558 <KE>
A:Cross-references: GB:J13721; NID:G455463; PIDN:BAA02874.1; PID:G460374
C:Comment: This protein contains the Rel homology domain in its amino-terminal 286 amino
C:Superfamily: rel transforming protein; rel homology
C:Keywords: DNA binding; phosphoprotein
F:25-310/Domain: rel homology <REL>
F:306-309/Region: nuclear location signal
F:281/Binding site: phosphate (Ser) (covalent): #status predicted

Query Match          71.4%; Score 35; DB 2; Length 558;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LGRPPPFET 8
      |||||
DB      429 LGRPPPFDT 436

RESULT 22
JG0196
protein kinase DYRK1B (EC 2.7.1.1) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 23-Jul-1999 #sequence_revision 16-Feb-2001 #text_change 16-May-2000
C:Accession: JG0196
R:Leder, S.; Weber, Y.; Altafaj, X.; Estivill, X.; Joost, H.; Becker, W.
Biochem. Biophys. Res. Commun. 254, 474-479, 1999
A:Title: Cloning and characterization of DYRK1B, a novel member of the DYRK family of p
A:Reference number: JG0195; MUID:99119336; PMID:9918863
A:Accession: JG0196
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-599 <LED>
A:Cross-references: GB:Y18280
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: phosphotransferase

Query Match          71.4%; Score 35; DB 2; Length 589;
Best Local Similarity 77.8%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 LGRPPPFETS 9
      |||||
DB      509 LGRPPSPTS 517

RESULT 21
JG0195
protein kinase DYRK1B (EC 2.7.1.1) - human
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```
C:Species: Homo sapiens (man)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C:Accession: JG0195
R:Leder, S.; Weber, Y.; Altafaj, X.; Estivill, X.; Joost, H.; Becker, W.
Biochem. Biophys. Res. Commun. 254, 474-479, 1999
A:Title: Cloning and characterization of DYRK1B, a novel member of the DYRK family of
A:Reference number: JG0195; MUID:99119336; PMID:9918863
A:Accession: JG0195
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-629 <LED>
A:Cross-references: GB:Y17999; NID:G4379096; PIDN:CAA76991.1; PID:G4379097
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: phosphotransferase

Query Match          71.4%; Score 35; DB 2; Length 629;
Best Local Similarity 77.8%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 LGRPPPFETS 9
      |||||
DB      549 LGRPPSPTS 557

RESULT 24
C85010
hypothetical protein: AT4G00750 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: C85010
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: C85010
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-633 <STO>
A:Cross-references: GB:NC_001268; NID:G7267414; PIDN:CAB80884.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4G00750
A:Map position: 4

Query Match          71.4%; Score 35; DB 2; Length 633;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPPF 6
      |||||
DB      382 LGRPPF 387

RESULT 25
T31072
heterocyst differentiation protein HetC - Anabaena sp.
C:Species: Anabaena sp.
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C:Accession: T31072
R:Khudyakov, I.; Wolk, C.P.
J. Bacteriol. 179, 6971-6978, 1997
A:Title: HetC, a gene coding for a protein similar to bacterial ABC protein exporter.
A:Reference number: Z20967; MUID:98037493; PMID:9371442
A:Accession: T31072
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1044 <KHU>
A:Cross-references: EMBL:U55386; NID:G2828797; PID:G2828798; PIDN:AAC38130.1
C:Genetics:
A:Gene: hetC
C:Function:
A:Description: involved in early regulation of heterocyst differentiation
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolo
```

Query Match 71.4%; Score 35; DB 2; Length 1044;
 Best Local Similarity 77.8%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
 |
 Db 444 LSRPQFETS 452

RESULT 26
 AB2158
 heterocyst differentiation protein [imported]; - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14 Dec-2001 #text_change 09-Dec-2002
 C:Accession: AB2158
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen fixing Cyanobacterium Anabaena PCC 7120
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AB2158
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1044 <KJR>
 A:Cross-references: GB:BA000019; PIDN:BAR74516.1; PID:G17111911; GSPDB:GN03179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: hnfC
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 71.4%; Score 35; DB 2; Length 1044;
 Best Local Similarity 77.8%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
 |
 Db 444 LSRPQFETS 452

RESULT 27
 T26902
 hypothetical protein Y41C4A.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
 C:Accession: T26902
 R;Steward, C.
 submitted to the EMBL Data Library, October 1998
 A:Reference number: Z20269
 A:Accession: T26902
 A:Status: preliminary; translated from GB:AF014044
 A:Molecule type: DNA
 A:Residues: 1-162 <WIL>
 A:Cross-references: EMBL:AL0332627; PIDN:CAA21546.1; CESP:Y41C4A.3
 A:Experimental source: clone Y41C4A
 C:Genetics:
 A:Gene: CESP:Y41C4A.3
 C:Superfamily: Caenorhabditis elegans hypothetical protein Y41C4A.3

Query Match 69.4%; Score 34; DB 2; Length 162;
 Best Local Similarity 85.7%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFE 7
 |
 Db 125 LGRPPFE 131

RESULT 28
 D83727
 RNA polymerase ECF-type sigma factor sigV [imported]; - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15 Jun-2001

C:Accession: D83727
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: D83727
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-177 <STQ>
 A:Cross-references: GB:AP001509; GB:BA000004; NID:G10173176; PIDN:BAR04339.1; GSPDB:GI
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: sigV

Query Match 69.4%; Score 34; DB 2; Length 177;
 Best Local Similarity 85.7%; Pred. No. 37;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFE 7
 |
 Db 11 LSRPPFE 17

RESULT 29
 B64621
 conserved hypothetical protein HP08i0 - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 24-Nov-1999
 C:Accession: B64621
 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKel
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: B64621
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-200 <TOM>
 A:Cross-references: GB:AE000592; GB:AE000511; NID:G2313929; PIDN:AAD07856.1; PID:G231
 C:Superfamily: Escherichia coli hypothetical 21.7K protein (ftsY-nika intergenic regi

Query Match 69.4%; Score 34; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPFETS 9
 |
 Db 134 PPFETS 139

RESULT 30
 A71895
 hypothetical protein jhp0746 - Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variety: strain J99
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Nov-1999
 C:Accession: A71895
 R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D
 ; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F
 Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: A71895
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-200 <ARN>
 A:Cross-references: GB:AE001505; GB:AE001439; NID:G4155295; PIDN:AAD06318.1; PID:G415
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: jhp0746
 C:Superfamily: Escherichia coli hypothetical 21.7K protein (ftsY-nika intergenic regi

Query Match 69.4%; Score 34; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPFETS 9
DB 334 PPFETS 139

RESULT 31
A89825
conserved hypothetical protein SA0525 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: A89825
S:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Jancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418149
A:Accession: A89825
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 <KJR>
A:Cross-references: GB:BA000018; PID:g13700459; PIDN:BA841756.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0525

Query Match 69.4%; Score 34; DB 2; Length 221;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPPFET 8
DB 49 LGNPPFAT 56

RESULT 32
H84064
hypothetical protein BH3320 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 14-Jun-2001
C:Accession: H84064
R:Takami, H.; Nakasone, K.; Takaki, F.; Nishii, R.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4319-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058130
A:Accession: H84064
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-227 <STO>
A:Cross-references: GB:AP001518; GB:BA001004; NID:g1010792; PIDN:BA807039.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3320

Query Match 69.4%; Score 34; DB 2; Length 227;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPPFET 8
DB 49 LGNPPFAT 56

RESULT 33
AE3528
flagellar m-ring protein flif [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

Query Match 69.4%; Score 34; DB 2; Length 242;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPPFET 8
DB 50 LGRPSYET 57

RESULT 34
E83469
hypothetical protein PA1406 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: E83469
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; I
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic p
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: E83469
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-252 <STO>
A:Cross-references: GB:AE004570; GB:AE004091; NID:g9947350; PIDN:AAG04795.1; GSPDB:G
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1406

Query Match 69.4%; Score 34; DB 2; Length 252;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPPE 7
DB 31 LARPPPE 37

RESULT 35
F72421
iron(III) ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 08-Sep-2000
C:Accession: F72421
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: F72421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <ARN>
A:Cross-references: GB:AE001694; GB:AE000512; NID:g4980558; PIDN:AAD35172.1; PID:g49
A:Experimental source: strain MSB8

C:Accession: AE3528
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanov
; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3528
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-242 <KJR>
A:Cross-references: GB:AE008918; PIDN:AAL53392.1; PID:g17984286; GSPDB:GN00191
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME110151
A:Map position: 11

Query Match 69.4%; Score 34; DB 2; Length 242;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

C;Genetics:
A;Gene: TM007A
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 69.4%; Score 34; DB 2; Length 266;
Best Local Similarity 77.8%; Pred. No. 55;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPPTS 9
DB 6 LGRIPWETS 71

RESULT 36
G71109
hypothetical protein PH0646 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 18-Aug-2000
C;Accession: G71109
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: G71109
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-303 <KAW>
A;Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29737.1; PID:di030680; PID:g32570
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0646
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0646

Query Match 69.4%; Score 34; DB 2; Length 303;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPPTS 9
DB 82 GKPPPTS 89

RESULT 37
T4322:
serine/threonine specific protein kinase (EC 2.7.11.1) 2 Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 14-Mar-2000
C;Accession: T4322;
R;Schumacher, J.M.; Golden, A.; Donovan, P.C.
J. Cell Biol. 143, 1635-1646, 1998
A;Title: AIR-2: An aurora/Ipl-related protein kinase associated with chromosomes and mi
A;Reference number: Z22347; MUID:99069487; PMID:9652156
A;Accession: T43221
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-305 <SCH>
A;Cross-references: EMBL:AF071207; PIDN:AAC70945.1
C;Genetics:
A;Gene: AIR-2
A;Map position: 1
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: phosphotransferase

Query Match 69.4%; Score 34; DB 2; Length 305;
Best Local Similarity 71.4%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPTS 7
DB 221 VGKPPPE 227

RESULT 38
AI2393
hypothetical protein all4705 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AI2393
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriugu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-320 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA876404.1; PID:g17133842; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4705

Query Match 69.4%; Score 34; DB 2; Length 320;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPPE 7
DB 122 LGRPPLE 128

RESULT 39
B87790
protein B0207.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: B87790
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A;Accession: B87790
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-329 <STC>
A;Cross-references: GB:chr_1; PIDN:AAB52459.1; PID:g1943805; GSPDB:GN00019; CESP:B020
C;Genetics:
A;Gene: B0207.4
A;Map position: 1
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 69.4%; Score 34; DB 2; Length 329;
Best Local Similarity 71.4%; Pred. No. 72;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPE 7
DB 245 VGKPPPE 251

RESULT 40
FB7524
histidinol-phosphate aminotransferase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: FB7524
R;Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: F87524
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <STC>
A:Cross-references: GB:AE005673; NID:g13423728; PIDN:AAK24194.1; SSPDB:GN00148
C:Genetics:
A:Gene: CC2223
C:Superfamily: probable histidinol-phosphate transaminase

Query Match 69.4%; Score 34; DB 2; Length 359;
Best Local Similarity 85.7%; Pred. NO. 79;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RPPETS 9
|||
Db 242 RPPETS 248

Search completed: November 14, 2003, 13:28:52
Job time : 11.8 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 14, 2003, 12:56:44 ; Search time 6.68571 Seconds
(without alignments:
63.305 Million cell updates/sec

Title: US-09-736-076-18
Perfect score: 49
Sequence: 1 LGRPPFETS 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	93.9	682	1 SNK_MOUSE	P53351 mus musculu
2	46	93.9	682	1 SNK_RAT	Q9r012 rattus norv
3	46	93.9	685	1 SNK_HUMAN	Q9nyy3 homo sapien
4	43	87.8	603	1 PLK1_HUMAN	P53350 homo sapien
5	43	87.8	603	1 PLK1_MOUSE	Q37832 mus musculu
6	43	87.8	603	1 PLK1_RAT	Q52673 rattus norv
7	39	79.6	282	1 STK6_MOUSE	Q88445 mus musculu
8	39	79.6	407	1 STK6_XENLA	Q91820 xenopus lae
9	39	79.6	408	1 ST6L_XENLA	Q91819 xenopus lae
10	39	79.6	576	1 PCLO_DROME	P52304 drosophila
11	36	73.5	220	1 NHAB_PSECE	P27763 pseudomonas
12	36	73.5	615	1 CNK_RAT	Q3r011 rattus norv
13	36	73.5	631	1 CNK_MOUSE	Q60806 mus musculu
14	36	73.5	646	1 CNK_HUMAN	Q9h4b4 homo sapien
15	36	73.5	660	1 PKN1_COREF	Q8fu15 corynebacte
16	35	71.4	396	1 HRG_BOVIN	P33433 bos taurus
17	35	71.4	403	1 STK6_HUMAN	Q14965 homo sapien
18	35	71.4	558	1 TF65_CHICK	P98152 gallus gali
19	35	71.4	589	1 DYRB_MOUSE	Q92188 mus musculu
20	35	71.4	629	1 DYRB_HUMAN	Q9y463 homo sapien
21	34	69.4	156	1 STKC_PIG	Q9r0x0 sus scrofa
22	34	69.4	344	1 STKC_HUMAN	Q963d4 homo sapien
23	34	69.4	359	1 H181_CAUCR	Q9a671 caulobacter
24	34	69.4	540	1 FLIF_BRUAB	C52069 brucella ab
25	34	69.4	830	1 GCL2_MOUSE	Q9jhd2 mus musculu
26	34	69.4	837	1 GCL2_HUMAN	Q92830 homo sapien
27	33	67.3	72	1 PN2A_PENVA	P81057 penaeus van
28	33	67.3	304	1 MTS1_STRCS	O52692 streptomyce
29	33	67.3	343	1 STKC_RAT	O55099 rattus norv
30	33	67.3	345	1 STKC_MOUSE	O70126 mus musculu
31	33	67.3	380	1 PKN5_MYXXA	P54737 myxococcus
32	33	67.3	646	1 PKN1_CORGL	Q8nu98 corynebacte
33	33	67.3	649	1 PLK1_CAEEL	P34331 caenorhabdi

34	33	67.3	839	1 TOP1_SYNP7	P34185 synchococc
35	33	67.3	1113	1 PER3_MOUSE	O70361 mus musculu
36	33	67.3	1188	1 HFM1_YEAST	P51979 saccharomyc
37	33	67.3	1210	1 PER3_HUMAN	P56645 homo sapien
38	33	67.3	1699	1 DPOL_THEG8	Q9hh84 thermococcu
39	33	67.3	1935	1 YBBA_SCHPO	O60072 schizosacch
40	32	65.3	207	1 RS8_ICTPU	Q90yr6 ictalurus p
41	32	65.3	238	1 YO97_CAEEL	P41847 caenorhabdi
42	32	65.3	309	1 STK6_HUMAN	Q9uqb9 homo sapien
43	32	65.3	314	1 PPAC_DEIRA	Q9rrb7 deinococcus
44	32	65.3	338	1 HM2C_CAEEL	P41779 caenorhabdi
45	32	65.3	406	1 O42A_DROME	Q9v912 drosophila

ALIGNMENTS

RESULT 1
SNK_MOUSE
ID SNK_MOUSE STANDARD; PRT; 682 AA.
AC P53351;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.-) (Serum inducible
DE kinase).
GN SNK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB:TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92375085; Pubmed=1508211;
RA Simmons D.L., Neel B.G., Stevens R., Evett G., Erikson R.L.;
RT "Identification of an early-growth-response gene encoding a novel
RT putative protein kinase."
RL Mol. Cell. Biol. 12:4164-4169(1992).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL
CC TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS,
CC WOUND HEALING OR NEOPLASIA.
CC -!- TISSUE SPECIFICITY: BRAIN, LUNG AND HEART.
CC -!- INDUCTION: BY SERUM AND PHORBOL ESTER.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M96163; -; NOT_ANNOTATED_CDS.
DR PIR; A44493; A44493.
DR MGD; MGI:1099790; Snk.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 54 59 POLY-HIS.
FT DOMAIN 79 331 PROTEIN KINASE.
FT NP_BIND 85 93 ATP (BY SIMILARITY).

FT BINDING 108 108 ATP (BY SIMILARITY)
FT ACT SITE 202 202 BY SIMILARITY
FT DOMAIN 507 570 POLO BOX 1
FT DOMAIN 603 674 POLO BOX 2
SQ SEQUENCE 682 AA; 77811 MW; 58C502EABFD7209A9D CRC64;

Query Match: 93.9%; Score 46; DB 1; Length 682;
Best Local Similarity 88.9%; Pred. No. 0.26;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPFETS 9
Db 272 LGRPPPFETT 280

RESULT 2

SNK_RAT STANDARD; PRT; 682 AA.
AC Q9R312; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
ET 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.-) (Serum inducible kinase).
GN SNK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID:10116;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=99452760; PubMed=10523297;
RA Kauselmann G., Weiler M., Wulff P., Jessberger S., Konietzko J., Scafield J., Staubli U., Bereiter-Hahn J., Streibhardt K., Kuhl D.;
RT "The polo-like protein kinases Pnk and Snk associate with a Ca(2+)- and integrin-binding protein and are regulated dynamically with synaptic plasticity."
RL EMBL J. 18:5528-5539(1999).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC ! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.

CC -----
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CC -----
CC EMBL: AF136583; AAF08366.1; 1;
CC InterPro: IPR000959; POLO box.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00069; pkinase; 1;
CC Pfam: PF00659; POLO box; 2;
CC ProDom: PD000001; Prot_kinase; 1;
CC SMART: SM0220; S_TKC; 1;
CC PROSITE: PS00078; POLO BOX; 2;
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1;
CC PROSITE: PS00108; PROTEIN_KINASE_ST;
CC Transferase; Serine/threonine-protein kinase; ATP binding; Repeat.
KW DOMAIN 54 59 POLY-HIS.
FT DOMAIN 79 331 PROTEIN_KINASE.
FT DOMAIN 85 93 ATP (BY SIMILARITY).
FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT SITE 202 202 BY SIMILARITY.
FT DOMAIN 507 570 POLO BOX 1;
FT DOMAIN 603 674 POLO BOX 2;

SQ SEQUENCE 682 AA; 77919 MW; 58C502E8DE83D5F3 CRC64;

Query Match: 93.9%; Score 46; DB 1; Length 682;
Best Local Similarity 88.9%; Pred. No. 0.26;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPFETS 9
Db 272 LGRPPPFETT 280

RESULT 3

SNK_HUMAN STANDARD; PRT; 685 AA.
AC Q9NY33; 060679; Q96CV7; Q9UE61;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.-) (Serum inducible kinase).
GN SNK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Ouyang B., Dai W.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN 12;
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Anderson K.M., Nerurkar S.S., Hansbury M.J., Fornwald J., Scott G., Bouzyk M., Mui P., Imbrugia C.S., Carlson K., Marshall L.A., Roshak A.K.;
RT "Identification and characterization of human serum-inducible kinase (SNK), a novel member of the polo-kinase family of cell cycle regulators: potential implication for regulation of vascular smooth muscle proliferation."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN 13;
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 14;
RP SEQUENCE OF 110-408 FROM N.A.
RA Fidler C., Boultonwood J., Wang Jabs E., Wainscoat J.S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.

```
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC -----
CC EMBL: AF059617; AAC14573.1; -
CC EMBL: AF223574; AAF62897.1; -
CC EMBL: J85755; AAD00575.1; -
CC EMBL: BC013879; AAH13879.1; -
CC MIM: 607023; -
CC InterPro: IPR000959; POLO box.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF00659; POLO box; 2.
CC ProDom: PDC00001; Prot_kinase; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS00078; POLO BOX; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00117; PROTEIN_KINASE_DCM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 57 64 POLY-HIS.
FT NP_BIND 82 334 PROTEIN_KINASE.
FT BINDING 111 111 ATP (BY SIMILARITY).
FT ACT_SITE 205 205 BY SIMILARITY.
FT DOMAIN 510 573 POLO BOX 1.
FT DOMAIN 606 677 POLO BOX 2.
FT CONFLICT 28 28 A -> G (IN REF. 1).
SQ SEQUENCE 685 AA; 78236 MW; 6429F6EFD830B333 CRC64;

Query Match 93.9%; Score 46; DB 1; Length 685;
Best local similarity 89.9%; Pred. No. 0.27;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPFFETS 9
DB 275 LGPPFFETT 283

RESULT 4
P.K1_HUMAN
ID P.K1_HUMAN STANDARD; PRT; 283 AA.
AC P53350;
DT 01-OCT-1996 (Ref. 34, Created)
DT 01-OCT-1996 (Ref. 34, Last sequence update)
DT 15-SEP-2003 (Ref. 42, Last annotation update)
DE Serine/threonine-protein kinase PLK (EC 2.7.1.-) (PLK-1) (Serine-
DE threonine protein kinase 13) (STPK13).
GN PLK OR PLK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94289293; PubMed=8018557;
RA Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.L.,
RA Ferris D.K.;
RT "Cloning and characterization of human and murine homologues of the
RT Drosophila polo serine-threonine kinase.";
RL Cell Growth Differ. 5:249-257(1994);
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94067140; PubMed=7902533;
RA Lake R.J., Celinek W.R.;
```

```
RT "Cell cycle- and terminal differentiation-associated regulation of
RT the mouse mRNA encoding a conserved mitotic protein kinase.";
RL Mol. Cell. Biol. 13:7793-7801(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95051109; PubMed=7962193;
RA Golsteyn R.M., Schultz S.J., Bartek J., Ziemiecki A., Ried T.,
RA Nigg E.A.;
RT "Cell cycle analysis and chromosomal localization of human Plk1, a
RT putative homologue of the mitotic kinases Drosophila polo and
RT Saccharomyces cerevisiae Cdc5.";
RL J. Cell Sci. 107:1509-1517(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94173904; PubMed=8127874;
RA Holtrich U., Wolf G., Braeuninger A., Karn T., Boehme B.,
RA Ruebsamen-Waigmann H., Strebhardt K.;
RT "Induction and down-regulation of PLK, a human serine/threonine
RT kinase expressed in proliferating cells and tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:1736-1740(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: PLACENTA AND COLON.
CC -!- DEVELOPMENTAL STAGE: ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
CC DURING S PHASE.
CC -!- INDUCTION: BY GROWTH-STIMULATING AGENTS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC -----
CC EMBL: U01038; AAA56634.1; -
CC EMBL: L19559; AAA36659.1; -
CC EMBL: X73458; CAA51837.1; -
CC EMBL: X75932; CAA53536.1; -
CC EMBL: BC002369; AAH02369.1; -
CC EMBL: BC003002; AAH03002.1; -
CC EMBL: BC014846; AAH14846.1; -
```


DR PIR: S34130; S34130.
DR Genew: HGNC:9077; PLK.
DR GK: P53350; -
DR MIM: 602096; -
DR GO: GO:0004674; Eiprotein serine/threonine kinase activity; TAS.
DR GO: GO:0007067; Pmitosis; TAS.
DR GO: GO:0007048; Pioncogenesis; TAS.
DR GO: GO:0000074; Piregulation of cell cycle; TAS.
DR InterPro: IPR003959; POLO_box.
DR InterPro: IPR003719; Prot_kinase.
DR InterPro: IPR002293; Ser_thr_pkinase.
DR Pfam: PF00659; pkinase; 1.
DR Pfam: PF00659; POLO_box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00078; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Nuclear protein.
FT DOMAIN 53 305 PROTEIN KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 480 POLO_BOX_1.
FT DOMAIN 515 584 POLO_BOX_2.
FT CONFLICT 2 2 S -> T (IN REF. 1).
FT CONFLICT 11 11 A -> E (IN REF. 1).
FT CONFLICT 58 58 E -> L (IN REF. 1).
FT CONFLICT 60 60 G -> S (IN REF. 1).
FT CONFLICT 73 73 A -> V (IN REF. 2).
FT CONFLICT 141 141 L -> P (IN REF. 4).
FT CONFLICT 227 227 G -> E (IN REF. 4).
FT CONFLICT 301 301 N -> G (IN REF. 2).
FT CONFLICT 495 495 A -> G (IN REF. 2).
FT CONFLICT 501 501 E -> Q (IN REF. 2).
SQ SEQUENCE 603 AA; 68254 MW; 17802F3C1CE8256 CR; 64,
Query Match 87.8% Score 437 DB 1 Length 603;
Best Local Similarity 77.8% Pred No 0.9;
Matches 77 Conservative 27 Mismatches 0 Indels 0 Gaps 0;
QY 1 LGRPPFFETS 9
DB 246 VGRPPFFETS 254
RESULT 5
PLK1_MOUSE STANDARD; EFT: 3 AA
AC Q07812;
DT 01 FEB 1995 (Rel. 31, Created);
DT 01 OCT 1996 (Rel. 34, Last sequence update);
DT 16 OCT 2001 (Rel. 40, Last annotation update);
DE Serine/threonine-protein kinase PLK1 (EC 2.7.11.1) (PK-1); Serine-
threonine protein kinase 13) (STPK1).
GN PLK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Bone marrow.
RX MEDLINE=93281660; PubMed=8099445;
RA Clay F.C., McEwen S.C., Bertoncello I., Wilks A.P., Dunn A.R.;
RT "Identification and cloning of a protein kinase encoding mouse gene,
RT plk, related to the polo gene of Drosophila";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4842-4845(1993).
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus.

RX MEDLINE=94289293; PubMed=8018557;
RA Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.L.,
RA Ferris D.K.;
RT "Cloning and characterization of human and murine homologues of the
RT Drosophila polo serine-threonine kinase";
RL Cell Growth Differ. 5:249-257(1994).
RN 13;
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=94067140; PubMed=7902533;
RA Lake R.J., Jelinek W.R.;
RT "Cell cycle- and terminal differentiation-associated regulation of
RT the mouse mRNA encoding a conserved mitotic protein kinase";
RL Mol. Cell. Biol. 13:7793-7801(1993).
CC -!- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: NEWBORN AND ADULT SPLEEN, FETAL AND NEWBORN
CC KIDNEY, LIVER, BRAIN, THYMUS AND ADULT BONE MARROW, THYMUS,
CC OVARY AND TESTES.
CC -!- DEVELOPMENTAL STAGE: IN THE THYMUS, LEVELS INCREASED DURING FETAL
CC DEVELOPMENT, WERE HIGHEST IN NEWBORN ANIMALS AND DECREASED IN THE
CC ADULT. IN THE TESTES, THE PLK LEVELS WERE HIGHER IN THE ADULT THAN
CC IN PREPUBESCENT MICE WHILE IN THE OVARY, THE LEVELS WERE HIGHER IN
CC THE PREPUBESCENT MICE. ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
CC DURING S PHASE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.

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CC EMBL: L06144; AAA39948.1;
CC EMBL: U01063; AAA56635.1;
CC EMBL: L19558; AAA16071.1;
CC PIR: A47545; A47545;
CC PIR: A54596; A54596;
CC MGD: MGI:97621; Plk.
CC InterPro: IPR000959; POLO_Box.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002293; Ser_thr_pkinase.
CC Pfam: PF00659; pkinase; 1.
CC Pfam: PF00659; POLO_box; 2.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS00078; POLO_BOX; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Nuclear protein.
FT DOMAIN 53 305 PROTEIN KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 480 POLO_BOX_1.
FT DOMAIN 515 584 POLO_BOX_2.
FT CONFLICT 4 4 A -> V (IN REF. 1).
FT CONFLICT 15 15 A -> T (IN REF. 1).
FT CONFLICT 23 23 P -> L (IN REF. 1).
FT CONFLICT 27 27 V -> A (IN REF. 1).
FT CONFLICT 29 29 G -> S (IN REF. 1).
FT CONFLICT 41 41 P -> L (IN REF. 1).
FT CONFLICT 54 54 V -> I (IN REF. 1).
FT CONFLICT 495 495 A -> R (IN REF. 1).

SQ SEQUENCE 603 AA; 68300 MW; 1B9806463666EFA10 CRC64;
Query Match 87.8%; Score 43; DB 1; Length 603;
Best local Similarity 77.8%; Pred. No. 0.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGKPPFETS 9
|:|:|:|:|
Db 246 VGRPPFETS 254

RESULT 6
PLK1_RAT STANDARD; PRT: 603 AA.
AC Q62673;
DT 16-OCT-2001 (Rel. 40, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update);
DT 16-OCT-2001 (Rel. 40, Last annotation update);
DE Serine/threonine-protein kinase PLK (EC 2.7.1.1.) (PLK-1).
GN PLK
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Arstorp J., Hansen J.A., Hxirlis Nielsen J.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC ! FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE (BY SIMILARITY).
CC ! SUBCELLULAR LOCATION: Nuclear (BY SIMILARITY).
CC ! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDS/POLO SUBFAMILY.
CC ! SIMILARITY: Contains 2 POLO box domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U10188; AAA1885.1;
CC InterPro: IPR000959; POLO_box
CC InterPro: IPR000719; Prot_kinase
CC InterPro: IPR002290; Ser_thr_kinase
CC Pfam: PF00069; pkinase; 1;
CC Pfam: PF00659; POLO_box; 2;
CC ProDom: PD000001; Prot_kinase; 1;
CC SMART: SM00220; S_TKC; 1;
CC PROSITE: PS50078; POLO_BOX; 2;
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1;
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1;
CC Transferase; Serine/threonine-protein kinase, ATP binding; Repeat;
KW Nuclear protein.
KW DOMAIN 53 305 PROTEIN_KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 480 POLO_BOX 1;
FT DOMAIN 515 584 POLO_BOX 2;
SQ SEQUENCE 603 AA; 68313 MW; 1C7AFF53B7EDCC02 CRC64;

Query Match 87.8%; Score 43; DB 1; Length 603;
Best local Similarity 77.8%; Pred. No. 0.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGKPPFETS 9
|:|:|:|:|
Db 246 VGRPPFETS 254

RESULT 7
STKD_MOUSE STANDARD; PRT: 282 AA.
AC O88445; Q9JLC2;
DT 28-FEB-2003 (Rel. 41, Created);
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Serine/threonine protein kinase 13 (EC 2.7.1.37) (Aurora/pl1/Eg2
protein 1) (Aurora-C).
GN STK13 OR AIE1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=99025616; PubMed=9809744;
RA Tseng T.C., Chen S.H., Hsu Y.P., Tang T.K.;
RT "Protein kinase profile of sperm and eggs: cloning and
RT characterization of two novel testis-specific protein kinases (AIE1,
RT AIE2) related to yeast and fly chromosome segregation regulators.";
RL DNA Cell Biol. 19:679-688(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=20551164; PubMed=11098217;
RA Hu H.M., Chuang C.K., Lee M.J., Tseng T.C., Tang T.K.;
RT "Genomic organization, expression, and chromosome localization of a
RT third aurora-related kinase gene, Aie1.";
RL DNA Cell Biol. 19:679-688(2000).
CC !- FUNCTION: May play a part in organizing microtubules in relation
CC to the function of the centrosome/spindle pole during mitosis.
CC !- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC !- SUBCELLULAR LOCATION: Localized to spindle pole from anaphase to
CC cytokinesis (BY SIMILARITY).
CC !- TISSUE SPECIFICITY: Expressed only in testis.
CC !- DEVELOPMENTAL STAGE: Expressed on day 14 dpc in prepubertal
CC testis, expression reached its plateau on day 21 dpc and remained
CC at a high level in adult.
CC !- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF054620; AAC25954.1;
CC EMBL: AF195272; AAF25838.1;
CC HSSP: Q63450; 1A06.
CC MGD: MGI:1321119; Stk13.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC InterPro: IPR001245; Tyr_kinase.
CC Pfam: PF00069; pkinase; 1;
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000001; Prot_kinase; 1;
CC SMART: SM00220; S_TKC; 1;
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1;
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1;
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 16 266 PROTEIN_KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT CONFLICT 74 74 R -> P (IN REF. 2).

SQ SEQUENCE 282 AA; 32907 MW; 7CB8AEC4984E7853 CRC64;

Query Match 79.6%; Score 39; DB 1; Length 282;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
Db 207 VGKPPFFES 215

RESULT 8

STK6_XENLA STANDARD; PRT; 407 AA.
AC Q91820;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine protein kinase Eg2 (EC 2.7.1.37) (pEg2) (p46Eg265).
GN EG2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RX MEDLINE=9812285; PubMed=9454730;
RA Couturier A., Doree M., Philippe M., Prigent C., Roghi C., Giet R., Uzbekov R., Morin N., Chartrain L., Le Guellec R.,
RT "The Xenopus protein kinase pEg2 associates with the centrosome in a cell cycle-dependent manner, binds to the spindle microtubules and is involved in bipolar mitotic spindle assembly.";
RL J. Cell Sci. 111:557-572(1998).
CC -!- FUNCTION: Associates with the centrosome in a cell-cycle dependent manner and invades the microtubules at the poles of the spindle during mitosis suggesting that it may be involved in the correct formation of bipolar mitotic spindles.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis especially from prophase through anaphase. Partially colocalised with gamma tubulin in the centrosome, from S to M phase.
CC -!- TISSUE SPECIFICITY: Highly expressed in ovary and testis.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.

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EMBL; Z17207; CAA78915.1; -
PIR; S52243; S52243.
HSSP; P24941; 1AQ1.
InterPro; IPR002290; Prot_kinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
KW DOMAIN 140 390 PROTEIN KINASE.
FT NP_BIND 146 154 ATP (BY SIMILARITY).
FT BINDING 169 169 ATP (BY SIMILARITY).
FT ACT_SITE 263 263 BY SIMILARITY.

SQ SEQUENCE 407 AA; 46372 MW; DE1628A2C6D11277 CRC64;

Query Match 79.6%; Score 39; DB 1; Length 407;
Best Local Similarity 75.0%; Pred. No. 3.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPFET 8
Db 331 VGKPPPFET 338

RESULT 9

ST6L_XENLA STANDARD; PRT; 408 AA.
AC Q91819;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine protein kinase Eg2-like (EC 2.7.1.37) (p46XLEg22).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RA Roghi C., Le Guellec R., Paris J., Couturier A., Philippe M.,
RT "Eg2, selected by differential screening encodes a new Xenopus protein kinase family.";
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis especially from prophase through anaphase. Partially colocalised with gamma tubulin in the centrosome, from S to M phase (By similarity).
CC -!- PTM: Phosphorylated (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.

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EMBL; Z17206; CAA78914.1; ALT_INIT.
HSSP; P24941; 1AQ1.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_kinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
KW DOMAIN 140 390 PROTEIN KINASE.
FT NP_BIND 146 154 ATP (BY SIMILARITY).
FT BINDING 169 169 ATP (BY SIMILARITY).
FT ACT_SITE 263 263 BY SIMILARITY.
SQ SEQUENCE 408 AA; 46461 MW; 97F6A69C7357AEE8 CRC64;

Query Match 79.6%; Score 39; DB 1; Length 408;
Best Local Similarity 75.0%; Pred. No. 3.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPFET 8
Db 331 VGKPPPFET 338

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Cc      331 VGKPPFET 338
-----
RESULT 13
POLO DROME
ID POLO DROME STANDARD; PRT: 536 AA.
AC P52304; Q9VWB2;
DT 31-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase polo (EC 2.7.1.1).
GN POLO OR CGL2306.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=92084090; PubMed=1660828;
RA Liamazares S., Moreira A., Tavares A., Girdham C., Spruce B.A.,
RA Gonzalez C., Kares R.E., Glover D.M., Sunkel C.E.;
RT "Polo encodes a protein kinase homolog required for mitosis in
RT Drosophila.";
RL Genes Dev. 5:2153-2165(1991);
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkelley;
RX MEDLINE=20196036; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans G.A., Gocayne J.D.,
RA Amarantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blake R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoen C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew J., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell C.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez C.F., Houck C.,
RA Hostin D., Houston K.A., Howland T., Wei M., Huo T.-wan C.,
RA Jalali M., Kalush F., Karpen G.R., Ku G., Koenig M., Ketchum K.A.,
RA Kimrei B.E., Kodira C.D., Kraft C., Kravitz S., Kung D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li C., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McKernson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy M., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pachle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: MAY PLAY A ROLE IN REGULATING BOTH NUCLEAR AND
CC CYTOPLASMIC ASPECTS OF THE MITOTIC CYCLE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: LARVAL DISCS, BRAIN AND TESTIS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-----
Cc      CDC5/POLO SUBFAMILY.
Cc      -!- SIMILARITY: Contains 2 POLO box domains.
Cc      -----
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Cc      or send an email to license@isb-sib.ch).
Cc      -----
Cc      EMBL; X63361; CAA44963.1;
Cc      EMBL; AE003514; AAF49036.1;
Cc      PIR; S22127; S22127.
Cc      HSSP; Q63450; 1A06.
Cc      FlyBase; FBgn003124; polo.
Cc      GO; GO:0005813; C:centrosome; IDA.
Cc      GO; GO:0005819; C:spindle; IDA.
Cc      GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
Cc      GO; GO:0007140; P:male meiosis; IMP.
Cc      GO; GO:0007067; P:mitosis; IMP.
Cc      InterPro; IPR000959; POLO_box.
Cc      InterPro; IPR000719; Prot_kinase.
Cc      InterPro; IPR002290; Ser_thr_kinase.
Cc      Pfam; PF00069; pkinase; 1.
Cc      Pfam; PF00659; POLO_box; 2.
Cc      ProDom; PD000001; Prot_kinase; 1.
Cc      SMART; SMC0220; S_TKC; 1.
Cc      PROSITE; PS50078; POLO_BOX; 2.
Cc      PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
Cc      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Cc      PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
Cc      TRANSferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
Cc      DOMAIN 25 277 PROTEIN_KINASE.
Cc      NP_BIND 31 39 ATP (BY SIMILARITY).
Cc      BINDING 54 54 ATP (BY SIMILARITY).
Cc      ACT_SITE 148 148 BY SIMILARITY.
Cc      DOMAIN 398 461 POLO_BOX_1.
Cc      DOMAIN 496 564 POLO_BOX_2.
Cc      CONFLICT 187 187 P -> A (IN REF. 1).
Cc      SEQUENCE 576 AA; 66973 MW; 5022B9AC0E88FAD CRC64;
-----
Cc      Query Match 77.6%; Score 38; DB 1; Length 576;
Cc      Best Local Similarity 75.0%; Pred. No. 8.1;
Cc      Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Cc      OY 1 IGRPPFET 8
Cc      1 IGRPPFET
Cc      218 VGQPPFET 225
Cc      -----
Cc      RESULT 11
Cc      NHAB_PSECL STANDARD; PRT: 220 AA.
Cc      ID NHAB_PSECL STANDARD; PRT: 220 AA.
Cc      AC P27763;
Cc      DT 01-AUG-1992 (Rel. 23, Created)
Cc      DT 01-AUG-1992 (Rel. 23, Last sequence update)
Cc      DT 28-FEB-2003 (Rel. 41, Last annotation update)
Cc      DE Nitrile hydratase subunit beta (EC 4.2.1.84) (Nitrilase) (NHase).
Cc      GN NTHB.
Cc      OS Pseudomonas chlororaphis (Pseudomonas aureofaciens).
Cc      OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Cc      OC Pseudomonadaceae; Pseudomonas.
Cc      OX NCBI_TaxID=333;
Cc      RN [1]
Cc      RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-23 AND 158-170.
Cc      RC STRAIN=B23;
Cc      RX MEDLINE=91193202; PubMed=2013568;
Cc      RA Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
Cc      Beppu T.;
Cc      RT "Cloning and characterization of genes responsible for metabolism of
Cc      nitrile compounds from Pseudomonas chlororaphis B23.";
Cc      RL J. Bacteriol. 173:2465-2472(1991).

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CC FUNCTION: NHASE CATALYZES THE HYDRATION OF VARIOUS NITRILE
CC COMPOUNDS TO THE CORRESPONDING AMIDES. INDUSTRIAL PRODUCTION OF
CC ACRYLAMIDE IS NOW BEING DEVELOPED USING SOME OF THESE ENZYMES.
CC
CC CATALYTIC ACTIVITY: An aliphatic amide = a nitrile + H(2)O.
CC
CC SUBUNIT: Heterodimer of an alpha and a beta chain.
CC
CC SIMILARITY: BELONGS TO THE NITRILE HYDRATASE SUBUNIT BETA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: D90216; BAA14246.1; -
CC PIR: B42725; B42725.
CC HSSP: P13449; 2AH3.
CC InterPro: IPR003168; NHase beta
CC Pfam: PF02211; NHase_beta; 1.
KW Lyase.
SQ SEQUENCE 220 AA; 24545 MW; 191AE1C5F14D4864 CRC64;

Query Match 73.5%; Score 36; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPE 7
DB 120 GRPPE 125

RESULT 12
CNK_RAT STANDARD; PRT; 615 AA.
AC Q9R011;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytokine-inducible serine/threonine-protein kinase (EC 2.7.1.37) (FGF-
DE inducible kinase) (Fragment).
GN CNK OR FNK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1;
RP MEDLINE=99452760; PubMed10523297;
RA Kauselmann G., Weiler M., Wolf F., Kauselmann S., Kuhl D.,
RA Scaife J., Staabli J., Berer-Haas M., Strobel K., Kuhl D.,
RA "The polo-like protein kinases Pnk and Snk associate with a Cal(2+) and
RT integrin-binding protein and are regulated dynamically with synaptic
RT plasticity";
RT EMBO J. 18:5528-5539(1999).
CC
CC FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN REGULATING M
CC PHASE FUNCTIONS DURING THE CELL CYCLE. MAY ALSO BE PART OF THE
CC SIGNALING NETWORK CONTROLLING CELLULAR ADHESION. IN VITRO, IS ABLE
CC TO PHOSPHORYLATE CDC25C AND CASEIN (BY SIMILARITY).
CC
CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC
CC SUBUNIT: BINDS TO THE CALCIUM/INTEGRIN-BINDING PROTEIN (CIB). THIS
CC INTERACTION PROBABLY OCCURS VIA THE POLO-BOX DOMAIN.
CC
CC SUBCELLULAR LOCATION: WHEN INDUCED, IT TRANSLOCATES INTO THE
CC DENDRITES OF ACTIVATED NEURONS.
CC
CC TISSUE SPECIFICITY: CONSTITUTELY EXPRESSED IN POST MITOTIC
CC NEURONS.
CC
CC INDUCTION: BY THE INTENSE ACTIVITY ASSOCIATED WITH SEIZURES.
CC
CC PTM: PHOSPHORYLATED AS CELLS ENTER MITOSIS AND DEPHOSPHORYLATED AS
CC CELLS EXIT MITOSIS (BY SIMILARITY).
CC
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC
CC CDC5/POLO SUBFAMILY.
CC
CC SIMILARITY: Contains 2 POLO box domains.
CC

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF136584; AAF08367.1; -
CC InterPro: IPR000959; POLO_box.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF00659; POLO_box; 2.
CC ProDom: PD00001; Prot_kinase; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS50078; POLO_BOX; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00311; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Phosphorylation.
FT NON_TER 1
FT DOMAIN 31 283 PROTEIN KINASE.
FT NP_BIND 37 45 ATP (BY SIMILARITY).
FT BINDING 60 60 ATP (BY SIMILARITY).
FT ACT_SITE 154 154 BY SIMILARITY.
FT DOMAIN 440 503 POLO_BOX 1.
FT DOMAIN 537 607 POLO_BOX 2.
FT NON_TER 615
SQ SEQUENCE 615 AA; 68800 MW; 06584C229B5D71BD CRC64;

Query Match 73.5%; Score 36; DB 1; Length 615;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPE 9
DB 225 GSPPE 232

RESULT 13
CNK_MOUSE STANDARD; PRT; 631 AA.
AC Q60806; Q60822; Q9R009;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytokine-inducible serine/threonine-protein kinase (EC 2.7.1.37) (FGF-
DE inducible kinase).
GN CNK OR FNK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=NIH Swiss;
RX MEDLINE=95247749; PubMed=7730342;
RA Donohue P.J., Alberts G.F., Guo Y., Winkles J.A.,
RA "Identification by targeted differential display of an immediate early
RT gene encoding a putative serine/threonine kinase";
RL J. Biol. Chem. 270:10351-10357(1995).
RN 2;
RP SEQUENCE OF 333-437 FROM N.A. (ISOFORM 2).
RC STRAIN=NIH Swiss;
RA Kauselmann G., Weiler M., Kuhl D.,
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN 3;
RP FUNCTION, AND PHOSPHORYLATION.
RX MEDLINE=98343954; PubMed=9677325;
RA Chase D., Feng Y., Hanstew B., Winkles J.A., Longo D.L., Ferris D.K.,
RA "Expression and phosphorylation of fibroblast-growth-factor-inducible
RT

RT Kinase (Fnk) during cell-cycle progression.";
RL Biochem. J. 333:655-660(1998).
CC -!- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN REGULATING M
CC PHASE FUNCTIONS DURING THE CELL CYCLE. MAY ALSO BE PART OF THE
CC SIGNALING NETWORK CONTROLLING CELLULAR ADHESION. IN VITRO, IS ABLE
CC TO PHOSPHORYLATE CDC25C AND CASEIN (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: BINDS TO THE CALCIUM/INTEGRIN-BINDING PROTEIN (CIB). THIS
CC INTERACTION PROBABLY OCCURS VIA THE POLO-BOX DOMAIN (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
CC ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q60806-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q60806-2; Sequence=VSP_004927;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN SKIN.
CC -!- PTM: PHOSPHORYLATED AS CELLS ENTER MITOSIS AND DEPHOSPHORYLATED AS
CC CELLS EXIT MITOSIS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U21392; AAC52191.1; -;
DR EMBL: U22434; AAC52192.1; -;
DR EMBL: AF136586; AAF08369.1; -;
DR PIR: A57286; A57286;
DR MGD: MGI:109604; Crk.
DR InterPro: IPR000959; POLO box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00659; POLO_box; 2.
DR ProDom: PDC00001; Prot_kinase; 1.
DR SMART: SM0220; S_TKC; 1.
DR PROSITE: PS00078; POLO_BOX; 2.
DR PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00117; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine protein kinase; All domain; Repeat;
KW Phosphorylation; Alternative splicing;
FT DOMAIN 63 315 PROTEIN KINASE
FT NP_BIND 69 77 ATP (BY SIMILARITY)
FT BINDING 92 92 ATP (BY SIMILARITY)
FT ACT_SITE 186 186 BY SIMILARITY
FT DOMAIN 455 518 POLO_BOX_1
FT DOMAIN 552 622 POLO_BOX_2
FT VARSPLIT 373 373 L -> LVSGLNRTSIGHGVVRIE (in isoform 2).
FT /FTID=VSP_004927.
FT CONFLICT 386 386 I -> V (IN REF. 2).
SQ SEQUENCE 631 AA; 70012 MW; 208573418705BID2 (C0064);
Query Match 73.5%; Score 16; DB 1; Length 631;
Best local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 GRPFETS 9
ID 257 GSPFETA 264
RESULT 14
CRK HUMAN
ID CRK HUMAN STANDARD; PRT; 346 AA

AC Q9H4B4; Q15767;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytokine-inducible serine/threonine-protein kinase (EC 2.7.1.37) (FGF-
DE inducible kinase) (Proliferation-related kinase).
GN CNK OR FNK OR PRK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB:TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=20493044; PubMed=11039900;
RA Holtrich U., Wolf G., Yuan J., Bereiter-Hahn J., Karn T., Weiler M.,
RA Kauselmann G., Rehli M., Andreesen R., Kaufmann M., Kuhl D.,
RA Strebhardt K.;
RT "Adhesion induced expression of the serine/threonine kinase Pnk in
RT human macrophages.";
RL Oncogene 19:4832-4839(2000).
RN [2]
RP SEQUENCE OF 28-646 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96325053; PubMed=8702627;
RA Li B., Ouyang B., Pan H., Reissmann P.T., Slamon D.J., Arceci R.,
RA Lu L., Dai W.;
RT "Prk, a cytokine-inducible human protein serine/threonine kinase whose
RT expression appears to be down-regulated in lung carcinomas.";
RL J. Biol. Chem. 271:19402-19408(1996).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98019242; PubMed=9353331;
RA Ouyang B., Pan H., Lu L., Li J., Stambrook P., Li B., Dai W.;
RT "Human Prk is a conserved protein serine/threonine kinase involved in
RT regulating M phase functions.";
RL J. Biol. Chem. 272:28646-28651(1997).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=20027391; PubMed=10557092;
RA Ouyang B., Li W., Pan H., Meadows J., Hoffmann I., Dai W.;
RT "The physical association and phosphorylation of Cdc25C protein
RT phosphatase by Prk.";
RL Oncogene 18:6029-6036(1999).
CC -!- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN REGULATING M
CC PHASE FUNCTIONS DURING THE CELL CYCLE. MAY ALSO BE PART OF THE
CC SIGNALING NETWORK CONTROLLING CELLULAR ADHESION. IN VITRO, IS ABLE
CC TO PHOSPHORYLATE CDC25C AND CASEIN.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: BINDS TO THE CALCIUM/INTEGRIN-BINDING PROTEIN (CIB). THIS
CC INTERACTION PROBABLY OCCURS VIA THE POLO-BOX DOMAIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- TISSUE SPECIFICITY: TRANSCRIPTS ARE HIGHLY DETECTED IN PLACENTA,
CC LUNG, FOLLOWED BY SKELETAL MUSCLE, HEART, PANCREAS, OVARIES AND
CC KIDNEY AND WEAKLY DETECTED IN LIVER AND BRAIN. MAY HAVE A SHORT
CC HALF-LIFE. IN CELLS OF HEMATOPOIETIC ORIGIN, STRONGLY AND
CC EXCLUSIVELY DETECTED IN TERMINALLY DIFFERENTIATED MACROPHAGES.
CC TRANSCRIPTS EXPRESSION APPEARS TO BE DOWN-REGULATED IN PRIMARY
CC LUNG TUMOR.
CC -!- INDUCTION: CYTOKINE AND CELLULAR ADHESION TRIGGER FNK INDUCTION.
CC -!- PTM: PHOSPHORYLATED AS CELLS ENTER MITOSIS AND DEPHOSPHORYLATED AS
CC CELLS EXIT MITOSIS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC -----
DR EMBL: AC293866; CAC10659.1;
DR EMBL: J56998; AAC50637.1; ALT_INIT
DR Genew; HGNC:2154; CNK.
DR GK; Q9H4B4;
DR MIM; 602913;
DR GO: GO:0004674; Eiprotein serine/threonine kinase activity; TAS.
DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO: GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 2.
DR ProDom; PDC00001; Prot_kinase; 1.
DR SMART; SMC0220; S_TKG; 1.
DR PROSITE; PS00078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Phosphorylation.
FT DOMAIN 62 314 PROTEIN KINASE.
FT NP_BIND 68 76 ATP (BY SIMILARITY).
FT BINDING 91 91 ATP (BY SIMILARITY).
FT ACT_SITE 185 185 BY SIMILARITY.
FT DOMAIN 470 537 POLO_BOX_1.
FT DOMAIN 567 637 POLO_BOX_2.
FT CONFLICT 99 99 V -> A (IN REF. 2).
FT CONFLICT 353 353 V -> G (IN REF. 2).
FT CONFLICT 419 419 H -> D (IN REF. 2).
FT CONFLICT 464 470 FSEWVG -> VSKWVDY (IN REF. 2).
FT CONFLICT 522 522 R -> P (IN REF. 2).
SQ SEQUENCE 646 AA; 71789 MW; C2014720FC8A3B4 CRC64;

Query Match 73.5%; Score 36; DB 1; Length 646;
Best Local Similarity 75.0%; Pred.No 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPFFTS 9
Db 256 GSPFFETA 263

RESULT 15
PKNI COREF STANDARD; FRT; 450 AA
AC Q8FJ15;
DT 15-SEP-2003 (Rel. 42, Created);
DT 15-SEP-2003 (Rel. 42, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Probable serine/threonine protein kinase C50043 (E1 2.7.1.37).
GN C50043.
OS Corynebacterium efficiens.
CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
CC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
CX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawayabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeno K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC SIMILARITY: Contains 3 PASTA domains.
CC
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CC -----
DR EMBL: AP005214; BAC16843.1;
DR InterPro; IPR005543; PASTA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF03793; PASTA; 3.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PDC00001; Prot_kinase; 1.
DR SMART; SM00740; PASTA; 3.
DR SMART; SM00220; S_TKG; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding; Repeat; Complete proteome.
FT DOMAIN 9 278 PROTEIN KINASE.
FT DOMAIN 377 443 PASTA_1.
FT DOMAIN 444 512 PASTA_2.
FT DOMAIN 513 577 PASTA_3.
FT NP_BIND 15 23 ATP (BY SIMILARITY).
FT BINDING 38 38 ATP (BY SIMILARITY).
FT ACT_SITE 136 136 BY SIMILARITY.
SQ SEQUENCE 660 AA; 69646 MW; D33D797EB02D44B1 CRC64;

Query Match 73.5%; Score 36; DB 1; Length 660;
Best Local Similarity 100.0%; Pred.No 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
Db 210 GRPFFE 215

RESULT 16
HRG_BOVIN
ID HRG_BOVIN STANDARD; FRT; 396 AA.
AC P33433;
DT 01-FEB-1994 (Rel. 28, Created);
DT 01-FEB-1994 (Rel. 28, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Histidine-rich glycoprotein (Histidine-proline rich glycoprotein)
DE (HRG) (Fragments).
GN HRG.
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
CX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=93351678; PubMed=8348977;
RA Soerensen C.B., Krogh-Pedersen H., Petersen T.E.;
RT "Determination of the disulphide bridge arrangement of bovine
RT histidine-rich glycoprotein."
RL FEBS Lett. 328:285-290(1993).
CC FUNCTION: THE PHYSIOLOGICAL FUNCTION IS NOT YET KNOWN. IT BINDS
CC HEME, DYES AND DIVALENT METAL IONS. IT CAN INHIBIT ROSETTE
CC FORMATION AND IS KNOWN TO INTERACT WITH HEPARIN, THROMBOSPONDIN,
CC AND THE LYSINE-BINDING SITE OF PLASMINOGEN. ON THE BASIS OF ITS
CC HOMOLOGUE WITH HMW KININOGEN, THE HIS-RICH REGION OF THIS PROTEIN
CC MAY MEDIATE THE CONTACT ACTIVATION PHASE OF INTRINSIC BLOOD
CC COAGULATION CASCADE.
CC SUBCELLULAR LOCATION: Secreted.
CC TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
CC DOMAIN: IN ADDITION TO HAVING A HIGH HIS AND PRO CONTENT, THIS
CC PROTEIN HAS MANY INTERNAL REPEATS. 12 TANDEM REPEATITIONS OF A 5-
CC RESIDUE SEQUENCE (GHHPH, CONSENSUS) FORM A HISTIDINE-RICH REGION.
CC SIMILARITY: Contains 2 cystatin-like domains.
```

KW Glycoprotein; Heparin-binding; Repeat.
FT DOMAIN 1 102 CYSSTATIN-LIKE 1.
FT DOMAIN 103 169 CYSSTATIN-LIKE 2.
FT DOMAIN 191 238 PRO-RICH.
FT DOMAIN 243 368 PRO/HIS-RICH.
FT DISULFID 7 375
FT DISULFID 56 67
FT DISULFID 77 92
FT DISULFID 123 297
FT DISULFID 137 160
FT DISULFID 212 242
FT NON-CONS 52 53
FT CARBOHYD 70 72
FT NON-CONS 71 72
FT NON-CONS 78 79
FT CARBOHYD 92 91
FT NON-CONS 103 104
FT CARBOHYD 122 122
FT NON-CONS 163 164
FT CARBOHYD 220 220
FT NON-CONS 263 264
FT NON-CONS 303 304
FT VARIANT 86 86
FT VARIANT 309 309
FT VARIANT 322 322
SQ SEQUENCE 396 AA; 44470 MW; 128AE2234959DE6FC CRC64;

Query Match 71.4%; Score 35; DB 1; Length 396;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 2 GRPPFKTS 9
DI 189 GRPPFKPS 196

RESULT 17
STK6 HUMAN STANDARD; PRT; 403 AA.
ID STK6 HUMAN STANDARD; PRT; 403 AA.
AC Q14965; Q60445; Q75873; Q9BQD6; Q9JF35;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine kinase 6 (EC 2.7.11.37) (Serine/threonine kinase 15)
DE (Aurora)/IPL1-related kinase 2 (Aurora related kinase 1) (ARK1)
DE (Aurora-A) (Breast-tumor-amplified kinase)
GN STK6 OR STK15 OR AIK OR ARK1 (P. ASPA OR BTAK)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catartida; Rodentia; Muridae
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=97298083; PubMed=9153231;
RA Kimura M., Kotani S., Hattori T., Sumi N., Yoshioka T., Todokoro K.,
RA Okano Y.;
PT "Cell cycle dependent expression and spindle pole localization of a
RT novel human protein kinase, Ark, related to Aurora of Drosophila and
RT yeast Ipl1.";
RL J. Biol. Chem. 272:13766-13771(1997);
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=98183439; PubMed=9514916;
RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
RC "cDNA cloning, expression, subcellular localization, and chromosomal
RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
RT 1 and 2.";
RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
RN 1;
RP SEQUENCE FROM N.A.
PC TISSUE=Breast;

RX MEDLINE=98442657; PubMed=9771714;
RA Zhou H., Kuang J., Zhong L., Kuo W.-L., Gray J.W., Sahin A.,
RA Brinkley B.R., Sen S.;
RT "Tumour amplified kinase STK15/BTAK induces centrosome amplification,
RT aneuploidy and transformation.";
RL Nat. Genet. 20:189-193(1998).
RN 4;
RP SEQUENCE FROM N.A.
RA Wang L., Thiobodeau S.N.;
RT "Mutational analysis of the STK15 gene in human tumors.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
RN 5;
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser J., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levasseur M.H., Levensha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McKay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN 6;
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix, Colon, Kidney, and Muscle;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapietou M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 7;
RP CELL-CYCLE REGULATION.
RX MEDLINE=21895866; PubMed=11790771;
RA Tanaka M., Ueda A., Kanamori H., Ideguchi H., Yang J., Kitajima S.,
RA Ishigatsubo Y.;
RT "Cell-cycle-dependent regulation of human aurora A transcription is
RT mediated by periodic repression of E4TF1.";
RL J. Biol. Chem. 277:10719-10726(2002).

[8]
 REVIEW.
 MEDLINE=21306577; PubMed=11413462;
 Nigg E.A.;
 "Mitotic kinases as regulators of cell division and its checkpoints.";
 Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
 -!- FUNCTION: May play a role in cell cycle regulation during anaphase and/or telophase, in relation to the function of the centrosome/spindle pole region during chromosome segregation. Maybe involved in microtubule formation and/or stabilization. May play a key role during tumor development and progression.
 -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 -!- SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells and at each spindle pole in mitosis.
 -!- TISSUE SPECIFICITY: Highly expressed in testis and weakly in skeletal muscle, thymus and spleen. Also highly expressed in colon, ovarian, prostate, neuroblastoma, breast and cervical cancer cell lines. Expression is cell-cycle regulated, low in G1/S, accumulates during G2/M, and decreases rapidly after.
 -!- PTM: Phosphorylated.
 -!- DISEASE: Defects in STK6 are responsible for numerical centrosome aberrations including aneuploidy.
 -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 -!- AURORA SUBFAMILY.
 -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts in positions 105, 125, 129, 235 and 241.
 -!- CAUTION: Although authors have considered STK6 and STK15 as two different proteins, it is clear that they are the same protein.

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 EMBL: D84212; BAA23592.1; ALT FRAME.
 EMBL: AF008551; AAC12708.1;
 EMBL: AF011467; AAC23448.1;
 EMBL: AF011468; AAC63902.1;
 EMBL: AF195947; AAF29508.1;
 EMBL: AF195942; AAF29508.1; JOINED.
 EMBL: AF195943; AAF29508.1; JOINED.
 EMBL: AF195944; AAF29508.1; JOINED.
 EMBL: AF195945; AAF29508.1; JOINED.
 EMBL: AF195946; AAF29508.1; JOINED.
 EMBL: AF121914; CAC12717.1;
 EMBL: BC001280; AAH01280.1;
 EMBL: BC002498; AAH02499.1;
 EMBL: BC006423; AAH06423.1;
 EMBL: BC027464; AAH27464.1;
 GK: C14965;
 MIM: 602687;
 MIM: 603372;
 HSP: P24941; IBUH.
 Genew: HGNC:11409; STK6.
 Genew: HGNC:11393; STK15.
 GO: GO:0005634; C:nucleus; TAS.
 GO: GO:0005819; C:spindle; TAS.
 GO: GO:0007067; P:mitosis; TAS.
 GO: GO:006468; P:protein amino acid phosphorylation; TAS.
 InterPro: IPR003719; Prot_kinase.
 InterPro: IPR002290; Ser_thr_kinase.
 InterPro: IPR001245; Tyr_kinase.
 Pfam: PF00069; pkinase; 1.
 ProDom: PD000001; Prot_kinase; 1.
 SMART: SM00220; S_TKc; 1.
 SMART: SM00219; TyrKc; 1.
 PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 PROSITE: PS00011; PROTEIN_KINASE_DCM; 1.
 Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW

```

KW Phosphorylation.
FT DOMAIN 133 383 PROTEIN KINASE.
FT NP_BIND 139 147 ATP (BY SIMILARITY).
FT BINDING 162 162 ATP (BY SIMILARITY).
FT ACT_SITE 256 256 BY SIMILARITY.
FT CONFLICT 31 31 F -> I (IN REF. 3).
FT CONFLICT 57 57 V -> I (IN REF. 2).
SQ SEQUENCE 403 AA; 45809 MW; 125F3594834CD157 CRC64;

Query Match 71.4%; Score 35; DB 1; Length 403;
Best Local Similarity 55.6%; Pred. No. 21;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
   :|:|:|:|:
Db 324 VGKPPFEAN 332

RESULT 18
TF65_CHICK
ID TF65_CHICK STANDARD; PRT; 558 AA.
AC P98152;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transcription factor p65 (Nuclear factor NF-kappa-B p65 subunit).
GN RELA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=94040817; PubMed=7916720;
RA Ikeda T., Honjo K., Hirota Y., Onodera T.;
RT "Isolation of the chicken NF-kappa B p65 subunit-encoding cDNA and
RT characterization of its products.";
RL Gene 133:237-242(1993).
CC -!- FUNCTION: P65 IS A SUBUNIT OF THE NUCLEAR FACTOR KAPPA-B, A SECOND
CC MESSENGER, WHICH ACTIVATES THE TRANSCRIPTION OF A NUMBER OF GENES
CC IN MULTIPLE TISSUES. THE INHIBITORY EFFECT OF I-KAPPA-B UPON
CC NF-KAPPA-B IN THE CYTOPLASM IS EXERTED PRIMARILY THROUGH THE
CC INTERACTION WITH P65. P65 SHOWS A WEAK DNA-BINDING SITE WHICH
CC COULD CONTRIBUTE DIRECTLY TO DNA BINDING IN THE NF-KAPPA-B
CC COMPLEX.
CC -!- SUBUNIT: ACTIVE NF-KAPPA-B IS A HETERODIMER OF AN ABOUT 50 kDa
CC DNA-BINDING SUBUNIT AND THE WEAK DNA-BINDING SUBUNIT P65. TWO
CC HETERODIMERS MIGHT FORM A LABILE TETRAMER.
CC -!- SUBCELLULAR LOCATION: NUCLEAR, BUT ALSO FOUND IN THE CYTOPLASM
CC IN AN INACTIVE FORM COMPLEXED TO AN INHIBITOR (I-KAPPA-B).
CC -!- TISSUE SPECIFICITY: SPLEEN; LOWER LEVEL IN BRAIN.
CC -!- SIMILARITY: BELONGS TO THE REL/DORSAL FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D13721; BAA02874.1; -
DR PIR; JC2004; JC2004.
DR HSSP; Q04207; 1IKV.
DR InterPro; IPR002909; IPT_TIG
DR InterPro; IPR000451; NF_Rel_dor_fam.
DR Pfam; PF00554; RHD; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00057; NFKBTNSCPFCT.
DR SMART; SM03429; IPT; 1.
DR PROSITE; PS01204; REL_1; 1.

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DR PROSITE; PS50254; REL_2; 1.
KW DNA-binding; Transcription regulation; Activator; Nuclear protein;
KW Phosphorylation.
FT DOMAIN 25 311 REL-LIKE (RHD).
FT DOMAIN 306 309 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MCD RES 281 281 PHOSPHORYLATION (BY PKA) (POTENTIAL).
SQ SEQUENCE 558 AA; 60071 MW; 0528D159A4D47B36 CRC64;

Query Match 71.4%; Score 35; DB 1; Length 558;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPPFET 8
Db 429 LGRPPPFET 436

RESULT 19
DYRB_MOUSE
ID DYRB_MOUSE STANDARD; PRT; 589 AA.
AC Q9Z188;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dual specificity tyrosine-phosphorylation regulated kinase 1B
DE (EC 2.7.1.1).
GN DYRK15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=NMRI; TISSUE=Testis;
RX MEDLINE=99119336; PubMed=9918863;
RA Leder S., Weber Y., Altafaj X., Estivill X., Joost H.-G., Becker W.;
RT "Cloning and characterization of DYRK15, a novel member of the DYRK
family of protein kinases."
RL Biochem. Biophys. Res. Commun. 254:474-479(1999).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- PTM: PHOSPHORYLATED BY MAP KINASE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MNB/DYRK SUBFAMILY.

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EMBL; Y18280; CAA77101.2; -;
HSSP; P24941; 1CKP.
DR MGD; MGI:1330302; Dyrlb.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; Tyrosine protein kinase;
KW ATP-binding; Nuclear protein; Phosphorylation.
FT DOMAIN 69 86 BIPARTITE NUCLEAR LOCALIZATION SIGNAL
(POTENTIAL).
FT DOMAIN 111 391 PROTEIN KINASE.
FT NP_BIND 117 125 ATP (BY SIMILARITY).
FT BINDING 140 140 ATP (BY SIMILARITY).
FT ACT_SITE 239 239 BY SIMILARITY.
FT DOMAIN 518 521 POLY-PRO.
FT DOMAIN 537 544 POLY-PRO.

SQ SEQUENCE 589 AA; 64914 MW; 48B4242AD6E8401E CRC64;

Query Match 71.4%; Score 35; DB 1; Length 589;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPPFETS 9
Db 509 LGRPPPFETS 517

RESULT 20
DYRB_HUMAN
ID DYRB_HUMAN STANDARD; PRT; 629 AA.
AC Q9Y463; O75258; O75788; O75789;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dual specificity tyrosine-phosphorylation regulated kinase 1B
DE (EC 2.7.1.1) (Mirk protein kinase).
GN DYRK1B OR MIRK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Testis;
RX MEDLINE=99119336; PubMed=9918863;
RA Leder S., Weber Y., Altafaj X., Estivill X., Joost H.-G., Becker W.;
RT "Cloning and characterization of DYRK1B, a novel member of the DYRK
family of protein kinases."
RL Biochem. Biophys. Res. Commun. 254:474-479(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Colon carcinoma;
RA Lee K., Deng X., Friedman E.;
RT "Mirk protein kinase is a MAP kinase substrate."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Sperm;
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K.J., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Barnes J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Frankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of a 2.2 Mb region in 19q13.1 containing the RYR
gene."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q9Y463-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9Y463-2; Sequence=VSP_004925;
CC Name=3;
CC IsoId=Q9Y463-3; Sequence=VSP_004926;
CC -!- TISSUE SPECIFICITY: HIGH LEVELS IN TESTIS AND SKELETAL MUSCLE, LOW
LEVELS IN BRAIN.
CC -!- PTM: PHOSPHORYLATED BY MAP KINASE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MNB/DYRK SUBFAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y17999; CAA76991.1; -.
CC EMBL; Y17999; CAA76990.1; -.
CC EMBL; Y17999; CAA76989.1; -.
CC EMBL; AF205861; AAF15893.1; -.
CC EMBL; AC005393; AAC28914.1; ALT_SEQ.
CC FIR; JG0195; JG0195.
CC HSSP; P24943; LHCU.
CC Genew; HGNC:3092; DYRK1B.
CC MIM; 604556; -.
CC GC; GO:0005634; C:nucleus; TAS.
CC GC; GO:0006468; P:protein amino acid phosphorylation; TAS.
CC InterPro; IPR00719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TK; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
KW ATP-binding; Nuclear protein; Alternative splicing; Phosphorylation.
FT DOMAIN 69 86 HIPARTITE NUCLEAR LOCALIZATION SIGNAL
(POTENTIAL).
FT DOMAIN 111 431 PROTEIN KINASE.
FT NF BIND 117 125 ATP (BY SIMILARITY).
FT BINDING 140 143 ATP (BY SIMILARITY).
FT ACT SITE 239 239 BY SIMILARITY.
FT DOMAIN 558 561 POLY-PRO.
FT VARSPLIC 366 405 Missing (in isoform 2)
/FTID=VSP_004925.
FT VARSPLIC 378 405 Missing (in isoform 3)
/FTID=VSP_004926.
FT SEQUENCE 629 AA; 69197 MW; D7Q354AC55943A8B CR664;

Query Match 71.4%; Score 35; DB 1; Length 629;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
Db 549 LGRPPSPTS 557

RESULT 21
STKC_PIG
ID STKC_PIG STANDARD; PRT; 156 AA.
AC Q9NXX0;
DT 28-FEB-2003 (Rel. 41, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora B)
DE (Fragment).
GN STK12.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=2232238; PubMed=12270407;
RA Braun F., Hosseini S.M., Lorf T., Laabs S., Ringe B.;
RT "Differential gene expression during intestinal ischemia-reperfusion
injury.";
RL Transplant. Proc. 34:2301-2302(2002).
CC -!- FUNCTION: Maybe directly involved in regulating the cleavage of
CC polar spindle microtubules and is a key regulator for the onset of
CC cytokinesis during mitosis (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
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CC in late anaphase and concentrated into the midbody in telophase
CC and cytokinesis. Colocalized with gamma tubulin in the mid-body
CC (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC -----
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CC -----
CC EMBL; AF244364; AAF61735.1; -.
CC InterPro; IPR002052; N6_Mtase.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
FT NON_TER 1 1
FT DOMAIN 41 156 PROTEIN KINASE.
FT ACT SITE 51 51 BY SIMILARITY.
FT NON_TER 156 156
FT SEQUENCE 156 AA; 17867 MW; CD23040EDB633FCE CR664;

Query Match 69.4%; Score 34; DB 1; Length 156;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
Db 119 VGNPPFESA 127

RESULT 22
STKC_HUMAN
ID STKC_HUMAN STANDARD; PRT; 344 AA.
AC Q96GD4; Q14630; Q60446; Q95083; Q96DV5; Q9UQ46;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora- and Ipl1-
DE like midbody-associated protein 1) (AIM-1) (Aurora/IPL1-related kinase
DE 2) (Aurora-related kinase 2) (STK-1) (Aurora-B).
GN STK12 OR AIM1 OR ARK2 OR AIK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98183439; PubMed=9514916;
RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
RT "cDNA cloning, expression, subcellular localization, and chromosomal
RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
RT 1 and 2.";
RT Biochem. Biophys. Res. Commun. 244:285-292(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99025855; PubMed=9809983;
RA Tatsuka M., Katayama H., Ota T., Tanaka T., Odashima S., Suzuki F.,
RA Terada Y.;
RT "Multinuclearity and increased ploidy caused by overexpression of the
RT aurora- and ipl1-like midbody-associated protein mitotic kinase in
RT human cancer cells";
RT Cancer Res. 58:4811-4816(1998).
RL
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PA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Jutterback T., Tran K., Wolf A., Vamathevan C., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro J., Fraser C.M.,
R7 "Complete genome sequence of Caulobacter crescentus.";
R5 Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001);
CC ... CATALYTIC ACTIVITY: L-histidinol phosphate + 2-oxoglutarate ->
CC (imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate.
CC Cofactor: pyridoxal phosphate (By similarity);
CC PATHWAY: Histidine biosynthesis; seventh step.
CC SIMILARITY: BELONGS TO CLASS-1 OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES. HISTIDINOL-PHOSPHATE AMINOTRANSFERASES
CC SUBFAMILY.
CC
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CC
CC EMBL; AEC05893; AAK24194.1;
DR PIR; F87524; F87524.
DR TIGR; CC2223; .
DR HAMAP; MF 01023; .; 1.
DR InterPro; IPR004839; Aminotransf.; 2.
DR InterPro; IPR005861; HisP_aminotransf.
DR InterPro; IPR001917; NHtransf. 2.
DR Pfam; PF00155; aminotran_1_2; 1.
DR TIGRFAMs; TIGR01141; hisC; 1.
DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; FALSE_NEG.
KW Histidine biosynthesis; Transferase; Aminotransferase;
KW Pyridoxal phosphate; Complete proteome.
RT BINDING 216 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 359 AA; 39261 MW; A3BFA7EDAGB6C65 CAC64;

Query Match 69.4%; Score 34; DB 1; Length 359;
Best Local Similarity 95.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RPPPTS 9
DB 242 RPPPTS 248

RESULT 34
FLIF_BRUAR STANDARD; PRT; 33 AA
AC Q52269;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar M-ring protein.
GN FLIF
OS Brucella abortus.
OC Bacteria; Proteobacteria; Alphaproteobacteria, Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-544 / Biovar 1;
RX MEDLINE=20468005; PubMed=11013709;
RA Halling S.M.;
RT "On the presence and organization of open reading frames of the
RT nonmotile pathogen Brucella abortus similar to class II, III, and IV
RT flagellar genes and to Yersinia enterocolitica.";
R5 Microb. Comp. Genomics 3:21-29(1998)
CC ... FUNCTION: THE M-RING MAY BE ACTIVELY INVOLVED IN ENERGY
CC TRANSDUCTION (BY SIMILARITY);
CC ... SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PART OF THE
CC FLAGELLAR ORGANELLE AND CONSISTS OF FIVE RINGS (E, P, L, S, AND M)
CC MOUNTED ON A CENTRAL ROD. THE M-RING IS INTEGRAL TO THE INNER
CC MEMBRANE OF THE CELL AND MAY BE CONNECTED TO THE FLAGELLAR ROD
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CC VIA THE S-RING. THE S (SUPRAMEMBRANE RING) LIES JUST DISTAL TO
CC THE M-RING. THE L AND P RINGS LIE IN THE OUTER MEMBRANE AND THE
CC PERIPLASMIC SPACE, RESPECTIVELY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC, MEMBRANE-ASSOCIATED (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FLIF FAMILY.
CC
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CC
CC EMBL; AF019251; AAC01568.1; .
DR InterPro; IPR000067; FlgMring_FLIF.
DR InterPro; IPR003282; SecIIOMPX.
DR InterPro; IPR006182; YscJ_FlIF.
DR Pfam; PF01514; YscJ_FlIF; 1.
DR PRINTS; PR01009; FLOMRINGFLIF.
DR PRINTS; PR01338; TYPE3OMKPROT.
DR TIGRFAMs; TIGR00206; flif; 1.
KW Flagella; Membrane.
SQ SEQUENCE 540 AA; 57447 MW; 43B309168BA32492 CRC64;

Query Match 69.4%; Score 34; DB 1; Length 540;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPPFET 8
DB 50 LGRPSYET 57

RESULT 25
GCJ2_MOUSE STANDARD; PRT; 830 AA.
AC Q9JHD2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE General control of amino acid synthesis protein 5-like 2 (EC 2.3.1.-)
DE (Histone acetyltransferase GCN5) (MGCN5).
GN GCN5L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=98414582; PubMed=9742083;
RA Xu W., Edmondson D.G., Roth S.Y.;
RT "Mammalian GCN5 and P/CAF acetyltransferases have homologous
RT amino-terminal domains important for recognition of nucleosomal
RT substrates.";
R5 Mol. Cell. Biol. 18:5659-5669(1998).
CC -!- FUNCTION: Functions as a histone acetyltransferase (HAT) to
CC promote transcriptional activation. Has significant histone
CC acetyltransferase activity with core histones, but not with
CC nucleosome core particles (By similarity).
CC -!- SUBUNIT: INTERACTS WITH P300, CBP AND ADA2.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Contains 1 bromodomain.
CC
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CC
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DR EMBL; AF254441; AAF70497.1; --
DR HSP; Q92831; 1891;
DR MGD; MG1:1343101; Gcn5l2.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR000182; Gcn5acetyltransf.
DR Pfam; PF00583; Acetyltransf; 1.
DR Pfam; PF00439; Bromodomain; 1.
DR SMART; SMART0297; BROMO; 1.
DR PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.
DR PROSITE; PS50014; BROMODOMAIN_2; 1.
KW Transcription regulation; Transferase; Nuclear protein;
KW Bromodomain.
FT DOMAIN 548 621 ACETYLTRANSFERASE.
FT DOMAIN 738 808 BROMODOMAIN.
SQ SEQUENCE 830 AA; 93391 MW; 89333C5SE0E734179 CRC64;

Query Match 69.4%; Score 34; DB 1; Length 830;
Best Local Similarity 85.7%; Pred. NO. 72;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFE 7
Db 216 LGSPPE 222

RESULT 26
GCC2_HUMAN
ID GCL2 HUMAN STANDARD; PRT; 837 AA.
AC Q92830; Q9UCW1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE General control of amino acid synthesis protein 5-like 2 (EC 2.3.1.-)
DE (Histone acetyltransferase Gcn5) (hGcn5).
GN GCL2 CR Gcn5 OR HGCN5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1.
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Liver;
RX MEDLINE=98278910; PubMed=9611240;
PA Smith E.R., Belote J.M., Schlitz R.L., Yang X.-J., Moore P.A.,
RA Berger S.L., Nakatani Y., Allis C.D.;
RT "Cloning of Drosophila Gcn5: conserved features among metazoan Gcn5
family members.";
RL Nucleic Acids Res. 26:2948-2954(1998).
RN 2.
RP SEQUENCE OF 362-837 FROM N.A. (ISOFORM 1);
RC TISSUE=Brain;
RX MEDLINE=96300317; PubMed=8684459;
RA Yang X.-J., Ogryzko V.V., Nishikawa C., Howard B.H., Nakatani Y.;
RT "A p300/CBP-associated factor that competes with the adenoviral
oncoprotein E1A.";
RL Nature 382:319-324(1996).
RN 3.
RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
RC TISSUE=Testis;
RX MEDLINE=96140426; PubMed=8552087;
RA Candau R., Moore P.A., Wang L., Barlev N., Yang C.Y., Rosen C.A.,
RA Berger S.L.;
RT "Identification of human proteins functionally conserved with the
yeast putative adaptors ADA2 and Gcn5.";
RL Mol. Cell. Biol. 16:593-602(1996).
CC -! FUNCTION: Functions as a histone acetyltransferase (HAT) to
CC promote transcriptional activation. Has significant histone
CC acetyltransferase activity with core histones, but not with
CC nucleosome core particles.
CC -! SUBUNIT: INTERACTS WITH P300, CBP AND ADA2.
CC -! SUBCELLULAR LOCATION: Nuclear.
CC -! ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;

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CC Name=1; Synonyms=Gcn5-L;
CC IsoId=Q92830-1; Sequence=Displayed;
CC Name=2; Synonyms=Gcn5-S;
CC IsoId=Q92830-2; Sequence=VSP_000556;
CC -! TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED, WITH MOST
CC ABUNDANT EXPRESSION IN OVARY.
CC -! SIMILARITY: Contains 1 bromodomain.
CC
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CC
CC EMBL; AF029777; AAC39769.1; --
CC EMBL; U57316; AAC50641.1; --
CC PIR; S71789; S71789.
CC PDB; 1F68; 13-DEC-00.
CC TRANSFAC; T01686; --
CC Genew; HGNC:4201; GCN5L2.
CC MIM; 602301; --
CC GO; GO:0005679; C:nucleosome remodeling complex; TAS.
CC GO; GO:0003713; F:transcription co-activator activity; TAS.
CC GO; GO:0006338; P:chromatin modeling; TAS.
CC GO; GO:0006473; P:protein amino acid acetylation; TAS.
CC GO; GO:0006357; P:regulation of transcription from pol II promoter; TAS.
CC InterPro; IPR001487; Bromodomain.
CC InterPro; IPR000182; Gcn5acetyltransf.
CC Pfam; PF00583; Acetyltransf; 1.
CC Pfam; PF00439; bromodomain; 1.
CC PRINTS; PR00503; BROMODOMAIN.
CC SMART; SMART0297; BROMO; 1.
CC PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.
CC PROSITE; PS50014; BROMODOMAIN_2; 1.
KW Transcription regulation; Transferase; Nuclear protein; Bromodomain;
KW Alternative splicing; 3D-structure.
FT DOMAIN 555 628 ACETYLTRANSFERASE.
FT DOMAIN 745 815 BROMODOMAIN.
FT VARSPLIC 1 410 Missing (in isoform 2).
FT /FTID=VSP_000556.
SQ SEQUENCE 837 AA; 93836 MW; 96D2F67C65627C4C CRC64;

Query Match 69.4%; Score 34; DB 1; Length 837;
Best Local Similarity 85.7%; Pred. NO. 73;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFE 7
Db 221 LGSPPE 227

RESULT 27
PN2A_PENVA
ID PN2A_PENVA STANDARD; PRT; 72 AA.
AC P81057;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Penaeidin-2a precursor (Pen-2a) (Pen-2) (P2).
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=6689;
RN 1.
RP SEQUENCE FROM N.A., SEQUENCE OF 22-71, FUNCTION, MASS SPECTROMETRY,
RP AND AMIDATION.
RC TISSUE=Hemocyte;
RX MEDLINE=98019209; PubMed=9353298;
RA Destoumieux D., Bulet P., Loew D., van Dorsellaer A., Rodriguez J.,
RA Bachere E.;

```


RT "penaeidins, a new family of antimicrobial peptides isolated from the
RT shrimp *Penaeus vannamei* (Decapoda).";
RL J. Biol. Chem. 272:28398-28406(1997);
RN [2]
RP SEQUENCE OF 22-72 FROM N.A., SEQUENCE OF 22-71, AND FUNCTION.
RX MEDLINE=21360118; PubMed=10561573;
RA Destoumieux D., Bulet P., Strub J.-M., van Dorsselaer A., Bache E.;
RT "Recombinant expression and range of activity of penaeidins,
RT antimicrobial peptides from penaeid shrimp.";
RJ Eur. J. Biochem. 266:335-346(2000).
RN [3]
RP CHITIN-BINDING ACTIVITY, TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND
RP DEVELOPMENTAL STAGE.
RX MEDLINE=20107129; PubMed=10639333;
RA Destoumieux D., Munoz M., Cosseau C., Rodriguez J., Bulet P.,
RA Comps M., Bache E.;
RT "Penaeidins, antimicrobial peptides with chitin-binding activity, are
RT produced and stored in shrimp granulocytes and released after
RT microbial challenge.";
RJ J. Cell Sci. 113:461-469(2000).
RN [4]
RP REVIEW.
RX MEDLINE=20479888; PubMed=11028917;
RA Destoumieux D., Munoz M., Bulet P., Bache E.;
RT "Penaeidins, a family of antimicrobial peptides from penaeid shrimp.";
RJ Cell. Mol. Life Sci. 57:1260-1271(2000).
CC [1] FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST *M. LUTENS* AND *E. COLI*.
CC BACTERIA: ANTIFUNGAL ACTIVITY AGAINST *N. CRASSA* AND *F. OXYSPORUM*.
CC PRESENTS CHITIN-BINDING ACTIVITY.
CC [2] SUBCELLULAR LOCATION: Cytoplasmic granules of hemocytes and to a
CC lesser extent in small granules of hemocytes.
CC [3] TISSUE SPECIFICITY: HIGHER EXPRESSION IN HEMOCYTES AND TO A LESSER
CC EXTENT IN HEART, TESTIS, GILLS, INTESTINE, LYMPHOID ORGAN AND
CC HEPATOPANCREAS. TRACES IN EYES AND SUBCUTICULAR EPITHELIUM. NOT
CC PRESENT IN THE BRAIN.
CC [4] DEVELOPMENTAL STAGE: EXPRESSION DECREASES 3 HOURS AFTER MICROBIAL
CC CHALLENGE TO RETURN TO CONTROL LEVELS AFTER 12 HOURS AND SLIGHTLY
CC INCREASES AFTER 24 HOURS.
CC [5] PTM: Three disulfide bonds are present.
CC [6] MASS SPECTROMETRY: MW=5520; METHOD=MAEDI; RANGE=22-71.
CC [7] SIMILARITY: BELONGS TO THE PENAEDIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch.
CC
CC EMBL; Y14925; CAA75142.1; --
KW Antibiotic; Fungicide; Chitin-binding; Amidation; Signal;
FT SIGNAL 1 21 POTENTIAL;
FT CHAIN 22 71 PENAEDIN-2A;
FT DOMAIN 29 43 PRO-RICH;
FT MOD RES 71 71 AMIDATION (G-72 PROVIDE AMIDE GROUP).
SQ SEQUENCE 72 AA; 7833 MW; 5743E69C59673954 CRC64;

Query Match 67.3%; Score 33; DB 1; Length 72;
Best Local Similarity 83.3%; Pred. No. 8.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : LGRPPF 6
: |||
Db 36 LGRPPF 41

RESULT 28
MTSI STRCS STANDARD; PRT; 304 AA;
ID MTSI STRCS
AC 052692;
DT 16-OCT-2001 (Rel. 40, Created,

RT "penaeidins, a new family of antimicrobial peptides isolated from the
RT shrimp *Penaeus vannamei* (Decapoda).";
RL J. Biol. Chem. 272:28398-28406(1997);
RN [2]
RP SEQUENCE OF 22-72 FROM N.A., SEQUENCE OF 22-71, AND FUNCTION.
RX MEDLINE=21360118; PubMed=10561573;
RA Destoumieux D., Bulet P., Strub J.-M., van Dorsselaer A., Bache E.;
RT "Recombinant expression and range of activity of penaeidins,
RT antimicrobial peptides from penaeid shrimp.";
RJ Eur. J. Biochem. 266:335-346(2000).
RN [3]
RP CHITIN-BINDING ACTIVITY, TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND
RP DEVELOPMENTAL STAGE.
RX MEDLINE=20107129; PubMed=10639333;
RA Destoumieux D., Munoz M., Cosseau C., Rodriguez J., Bulet P.,
RA Comps M., Bache E.;
RT "Penaeidins, antimicrobial peptides with chitin-binding activity, are
RT produced and stored in shrimp granulocytes and released after
RT microbial challenge.";
RJ J. Cell Sci. 113:461-469(2000).
RN [4]
RP REVIEW.
RX MEDLINE=20479888; PubMed=11028917;
RA Destoumieux D., Munoz M., Bulet P., Bache E.;
RT "Penaeidins, a family of antimicrobial peptides from penaeid shrimp.";
RJ Cell. Mol. Life Sci. 57:1260-1271(2000).
CC [1] FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST *M. LUTENS* AND *E. COLI*.
CC BACTERIA: ANTIFUNGAL ACTIVITY AGAINST *N. CRASSA* AND *F. OXYSPORUM*.
CC PRESENTS CHITIN-BINDING ACTIVITY.
CC [2] SUBCELLULAR LOCATION: Cytoplasmic granules of hemocytes and to a
CC lesser extent in small granules of hemocytes.
CC [3] TISSUE SPECIFICITY: HIGHER EXPRESSION IN HEMOCYTES AND TO A LESSER
CC EXTENT IN HEART, TESTIS, GILLS, INTESTINE, LYMPHOID ORGAN AND
CC HEPATOPANCREAS. TRACES IN EYES AND SUBCUTICULAR EPITHELIUM. NOT
CC PRESENT IN THE BRAIN.
CC [4] DEVELOPMENTAL STAGE: EXPRESSION DECREASES 3 HOURS AFTER MICROBIAL
CC CHALLENGE TO RETURN TO CONTROL LEVELS AFTER 12 HOURS AND SLIGHTLY
CC INCREASES AFTER 24 HOURS.
CC [5] PTM: Three disulfide bonds are present.
CC [6] MASS SPECTROMETRY: MW=5520; METHOD=MAEDI; RANGE=22-71.
CC [7] SIMILARITY: BELONGS TO THE PENAEDIN FAMILY.
CC
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CC
CC EMBL; Y14925; CAA75142.1; --
KW Antibiotic; Fungicide; Chitin-binding; Amidation; Signal;
FT SIGNAL 1 21 POTENTIAL;
FT CHAIN 22 71 PENAEDIN-2A;
FT DOMAIN 29 43 PRO-RICH;
FT MOD RES 71 71 AMIDATION (G-72 PROVIDE AMIDE GROUP).
SQ SEQUENCE 72 AA; 7833 MW; 5743E69C59673954 CRC64;

Query Match 67.3%; Score 33; DB 1; Length 72;
Best Local Similarity 83.3%; Pred. No. 8.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : LGRPPF 6
: |||
Db 36 LGRPPF 41

RESULT 28
MTSI STRCS STANDARD; PRT; 304 AA;
ID MTSI STRCS
AC 052692;
DT 16-OCT-2001 (Rel. 40, Created,

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Modification methylase ScaI (EC 2.1.1.113) (N-4 cytosine-specific
DE methyltransferase ScaI) (M.ScaI).
GN SCAIM.
OS Streptomyces caespitosus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=53502;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077292; PubMed=9862476;
RA Xu S.-Y., Xiao J.-P., Etlwiler L., Holden M., Aliotta J., Poh C.L.,
RA Dalton M., Robinson D.P., Petronzio F.R., Moran L., Ganatra M.,
RA Ware J., Slatko B., Benner J. II;
RT "Cloning and expression of the ApaLI, NspI, NspHI, SacI, ScaI, and
RT SspI restriction-modification systems in *Escherichia coli*.";
RL Mol. Gen. Genet. 260:226-231(1998).
CC [1] FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE
CC AGTACT, CAUSES SPECIFIC METHYLATION ON C-5 ON BOTH STRANDS, AND
CC PROTECTS THE DNA FROM CLEAVAGE BY THE SCAI ENDONUCLEASE.
CC [2] CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA cytosine = S-
CC adenosyl-L-homocysteine + DNA N(4)-methylcytosine.
CC [3] SIMILARITY: BELONGS TO THE N4-METHYLTRANSFERASE FAMILY.
CC
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CC
CC EMBL; AF044681; AAC97178.1; --
REBASE; 3498; M.ScaI.
DR InterPro; IPR0C1091; CN4_Metransf.
DR InterPro; IPR002295; D21N6_mtfase.
DR InterPro; IPR002941; N6/N4_Mtase.
DR Pfam; PF01555; N6_N4_Mtase; 1.
DR PRINTS; PR00506; D21N6MTFRASE.
DR PRINTS; PR00508; S21N4MTFRASE.
DR PROSITE; PS00093; N4_MTASE; 1.
KW Transferase; Methyltransferase; Restriction system.
SQ SEQUENCE 304 AA; 34187 MW; F589CF18B62C3634 CRC64;

Query Match 67.3%; Score 33; DB 1; Length 304;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY : LGRPPFFETS 9
: ||| : |||
Db 41 LGRPPFFETS 49

RESULT 29
STKC RAT
ID STKC RAT STANDARD; PRT; 343 AA.
AC O55099;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora- and Ipl1-
DE like midbody-associated protein 1) (AIM-1) (Aurora-B).
GN STK12 OR AIM1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96119810; PubMed=9450992;
RT Terada Y., Tatsuka M., Suzuki F., Yasuda Y., Fujita S., Otsu M.;


```
RT "AIM-1: a mammalian midbody-associated protein required for
RT cytokinesis.";
RL EMBL J. 17:667-676(1998).
CC -!- FUNCTION: Maybe directly involved in regulating the cleavage of
CC polar spindle microtubules and is a key regulator for the onset of
CC cytokinesis during mitosis (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
CC in late anaphase and concentrated into the midbody in telophase
CC and cytokinesis. Colocalized with gamma tubulin in the mid-body
CC (By similarity).
CC -!- TISSUE SPECIFICITY: High level expression seen in the testis. It
CC is also expressed in the spleen, lung and heart. Expressed in the
CC G2/M phase of the cell cycle.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC
CC EMBL; D99731; BAA23794.1; -.
CC HSSP; Q63450; 1A06.
CC InterPro; IPR002052; N6_Mtase.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC
CC Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
CC
CC DOMAIN 80 330 PROTEIN_KINASE.
CC NP_BIND 86 94 ATP (BY SIMILARITY).
CC BINDING 109 109 ATP (BY SIMILARITY).
CC ACT_SITE 203 203 BY SIMILARITY.
CC
CC SEQUENCE 343 AA; 39234 MW; 27B74C02A0E1B759E CPO-4;
CC
CC Query Match 67.3%; Score 33; DB 1; Length 343.
CC Best local Similarity 62.5%; Erez 8; 44.
CC Matches 5; Conservative 2; Miscellaneous 1; Idents 0; Gaps 0;
CC
CC QY 1 LGRPPFET 8
CC :|:|:|:
CC DB 271 VGNPPFES 278
CC
CC RESULT 30
CC STKC MOUSE
CC ID STKC_MOUSE STANDARD; PRT; 345 AA.
CC AC Q70126; Q61882;
CC DT 28-FEB-2003 (Rel. 41, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora-related
CC kinase 2) (Serine/threonine protein kinase 5) (STK-1) (Aurora-B).
CC GN STK12 OR STK5 OR ARK2 OR STK1.
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OX NCBI_TaxID=10090;
CC RN 1;
CC
CC SEQUENCE FROM N.A.
CC STRAIN=C57BL/6; TISSUE=Testis;
CC MEDLINE=96194801; PubMed=8647446;
CC Niwa H., Abe K., Kunitada T., Yamamura K.
CC "Cell-cycle-dependent expression of the STK-1 gene encoding a novel
```

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RT murine putative protein kinase";
RL Gene 169:197-201(1996).
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=98183439; PubMed=9514916;
RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
RT "cDNA cloning, expression, subcellular localization, and chromosomal
RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
RT 1 and 2.";
RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
RN 3;
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Maman A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be directly involved in regulating the cleavage of
CC polar spindle microtubules and is a key regulator for the onset of
CC cytokinesis during mitosis (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
CC in late anaphase and concentrated into the midbody in telophase
CC and cytokinesis. Colocalized with gamma tubulin in the mid body
CC (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in testis, intestine and spleen. All
CC of them are tissues that contain a large number of proliferating
CC cells. Expressed during S phase, in a cell-cycle-
CC dependent fashion.
CC -!- DEVELOPMENTAL STAGE: Strongly expressed in 8.5 and 12.5 dpc.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D21099; BAA04658.1; -.
CC EMBL; U69107; AAC12683.1; -.
CC EMBL; BC003261; AAH03261.1; -.
CC HSSP; Q63450; 1A06.
CC MGD; MGI:107168; Stk12.
CC InterPro; IPR002052; N6_Mtase.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
```

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP binding.
FT DOMAIN 82 332 PROTEIN KINASE.
FT NP BIND 88 96 ATP (BY SIMILARITY).
FT BINDING 111 111 ATP (BY SIMILARITY).
FT ACT SITE 205 205 BY SIMILARITY.
FT CONFLICT 44 44 R - S W (IN REF. 1).
SQ SEQUENCE 345 AA; 39324 MW; C1D1D8B6BDEA00A0 CRC64;

Query Match 67.3%; Score 33; DB 1; Length 345;
Best Local Similarity 62.5%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFFET 8
DB 273 VGNPPFES 280

RESULT 31
PKN5 MYXXA
ID PKN5 MYXXA STANDARD; PRT; 380 AA.
AC P54737;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase pkn5 (EC 2.7.1.37)
GN PKN5.
OS Myxococcus xanthus.
CC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
CC Cystobacterineae; Myxococcaceae; Myxococcus.
CX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DZFL;
RX MEDLINE=96310380; PubMed=8733241;
RA Zhang W., Inouye M., Inouye S.
RT "Reciprocal regulation of the differentiation of Myxococcus xanthus
by pkn5 and pkn6, eukaryotic-like Ser/Thr protein kinases".
RL Mol. Microbiol. 20:435-447(1996).
CC 1. FUNCTION: Pkn5 and pkn6 may have reciprocal roles in growth and
development. Pkn5 may be a kinase that negatively regulates
development.
CC 2. CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.
CC 3. SUBCELLULAR LOCATION: Cytoplasmic.
CC 4. DEVELOPMENTAL STAGE: Expressed abundantly in the early life
cycle, with slight increases at early stage of development.
CC 5. PTM: Autophosphorylated at serine residues.
CC 6. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

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DR EMBL; J03656; AAB40049.1; -
DR PIR; S70964; S70964.
DR PhosSite; P54737; -
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1
KW Transferase; Serine/threonine-protein kinase; ATP BINDING.
KW Phosphorylation.
FT DOMAIN 9 378 PROTEIN KINASE.
FT NP BIND 15 23 ATP (BY SIMILARITY).
FT BINDING 38 38 ATP (BY SIMILARITY).

Query Match 67.3%; Score 33; DB 1; Length 345;
Best Local Similarity 62.5%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFFET 8
DB 273 VGNPPFES 280

FT ACT SITE 244 244 BY SIMILARITY.
SQ SEQUENCE 380 AA; 41924 MW; DC3ADF824420C1F1 CRC64;

Query Match 67.3%; Score 33; DB 1; Length 380;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
DB 317 GRPPFD 322

RESULT 32
PKN1 CORGL
ID PKN1 CORGL STANDARD; PRT; 646 AA.
AC Q8NJ38;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine protein kinase Cgl0041 (EC 2.7.1.37).
GN CGL0041.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
CX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20330 / NCIB 10025;
RA Nakagawa S.
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC 1. CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.
CC 2. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC 3. SIMILARITY: Contains 3 PASTA domains.

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DR EMBL; AP005274; BAB397434.1; -
DR InterPro; IPR005543; PASTA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF03793; PASTA; 3.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
ATP-binding; Repeat; Complete proteome.
FT DOMAIN 9 278 PROTEIN KINASE.
FT DOMAIN 365 431 PASTA 1.
FT DOMAIN 432 500 PASTA 2.
FT DOMAIN 501 565 PASTA 3.
FT NP BIND 15 23 ATP (BY SIMILARITY).
FT BINDING 38 38 ATP (BY SIMILARITY).
FT ACT SITE 136 136 BY SIMILARITY.
SQ SEQUENCE 646 AA; 68237 MW; CF3B4980ECF73BFB CRC64;

Query Match 67.3%; Score 33; DB 1; Length 646;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
DB 210 GRPFFE 215

RESULT 33
PLK1-CABE...
ID PLK1-CABE... STANDARD: PRT: 649 AA.
AC P34331; C61662; C76763;
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase plk-1 (EC 2.7.1.1) (Polo like
kinase-1)
GN PLK-1 OR PLC1 OR C14B9.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID:6239;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=99304501; PubMed=10376213;
RA Guyang B., Wang Y., Dai W.;
RT "Caenorhabditis elegans contains structural homologs of human prk and
pk-1";
RL DNA Seq. 10:109-113(1999).
RN (2)
RP SEQUENCE FROM N.A. (ISOFORM A), FUNCTION, AND SUBCELLULAR LOCATION.
RC STRAIN=Bristol N2;
RX MEDLINE=20190108; PubMed=10660671;
RA Chase D., Serafinas C., Ashcroft N., Kosinski M., Longo D.,
RA Ferris D.K., Golden A.;
RT "The polo-like kinase PLK-1 is required for nuclear envelope breakdown
and the completion of meiosis in Caenorhabditis elegans";
RL Genesis 26:26-41(2000).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906395;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton J., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston D., Jones M., Kershaw J., Kirov G., Kister N.,
RA Latreille P., Lightning J., Lloyd C., Mottimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken B., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Schrammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock J., Wilkinson S., Winton J.,
RA Wohldman P.;
RT "2.2 kb of contiguous nucleotide sequence from chromosome III of C.
elegans";
RL Nature 368:32-38(1994).
RN (4)
RP REVISIONS, AND ALTERNATIVE SPLICING.
RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBS databases.
CC -!- FUNCTION: Required for oocyte nuclear envelope breakdown before
entry of oocyte into spermatheca. In mitotic cells, plays a role
in spindle organization and centrosome maturation. In meiotic
cells, required for spindle dynamics and probably for spindle
attachment to the chromosomes. Zygotic role in the development of
the germline and nerve cord.
CC -!- SUBCELLULAR LOCATION: In mitosis, remains associated with
centrosomes entering prophase through to anaphase. During
metaphase, found at the chromosomes of the metaphase plate. In
meiosis, detected at centrosomes after pronuclear meeting in post-
meiotic 1-cell embryos. Associated with chromatin during
chromosome segregation of anaphase and in the region between the
dividing chromosomes. Cytoplasmic in mature, unfertilized oocytes.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Name=isoform-2;
CC Name=b;
CC IsoId=P34331-1; Sequence=Displayed;
CC Name=a;
CC IsoId=P34331-2; Sequence=VSP_04929;
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
CC (DGS/POLO SUBFAMILY).

-!- SIMILARITY: Contains 2 POLO box domains.
CC
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CC
CC
CC EMBL: AF057165; AAC14129.1;
DR EMBL: AF080581; AAC34661.1;
DR EMBL: L15188; AAN27947.2;
DR EMBL: L15188; AAM22025.1;
DR PIR: T43337; T43337;
DR HSSP: Q63450; 1A06.
DR WormPep: C14B9.4a; CE26649.
DR WormPep: C14B9.4b; CE30602.
DR GO: GO:0005634; C:nucleus; IEP.
DR GO: GO:0005524; F:protein serine/threonine kinase activity; ISS.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; ISS.
DR GO: GO:0007417; P:central nervous system development; IMP.
DR GO: GO:0007098; P:centrosome cycle; IMP.
DR GO: GO:0007077; P:mitotic nuclear envelope breakdown; IMP.
DR GO: GO:0007052; P:mitotic spindle assembly; IMP.
DR GO: GO:0006468; P:protein amino acid phosphorylation; ISS.
DR InterPro: IPR000959; POLO box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00659; POLO_box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00078; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase; Repeat;
KW Nuclear protein; Alternative splicing.
FT DOMAIN 38 290 PROTEIN KINASE.
FT NP_BIND 45 52 ATP (BY SIMILARITY).
FT BINDING 57 67 ATP (BY SIMILARITY).
FT ACT_SITE 162 162 BY SIMILARITY.
FT DOMAIN 423 485 POLO_BOX_1.
FT DOMAIN 523 589 POLO_BOX_2.
FT VARSP_LIC 83 89 VSPERIL -> MTQEVQ (in isoform a).
FT /FTID=VSP_004928.
SQ SEQUENCE 649 AA; 73633 MW; 54D969F140D7A43B CRC64;

Query Match 67.3%; Score 33; DB 1; Length 649;
Best Local Similarity 71.4%; Pred. No. 87;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPPFET 8
|:|:|:
Db 232 GQPPFES 236

RESULT 34
TOP1-SYNP7
ID TOP1-SYNP7 STANDARD: PRT: 839 AA.
AC P34185;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
DE (Unwinding enzyme) (Swivelase).
GN TOPA.
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=1140;
RN (1)
RP SEQUENCE FROM N.A.

```
RX MEDLINE=95388763; PubMed=7659748;
RA Rotten-Tarazi M., Lieman-Hurwitz J., Gabay C., Orus V.I., Kaplan A.;
RT "The genomic region of rbcLs in Synechococcus sp. PCC 7942 contains
RT genes involved in the ability to grow under low CO2 concentration and
RT in chlorophyll biosynthesis.";
RL Plant Physiol. 108:1461-1469(1995).
CC -!- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE
CC CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
CC -!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
CC DNA, followed by passage and rejoining.
CC -!- SUBUNIT: Monomer.
CC -!- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
CC BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN
CC WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS
CC AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
CC -!- SIMILARITY: BELONGS TO THE PROKARYOTIC TYPE I/III TOPOISOMERASE
CC FAMILY.
CC -----
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CC -----
CC EMBL; X72391; CAA51086.1; --
CC PIR; S32158; S32158.
CC HSSP; P06612; IECJ.
CC InterPro; IPR005733; DNA_topI_bact.
CC InterPro; IPR003380; DNA_topoisomerase.
CC InterPro; IPR003601; DNATopI_ATP_bind.
CC InterPro; IPR003602; DNATopI_DNA_bind.
CC InterPro; IPR006171; Toprim_dom.
CC InterPro; IPR006154; Toprim_sub.
CC Pfam; PF01131; Topoisom_bac; 1.
CC Pfam; PF01751; Toprim; 1.
CC SMART; SM00437; TOP1AC; 1.
CC SMART; SM00436; TOP1BC; 1.
CC SMART; SM00493; TOPRIM; 1.
CC TIGRfam; TIGR01051; topA_bact; 1.
CC PROSITE; PS00336; TOPOISOMERASE_I_PROCK; 1.
KW isomerase; topoisomerase; DNA-binding.
LT ACT SITE 322 322 DNA CLEAVAGE (BY SIMILARITY;
SQ SEQUENCE 819 AA; 91236 MW; C756AC2EE8E1A680 CRC64.
Query Match 67.3%; Score 102; DB 1; Length 1113;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 RPPFFTS 9
Db 284 RPPFFTS 290
RESULT 35
PER3_MOUSE STANDARD; PRT: 1113 AA.
AC Q70361;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Period circadian protein 3 (PER3).
GN PER3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
PP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=98318231; PubMed=9655499;
RA Zyika M.J., Shearman L.P., Weaver D.R., Reppert S.M.;
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RT "Three period homologs in mammals: differential light responses in the
RT suprachiasmatic circadian clock and oscillatin transcripts outside of
RT brain.";
RL Neuron 20:1103-1110(1998).
CC -!- FUNCTION: CIRCADIAN REGULATOR THAT MAY ACT AS A TRANSCRIPTION
CC FACTOR. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN TRANSCRIPTIONAL
CC LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING INDIRECT
CC TRANSCRIPTIONAL INHIBITION (BY SIMILARITY). EXPRESSION OSCILLATES
CC IN THE SUPRACHIASMATIC NUCLEI (SCN) AND EYES. THE EXPRESSION
CC RHYTHMS APPEAR TO ORIGINATE FROM RETINA.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. EXPRESSED IN HEART, BRAIN,
CC LUNG, LIVER, SKELETAL MUSCLE, TESTIS, AND AT LOW LEVEL IN THE
CC SPLEEN AND KIDNEY. IN BRAIN, MAINLY FOUND IN THE SCN, HIPPOCAMPUS,
CC PIRIFORM CORTEX, AND CEREBELLUM. LOWER LEVEL OF EXPRESSION IN THE
CC NEOCORTEX. EXPRESSION EXHIBITS SYNCHRONOUS OSCILLATIONS IN LIVER,
CC SKELETAL MUSCLE AND TESTIS.
CC -!- INDUCTION: NOT ACUTELY INDUCED BY LIGHT IN SCN DURING SUBJECTIVE
CC NIGHT.
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC -----
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CC -----
CC EMBL; AF050182; AAC40147.1; --
CC PIR; T14260; T14260.
CC MGD; MGI:1277134; Per3.
CC InterPro; IPR001610; PAC.
CC InterPro; IPR000014; PAS_domain.
CC Pfam; PF00989; PAS; 1.
CC SMART; SM00066; PAC; 1.
CC SMART; SM00091; PAS; 1.
CC PROSITE; PS01112; PAS; 1.
KW Transcription regulation; Nuclear protein; Repeat; Biological rhythms.
LT ACT SITE 52 86 HELIX-LOOP-HELIX MOTIF.
SQ SEQUENCE 1113 AA; 120939 MW; 8121E235D100A627 CRC64;
Query Match 67.3%; Score 33; DB 1; Length 1113;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GRPFFTS 9
Db 327 GHPFFHS 334
RESULT 36
HFM1_YEAST STANDARD; PRT: 1188 AA.
ID HFM1_YEAST
AC P51979;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ATP-dependent DNA helicase MER3 (EC 3.6.1.-) (HFM1 protein).
GN HFM1 OR MER3 OR YGL251C OR NRE1046.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN 1;
PP SEQUENCE FROM N.A.
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RC STRAIN=S288C / FY1679;
RX MEDLINE=97127827; PubMed=8972578;
RA Coissac E., Mailhier E., Robineau S., Netter P.;
RT "Sequence of a 39,411 bp DNA fragment covering the left end of
X1 Chromosome VII of *Saccharomyces cerevisiae*.";
RL Yeast 12:1555-1562(1996).
RN 12;
RP SEQUENCE OF 20-1188 FROM N.A.
RA West R.W., Thomas S., Ma J.L.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN 13;
RP CHARACTERIZATION.
RX MEDLINE=99452777; PubMed=10523314;
RA Nakagawa T., Ogawa H.;
RT "The *mer3* helicase involved in meiotic crossing over is stimulated by
RT single-stranded dna-binding proteins and unwinds dna in the 3' to 5'
RT direction.";
RL J. Biol. Chem. 276:31487-31493(2001).
RN 15;
RP CONCEPTUAL TRANSLATION.
RA Linder P.;
RL Unpublished observations (AUG-2001).
CC -!- FUNCTION: DNA-dependent ATPase. Required in the control of double
CC strand breaks transition and crossover during meiosis. Unwinds DNA
CC in the 3' to 5' direction. Prefers single-stranded DNA.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: BELONGS TO THE HELICASE FAMILY. SKI2 SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EXBL: X94357; CRA64136.1; ALT_SEQ.
CC EXBL: Z72773; CAA96971.1; ALT_SEQ.
CC EXBL: U22156; AAA93159.1; ALT_INIT.
CC SGD: S000322; HFM1.
CC GC: G010005634; Cinnuleus; IDA.
CC GC: G010002678; F1DNA helicase activity; IDA.
CC GC: G010007126; P1meiosis; IDA.
CC InterPro: IPR003593; AAA ATPase.
CC InterPro: IPR001410; DEAD.
CC InterPro: IPR001650; Helicase_C.
CC InterPro: IPR004179; Sec63.
CC Pfam: PF00270; DEAD; 1.
CC Pfam: PF00271; helicase_C; 1.
CC Pfam: PF02889; Sec63; 1.
CC SMART: SM00382; AAA; 1.
CC SMART: SM00487; DEXDC; 1.
CC SMART: SM00490; HELICC; 1.
CC SMART: SM00611; SEC63; 1.
KW Nuclear protein; Zinc-finger; DNA-binding; Helicase; Hydrolase;
KW ATP-binding.
FT NP_BIND 160 167 ATP (POTENTIAL).
FT SITE 267 270 DEH BOX.
FT ZN_FING 1040 1055 C4-TYPE (POTENTIAL)
FT MUTAGEN 165 165 G->D: DECREASE OF ACTIVITY.
FT CONFLICT 552 553 MISSING (IN REF. 1).
SQ SEQUENCE 1188 AA; 135099 MW; C43CE08B93A565F8 CRC64;

Query Match 67.3%; Score 33; DR 1; Length 1188;
Best Local Similarity 85.7%; Pred. No. 17e-02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPFET 8
Db 493 GRPQFET 499

RESULT 37
PER3_HUMAN
ID PER3_HUMAN STANDARD; PRT; 1210 AA.
AC P56645; Q369K6; Q96S77; Q36S78; Q9C0J3; Q9NSP9; Q9UGU8;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Period circadian protein 3 (hPER3).
GN PER3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Nagase T., Kikuno R., Ohara O.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN 12;
RP SEQUENCE FROM N.A.
RA Rhodes S., Huckle E.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN 13;
RP SEQUENCE OF 44-1210 FROM N.A.
RA Pearce A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN 14;
RP SEQUENCE OF 114-379 FROM N.A.
RA Mistry S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN 15;
RP SEQUENCE OF 44-91 AND 732-890 FROM N.A., AND VARIANT ALA-864.
RA Ebisawa T., Uchiyama M., Kajimura N., Mishima K., Kamei Y., Katoh M.,
RA Matanabe T., Sekimoto M., Shibui K., Kim K., Kudo Y., Ozeki Y.,
RA Inoue Y., Yamada N., Nagase T., Ozaki N., Ohara O., Ishida N.,
RA Okawa M., Takahashi K.;
RT "Association of structural polymorphisms in human period3 gene with
RT delayed sleep phase syndrome.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CIRCADIAN REGULATOR THAT MAY ACT AS A TRANSCRIPTION
CC FACTOR. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN TRANSCRIPTIONAL
CC LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING INDIRECT
CC TRANSCRIPTIONAL INHIBITION. THE EXPRESSION RHYTHMS APPEAR TO
CC ORIGINATE FROM RETINA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AB047686; BAB32925.1; -
CC EMBL: AL157954; CAB76084.1; -
CC EMBL: Z98884; CAB63147.1; -
CC EMBL: AB047521; BAB63250.1; -
CC EMBL: AB047530; BAB63251.1; -
CC EMBL: AB047531; BAB63252.1; -
CC EMBL: AB047532; BAB63253.1; -
CC EMBL: AB047533; BAB63254.1; -
CC EMBL: AB047534; BAB63255.1; -


```
DR Genew; HGNC:8847; PER3.
DR MIM; 603427; -.
DR InterPro; IPR0000314; PAS_domain.
DR Pfam; PF00989; PAS; 1.
DR PROSITE; PS00112; PAS; 1.
KW Transcription regulation; Nuclear protein; Repeat; Biological rhythms;
KW Polymorphism.
FT DOMAIN 116 188 PAS 1.
FT DOMAIN 261 331 PAS 2.
FT DOMAIN 339 381 PAS.
FT VARIANT 864 864 F -> A.
FT /FTID=VAR_015514.
FT CONFLICT 198 215 AARYSCAPVKPFQRIK -> ENRTGCVKSTNIFNLLS
(IN REF. 4).
FT CONFLICT 200 200 MISSING (IN REF. 2 AND 3).
FT CONFLICT 248 248 MISSING (IN REF. 4).
FT CONFLICT 327 331 MISSING (IN REF. 3 AND 4).
FT CONFLICT 503 509 MISSING (IN REF. 2 AND 3).
FT CONFLICT 595 606 AGQIPAPKSE -> GNKNAPQK (IN REF. 3).
FT CONFLICT 835 835 P -> L (IN REF. 2 AND 3).
FT CONFLICT 951 951 R -> Q (IN REF. 2 AND 3).
FT CONFLICT 963 963 MISSING (IN REF. 2 AND 3).
SQ SEQUENCE 1210 AA; 132671 MW; 89E79321F8B33FF5 CRC64;

Query Match 67.3%; Score 33; DB 1; Length 1210;
Best Local Similarity 75.0%; Pred.No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GRPPFFES 9
| | | |
DB 332 GHPFFES 339

RESULT 38
DPOL THEG8
ID DPOL_THEG8 STANDARD; PRT; 1699 AA.
AC Q3HR84;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7) [Contains: Endonuclease PI-Tspge81
(EC 3.1.1.1)] (Tsp-GE8 pol-1 intein); Endonuclease PI-Tspge81;
DE (EC 3.1.1.1) (Tsp-GE8 pol-2 intein).
GN POL CR POL-1.
OS Thermococcus sp. (strain GE8).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=105583;
RN [1]
RP SEQUENCE FROM N.A.
RA Querellou C.J.E., Cambon M.A., Lesangher F., Barber G.;
PT "Thermococcales taxonomy and phylogeny based on the comparative use of
RT 16S rDNA, 16S-23S rDNA intergenic spacer and family B DNA polymerase
RT genes.";
RL Submitted (OCT-1999) to the EMBL/GenBank/CCBJ databases.
CC -!- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE
CC EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY (BY SIMILARITY).
CC -!- FUNCTION: PI-TSPGE81 AND PI-TSPGE81I ARE ENDONUCLEASES
CC (POTENTIAL).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {ENA}(N).
CC -!- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
CC A POST-TRANSLATIONAL EXCISION OF THE INTERVENING REGION (INTEIN)
CC FOLLOWED BY PEPTIDE LIGATION.
CC -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
CC -!- SIMILARITY: IN THE INTEIN SECTION; BELONGS TO THE HOMING
CC ENDONUCLEASE FAMILY.
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CC -----
DR EMBL; AJ250333; CAC12850.1; -.
DR HSSP; PS6689; ITGO.
DR InterPro; IPR006172; DNA_pol_B.
DR InterPro; IPR006134; DNA_pol_B_dom.
DR InterPro; IPR006133; DNA_pol_B_exo.
DR InterPro; IPR003586; Hedgehog_HintC.
DR InterPro; IPR003587; Hedgehog_HintN.
DR InterPro; IPR006141; INTEIN.
DR InterPro; IPR006142; INTEIN.
DR InterPro; IPR004842; INTEIN_endonuc.
DR InterPro; IPR004578; Pol2.
DR Pfam; PF00136; DNA_pol_B; 3.
DR Pfam; PF03104; DNA_pol_B_exo; 1.
DR PRINTS; PR00379; INTEIN.
DR SMART; SM00305; HintC; 2.
DR SMART; SM00306; HintN; 2.
DR SMART; SM00486; POLBc; 1.
DR TIGRFAMS; TIGR01443; intein_Cterm; 2.
DR TIGRFAMS; TIGR01445; intein_Nterm; 2.
DR TIGRFAMS; TIGR00592; pol2; 2.
DR PROSITE; PS00116; DNA_POLYMERASE_B; FALSE_NEG.
DR PROSITE; PS50818; INTEIN_C_TERM; 2.
DR PROSITE; PS50819; INTEIN_ENDONUCLEASE; 2.
DR PROSITE; PS50817; INTEIN_N_TERM; 2.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Hydrolase; Nuclease; Exonuclease; Multifunctional enzyme;
KW Protein splicing; Autocatalytic cleavage; Endonuclease; Intron homing.
FT CHAIN 1 491 DNA POLYMERASE, 1ST PART.
FT CHAIN 492 1026 ENDONUCLEASE PI-TSPGE81.
FT CHAIN 1027 1075 DNA POLYMERASE, 2ND PART.
FT CHAIN 1076 1464 ENDONUCLEASE PI-TSPGE81I.
FT CHAIN 1465 1699 DNA POLYMERASE, 3RD PART.
SQ SEQUENCE 1699 AA; 197323 MW; F389B4351F0B12D3 CRC64;

Query Match 67.3%; Score 33; DB 1; Length 1699;
Best Local Similarity 77.8%; Pred.No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPFFES 9
| | | |
DB 631 LGLPPEES 639

RESULT 39
YBBA_SCHPO
ID YBBA_SCHPO STANDARD; PRT; 1935 AA.
AC Q60072;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative helicase C13G1.10c (EC 3.6.1.-).
GN SPBC13G1.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Mule S., Mungall K., Murphy L., Niblett D., Odeli C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
```


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OM protein protein search, using sw model

Run on: November 14, 2003, 13:18:40 ; Search time 27 seconds
(without alignments)
86.018 Million cell updates/sec

Title: US-09-736-076-18
Perfect score: 49
Sequence: 1 LGRPPPFETS 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	93.9	316	Q9BDK4	Q9bdk4 sus scrofa
2	46	93.9	372	Q8N7M6	Q8n7m6 homo sapien
3	46	93.9	666	Q90XS4	Q90xs4 xenopus lae
4	46	93.9	682	Q8K226	Q8k226 mus musculu
5	43	87.8	526	Q9BDP8	Q9bdp8 sus scrofa
6	43	87.8	598	P70C32	P70c32 xenopus lae
7	43	87.8	623	Q8IU35	Q8iu35 asterina pe
8	42	85.7	769	Q97143	Q97143 drosophila
9	41	83.7	568	Q8MXG6	Q8mxg6 caenorhabd1
10	41	83.7	749	Q8MXG7	Q8mxg7 caenorhabd1
11	41	83.7	780	Q76360	Q76360 caenorhabd1
12	40	81.6	324	Q9CVR6	Q9cvr6 mus musculu
13	40	81.6	925	Q8R015	Q8r015 mus musculu
14	40	81.6	925	Q64702	Q64702 mus musculu
15	40	81.6	970	Q96Q95	Q96q95 homo sapien
16	40	81.6	970	Q00444	Q00444 homo sapien

17	40	81.6	970	4	Q8IYFC	Q8iyf0 homo sapien
18	39	79.6	80	13	Q91891	Q91891 xenopus lae
19	39	79.6	153	16	O84342	O84342 chlamydia t
20	39	79.6	425	13	Q90XS2	Q90xs2 xenopus lae
21	39	79.6	557	13	Q90XS3	Q90xs3 xenopus lae
22	39	79.6	582	5	Q9GRB7	Q9grb7 hemacentrot
23	38	77.6	434	16	Q8EMI2	Q8emi2 oceanobacil
24	38	77.6	605	10	Q93ZJ9	Q93zj9 arabidopsis
25	38	77.6	656	10	Q9S770	Q9s770 arabidopsis
26	38	77.6	767	5	O15882	O15882 trypanosoma
27	38	77.6	813	5	O76216	O76216 drosophila
28	38	77.6	813	5	Q9VTZ1	Q9vtz1 drosophila
29	37	75.5	301	8	Q950L6	Q950l6 rhizophydiu
30	37	75.5	346	13	Q8JGS8	Q8jgs8 brachydanio
31	37	75.5	582	11	Q8CIE3	Q8cie3 mus musculu
32	37	75.5	779	11	Q8R311	Q8r311 mus musculu
33	36	73.5	123	4	Q9HAB5	Q9hab5 homo sapien
34	36	73.5	256	16	Q9PPA6	Q9ppa6 campylobact
35	36	73.5	257	10	Q8H5W2	Q8h5w2 oryza sativ
36	36	73.5	310	16	Q8PIA4	Q8pia4 xanthomonas
37	36	73.5	321	2	Q93179	Q93179 pseudomonas
38	36	73.5	504	11	Q8K0J7	Q8k0j7 mus musculu
39	36	73.5	646	4	Q96CV1	Q96cv1 homo sapien
40	36	73.5	660	16	Q8FJ15	Q8fuj5 corynebacte
41	36	73.5	1051	12	Q91EU4	Q91eu4 cydia pomon
42	36	73.5	1058	11	Q8BZ02	Q8bz02 mus musculu
43	36	73.5	1207	6	Q9TT98	Q9tt98 sus scrofa
44	36	73.5	1210	4	Q9UHF9	Q9uhf9 homo sapien
45	36	73.5	1308	6	Q9MZF3	Q9mzf3 canis famil

ALIGNMENTS

RESULT 1
Q9BDK4
ID Q9BDK4 PRELIMINARY: PRT: 316 AA.
AC Q9BDK4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Serum-inducible kinase (Fragment).
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Anger M., Kues W.A., Klima J., Motlik J., Carnwath J.W., Niemann H.;
RT "Porcine serum-inducible kinase."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF348424; AAK27154.1; -.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO_box; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50078; POLO_BOX; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER 1
FT NON_TER 316
SQ SEQUENCE 316 AA; 35330 MW; F63BBE4A2691D62F CRC64;

Query Match 93.9%; Score 46; DB 6; Length 316;
Best Local Similarity 98.9%; Pred. No. 0.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPPFETS 9
D5 27 LGRPPPFETT 35

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RESULT 2
Q8N7M6
ID Q8N7M6 PRELIMINARY; PRT; 372 AA;
AC Q8N7M6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created);
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Hypothetical protein FLJ40844.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
GX NCBI TaxID=9606;
RN [1]
PP SEQUENCE FROM N.A.
RC PSSUE-Tianhua;
RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA Matsumura Y., Moriya S., Chiba E., Moriyama H., Onopawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
RA Kuja N., Kuroda A., Satoh I., Karata K., Takami S., Terashima Y.,
RA Watanabe M., Sugiyama T., Irie B., Otsuki T., Sato H., Ota T.,
RA Wakamatsu A., Ishii S., Yamamoto S., Isono Y., Kawai H., Saito K.,
RA Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
RA Sekine M., Kikuchi H., Kanda K., Wajitsuma Y., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
RA "NEDO human cDNA sequencing project";
RC Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DE EMBL: AK098163; FACC5247.1;
DE InterPro: IPR000719; Prot_kinase.
DE InterPro: IPR002290; Ser_thr_kinase.
DE InterPro: IPR001245; Tyr_kinase.
DE Pfam: PF00069; pkinase; 1.
DE PROSITE: PS00001; Prot_kinase; 1.
DE SMART: SM00220; S_TKC; 1.
DE SMART: SM00219; TyrKC; 1.
DE PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DE PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DE PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 372 AA; 42632 MW; 763031F6302A0C09 CRC64;

Query Match 93.9%; Score 46; DB 4; Length 372;
Best Local Similarity 98.9%; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
   |||||
DB 268 LGRPPFFET 276

RESULT 3
Q8KX84
ID Q8KX84 PRELIMINARY; PRT; 682 AA;
AC Q8KX84;
DT 01-DEC-2001 (TrEMBLrel. 19, Created);
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Polo like kinase 2.
OS Xenopus laevis (African clawed frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae.
GX NCBI TaxID=8355;
RN [1]
PP SEQUENCE FROM N.A.
RC MIMBLNE-21481843; PubMed=11591129;
RA Jackson D.L., Pollet N., Niers G., Korn E. A.,
RA "Cloning and Characterization of Flx and Flx2, Two Additional Polo
RA Like Kinases from Xenopus laevis."
RA Exp. Cell Res. 270:78-97(2001);
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
```

```
DR EMBL: AF357840; AAL30175.1; -;
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00659; POLO_box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00078; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 666 AA; 76322 MW; AB4D8F8BDFB5D4FC CRC64;

Query Match 93.9%; Score 46; DB 13; Length 666;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
   |||||
DB 256 LGRPPFFET 264

RESULT 4
Q8K226
ID Q8K226 PRELIMINARY; PRT; 692 AA;
AC Q8K226;
DT 01-OCT-2002 (TrEMBLrel. 22, Created);
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Serum-inducible kinase.
GN SNK.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
GX NCBI TaxID=10090;
RN [1]
PP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC034513; AAH34513.1; -;
DR MGD: MGI:1099790; Snk.
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00659; POLO_box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TyrKC; 1.
DR PROSITE: PS00078; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 692 AA; 77777 MW; 993A65C8DFAFFD95 CRC64;

Query Match 93.9%; Score 46; DB 11; Length 682;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
   |||||
DB 272 LGRPPFFET 280

RESULT 5
Q9BDP8
ID Q9BDP8 PRELIMINARY; PRT; 526 AA;
AC Q9BDP8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created);
```

DR 01 JUN-2003 (TrEMBLrel. 17, Last sequence update)
DT 01 MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Polio-like protein kinase (fragment)
OS Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Mammalia; Euteleostomi
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus
OX NCBI_TaxID:9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Alpert M., Kues W.A., Klima C., Mielenz M., Marik J., Varnath J.W.,
PA Nuemann H.
RT "Expression of Polio-like Kinase in Cell Cycle Synchronized Porcine
BT Fetal Fibroblasts";
PU Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC 1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF339023; AAK285017;
DR HSSP: Q63450; IAC6;
DR InterPro: IPR000959; POLO_BOX;
DR InterPro: IPR000719; Prot_kinase;
DR InterPro: IPR002290; Ser_thr_kinase;
DR Pfam: PF00069; pkinase; 1;
DR Pfam: PF00659; POLO_box; 2;
DR ProDom: PD000001; Prot_kinase; 1;
DR SMART: SM00220; S_TKC; 1;
DR PROSITE: PS50078; POLO_BOX; 2;
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1;
DR PROSITE: PS00109; PROTEIN_KINASE_ST; 1;
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER
FT NON_TER 526 526
SQ SEQUENCE 526 AA; 60399 MW; 1AFALESQ9B2CHB3 CRC64.

Query Match 87.8% Score 43; DB 6; Length 526;
Best local Similarity 77.8% Pred. No. 5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : LGKPPPPETS 9
DB 20: VGRPPPPETS 209

RESULT 4
Q97143
ID 097143 PRELIMINARY; PRT: 209 AA
AC 097143;
DT 01 FEB-1999 (TrEMBLrel. 02, Created)
DT 01 FEB-1999 (TrEMBLrel. 02, Last sequence update)
DT 01 MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fixl.
OS Xenopus laevis (African clawed frog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae
OC Xenophoridae; Xenopus.
OX NCBI_TaxID:9855;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 96355660; PubMed=8703070;
RA Kumagai A., Dunphy W.G.
RT "Purification and molecular cloning of Fixl, a dual regulatory kinase
RI from Xenopus egg extracts";
RI Science 273:1377-1380(1996).
CC 1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U58205; AAC60317;
DR HSSP: Q63450; IAC6;
DR InterPro: IPR000959; POLO_BOX;
DR InterPro: IPR000719; Prot_kinase;
DR InterPro: IPR002290; Ser_thr_kinase;
DR Pfam: PF00069; pkinase; 1;
DR Pfam: PF00659; POLO_box; 2;
DR ProDom: PD000001; Prot_kinase; 1;
DR SMART: SM00220; S_TKC; 1;
DR PROSITE: PS50078; POLO_BOX; 2;

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1;
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1;
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 598 AA; 69211 MW; 2467195911F225E6 CRC64;

Query Match 87.8% Score 43; DB 13; Length 598;
Best local Similarity 77.8% Pred. No. 5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGKPPPPETS 9
DB 237 VGRPPPPETS 245

RESULT 7
Q8IUJ35
ID 08IUJ35 PRELIMINARY; PRT: 623 AA
AC 08IUJ35;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Polio-like kinase.
GN PLK.
OS Asterina pectinifera (Starfish).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
OX NCBI_TaxID:7594;
RN [1]
RP SEQUENCE FROM N.A.
RA Uchida T.O., Tachibana K., Kishimoto T.;
RT "Starfish Plk.";
RI Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB084469; BAC226921;
KW Kinase.
SQ SEQUENCE 623 AA; 70929 MW; CPD1900802D724A CRC64;

Query Match 87.8% Score 43; DB 5; Length 623;
Best local Similarity 77.8% Pred. No. 5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGKPPPPETS 9
DB 222 VGRPPPPETS 240

RESULT 8
Q97143
ID 097143 PRELIMINARY; PRT: 269 AA
AC 097143;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SAK protein.
GN SAK OR CG7186.
OS Drosophila melanogaster (Fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID:7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandel M.D., Zhang C., Chen J.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter S.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrahams J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballaw R.M., Bass A., Baxendale J., Bayraktaroglu L., Beasley E.V.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Sorkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablos B., DeCher A., Deng Z., Mays A.D., Dew J., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Recha S., Dunkov B.C., Dunn P.,
RA Forbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan F., Harria M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.K., Houck J.,
RA Heston D., Houston K.A., Howland T.G., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison C.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Jasko P., Lei Y., Levitsky A.A., Li D., Li Z., Liang Y., Lin X.,
RA Liu X., Maitei P., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milisina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy J., Muzny D., Nelson D.,
RA Nelson C.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders P.D.C., Scheeler S., Shen H.,
RA Shue B.C., Sinden-Kiaros I., Simpson X., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao W., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
ET "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN (2)
RP SEQUENCE FROM N.A.
RA Hudson J.W., Dennis J.W.,
RI Submitted (NCV-1998) to the EMBL/GenBank/DBJ databases.
RI EXBL: AEO03594; AAF51737.1;
RI EXBL: AE106952; AAD19607.1;
RI ESSE, P00518; IEHK.
RI FlyBase: FBgn026171; SAK.
RI InterPro: IPR000959; POLO_box.
RI InterPro: IPR000719; Prot_kinase.
RI InterPro: IPR022290; Ser_thr_kinase.
RI InterPro: IPR001245; Tyr_kinase.
RI Pfam: PF00369; pkinase; 1.
RI PRINTS: PRC0109; TYRKINASE.
RI PRODom: PDC00001; Prot_kinase; 1.
RI SMART: SM00220; S_TK_X; 1.
RI PROSITE: PS00378; POLO_BOX; 1.
RI PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
RI PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
RI PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 769 AA; 85866 MW; F050BF6A5034AA4 CRC64;

Query Match 85.7%; Score 41; DB 5; Length 260;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
DB 204 VGRPPFET 215
RESULT 9
Q8MXG6 PRELIMINARY; PRT; 258 AA.
AC Q8MXG6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE EGL-4 protein (corresponding sequence F55A8.2d).
GN F55A8.2 OR EGL-4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Langston Y., Wehlmann P., Duckels G.;
RT "The sequence of C. elegans cosmid F55A8.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RI Submitted (AJG-2002) to the EMBL/GenBank/DBJ databases.
RI EMBL: AF067612; AAY9831.1;
RI WormPep; F55A8.2d; CE1542.
RI InterPro: IPR002373; cAMP_kin.
RI InterPro: IPR002374; cAMP_kin.
RI InterPro: IPR000595; cAMP_binding.
RI InterPro: IPR000961; pkinase_C.
RI InterPro: IPR000719; Prot_kinase.
RI InterPro: IPR02290; Ser_thr_kinase.
RI InterPro: IPR001245; Tyr_kinase.
RI Pfam: PF00369; pkinase; 1.
RI Pfam: PF00369; pkinase; 1.
RI PRINTS: PRC0433; pkinase_C; 1.
RI PRINTS: PRC0103; CAMPKINASE.
RI PRINTS: PRC0104; CGMPKINASE.
RI PRODom: PDC00001; Prot_kinase; 1.
RI SMART: SM00100; cNVP; 1.
RI SMART: SM00220; S_TK_X; 1.
RI SMART: SM00133; S_TK_X; 1.
RI SMART: SM00219; TyRK; 1.
RI PROSITE: PS00888; cNVP_BINDING_1; 1.
RI PROSITE: PS00889; cNVP_BINDING_2; 1.
RI PROSITE: PS00342; cNVP_BINDING_3; 2.
RI PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
RI PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
RI PROSITE: PS00108; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 568 AA; 65094 MW; 423AB3BD6E52ACF4 CRC64;
Query Match 83.7%; Score 41; DB 5; Length 568;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
DB 450 LGRPPFQAS 458

RESULT 10
Q8MXG7 PRELIMINARY; PRT; 749 AA.
AC Q8MXG7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE EGL-4 protein (corresponding sequence F55A8.2c).
GN F55A8.2 OR EGL-4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;


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RC TISSUE=Blood;
RX MEDLINE=21486437; PubMed=21489907;
RA Yamashita Y., Kajiigaya S., Yoshida K., Ueno S., Ota J., Ohnise K.,
RA Jeda M., Miyazato A., Ohya K., Kitamura T., Ozawa K., Mano H.;
RT "Sak Serine-Threonine Kinase Acts as an Effector of Tec Tyrosine
RT Kinase";
RL J. Biol. Chem. 276:39012-39020(2001)
DR EXBL: AB006972; BAB69958.1;
DR HSSP: P24941; 1BJH;
DR InterPro: IPR000959; POLO_BOX;
DR InterPro: IPR000719; Prot_kinase;
DR InterPro: IPR002293; Ser_thr_kinase;
DR InterPro: IPR001245; Tyr_pkinase;
DR Pfam: PF00069; pkinase; 1;
DR PRINTS: PS00109; TYRKINASE;
DR PRODOM: PDC00001; Prot_kinase; 1;
DR SMART: SM0220; S_TKC; 1;
DR PROSITE: PS00078; POLO_BOX; 1;
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1;
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1;
DR ATP-binding; Transferase;
KW SEQUENCE 970 AA; 109084 MW; 1F431FA607A1550A CRC64;

Query Match 81.6%; Score 40; DB 4; Length 970;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRRPFET 8
DB 206 IGRPPFDI 213

RESULT 18
Q91891 PRELIMINARY; PRT; 970 AA.
AC Q91891;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 9.4 kDa protein (Fragment);
OS Xenopus laevis (African clawed frog);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus;
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Bouvet P., Omilli F., ARLOT-BONNEVAIN Y., Legagneux V., Roghi C.,
RA Bassez T., OSBORNE H.;
RT "Deadenylation conferred by the 3'Untranslated region of a
RT developmentally controlled mRNA in xenopus embryos is switched to
RT polyadenylationby deletion of a short sequences element.";
RL Mol. Cell. Biol. 14:1893-1900(1995);
DR EMBL: Z24453; CAA80826.1;
DR InterPro: IPR000719; Prot_kinase;
DR Pfam: PF00069; pkinase; 1;
DR PRODOM: PDC00001; Prot_kinase; 1;
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1;
KW Hypothetical protein; ATP-binding; Transferase;
FT NON_TER 1
SQ SEQUENCE 80 AA; 9388 MW; 8DFCEDBA14BE14FB CRC64;

Query Match 79.6%; Score 39; DB 13; Length 80;
Best Local Similarity 75.0%; Pred. No. 4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRRPFET 8
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RC TISSUE=Blood;
RX MEDLINE=21486437; PubMed=21489907;
RA Yamashita Y., Kajiigaya S., Yoshida K., Ueno S., Ota J., Ohnise K.,
RA Jeda M., Miyazato A., Ohya K., Kitamura T., Ozawa K., Mano H.;
RT "Sak Serine-Threonine Kinase Acts as an Effector of Tec Tyrosine
RT Kinase";
RL J. Biol. Chem. 276:39012-39020(2001)
DR EXBL: AB006972; BAB69958.1;
DR HSSP: P24941; 1BJH;
DR InterPro: IPR000959; POLO_BOX;
DR InterPro: IPR000719; Prot_kinase;
DR InterPro: IPR002293; Ser_thr_kinase;
DR InterPro: IPR001245; Tyr_pkinase;
DR Pfam: PF00069; pkinase; 1;
DR PRINTS: PS00109; TYRKINASE;
DR PRODOM: PDC00001; Prot_kinase; 1;
DR SMART: SM0220; S_TKC; 1;
DR PROSITE: PS00078; POLO_BOX; 1;
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1;
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1;
DR ATP-binding; Transferase;
KW SEQUENCE 970 AA; 109084 MW; 1F431FA607A1550A CRC64;

Query Match 81.6%; Score 40; DB 4; Length 970;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRRPFET 8
DB 206 IGRPPFDI 213

RESULT 17
Q81YFC PRELIMINARY; PRT; 970 AA.
ID Q81YFC;
AC Q81YFC;
DI 01-MAR-2003 (TREMBLrel. 23, Created)
DI 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DI 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Similar to serine/threonine protein kinase.
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC036023; AAH36023.1;
KW Kinase; Serine/threonine-protein kinase;
SQ SEQUENCE 970 AA; 108971 MW; 4D56F5FD983211A6 CRC64;

Query Match 81.6%; Score 40; DB 4; Length 970;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRRPFET 8
DB 206 IGRPPFDI 213

RESULT 18
Q91891 PRELIMINARY; PRT; 80 AA.
ID Q91891;
AC Q91891;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 9.4 kDa protein (Fragment);
OS Xenopus laevis (African clawed frog);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus;
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Bouvet P., Omilli F., ARLOT-BONNEVAIN Y., Legagneux V., Roghi C.,
RA Bassez T., OSBORNE H.;
RT "Deadenylation conferred by the 3'Untranslated region of a
RT developmentally controlled mRNA in xenopus embryos is switched to
RT polyadenylationby deletion of a short sequences element.";
RL Mol. Cell. Biol. 14:1893-1900(1995);
DR EMBL: Z24453; CAA80826.1;
DR InterPro: IPR000719; Prot_kinase;
DR Pfam: PF00069; pkinase; 1;
DR PRODOM: PDC00001; Prot_kinase; 1;
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1;
KW Hypothetical protein; ATP-binding; Transferase;
FT NON_TER 1
SQ SEQUENCE 80 AA; 9388 MW; 8DFCEDBA14BE14FB CRC64;

Query Match 79.6%; Score 39; DB 13; Length 80;
Best Local Similarity 75.0%; Pred. No. 4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRRPFET 8
```


RA Yonemura I., Fujimoto H., Mabuchi I.;
 PT "Cloning of sea urchin pik.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RC [2]
 RP SEQUENCE FROM N.A.
 RA Yonemura I., Fujimoto H., Mabuchi I.;
 PT "Cloning of sea urchin polo-like kinase.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CR EMBL: AB043897; BAB18588.1;
 DR InterPro: IPR001395; Aldo/ket red.
 DR InterPro: IPR000959; POLO_box.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00659; POLO_box; 2.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00063; ALDO-KETO-REDUCTASE_3; 1.
 DR PROSITE: PS00078; POLO_BOX; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 582 AA; 66429 MW; A3774ACCAACPFDESD CRC64;

Query Match 79.6%; Score 29; DB 5; Length 582;
 Best Local Similarity 75.0%; Pred. No. 29;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
 |||||
 DB 220 VGRPPFET 227

RESULT 23
 Q8EM12 PRELIMINARY; PRT; 434 AA
 AC Q8EM12;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE C4-dicarboxylate transporter.
 GN CR2840.
 OS Oceanobacillus thelyensis.
 OC Bacteria; Firmicutes; Bacillales; Clostridiales
 CC NCBI TaxID=152710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HTE831 / DSM 14371 / JCM 11374;
 RX MEDLINE=22220767; PubMed=12235376;
 RA Takaki H., Takaki Y., Uchiyama I.;
 RT "Genome sequence of Oceanobacillus thelyensis isolated from the Iheya
 Ridge and its unexpected adaptive capabilities to extreme
 environments";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 DR EMBL: AP004602; BAC14816.1;
 KW Complete proteome.
 SQ SEQUENCE 434 AA; 46688 MW; C8DAE6500F954BEE CRC64;

Query Match 77.6%; Score 38; DB 16; Length 434;
 Best Local Similarity 77.8%; Pred. No. 34;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
 |||||
 DB 49 LGRTPFETS 57

RESULT 24
 Q93ZJ9 PRELIMINARY; PRT; 605 AA
 ID Q93ZJ9
 AC Q93ZJ9;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Atig80000/F19K16.3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesera E., Meyers M.C., Banh C.,
 RA Bowser C., Carninci P., Dale G.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY057486; AAL09720.1;
 SQ SEQUENCE 605 AA; 65693 MW; 7FF61B6C323EE41F CRC64;

Query Match 77.6%; Score 38; DB 10; Length 605;
 Best Local Similarity 77.8%; Pred. No. 48;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
 |||||
 DB 271 LGRPPPTETA 279

RESULT 25
 Q9S770 PRELIMINARY; PRT; 656 AA
 AC Q9S770;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE F19K16.3 protein.
 GN F19K16.3 OR F18B13.5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia.
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
 RA Maiti R., Renning C.M., Koo H., Fujii C.Y., Utterback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome 1 BAC F19K16 genomic sequence";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Altarfi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
 RA Gonzalez A., Kremenetskaia I., Kim C., Ienz C., Li J., Liu S.,
 RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
 RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC009322; AAC55481.1;
 SQ SEQUENCE 656 AA; 71630 MW; C7F04A188ACEA410 CRC64;

Query Match 77.6%; Score 38; DB 10; Length 656;
 Best Local Similarity 77.8%; Pred. No. 52;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
 |||||

DB 271 LGRPPFETA 279

RESULT 26
Q15882

ID Q15882 PRELIMINARY; PRT; 813 AA.
AC Q15882
DT 01-JAN-1998 (TrEMBLrel. 35, Created)
DI 01-JAN-1998 (TrEMBLrel. 35, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 23, Last annotation update)
DE Polo-like protein kinase (Fragment)
GN PLK.

OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN STIB247;
RX XELLINE:98172736; PubMed=9511745;
RA Graham T.M., Tail A., Hide G.,
RT "Characterisation of a polo-like protein kinase gene homologue from an
evolutionary divergent eukaryote, Trypanosoma brucei",
RL Gene 207:71-77(1998).

.. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DB EMBL: Y13969; CAA74301.1; -
DR InterPro: IPR000959; POLO_BOX.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR022903; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF03659; POLO_BOX; 2.
DR PRINTS: PR0109; TYRKINASE.
DR PRODOM: PD02001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00649; POLO_BOX; 2.
DR PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
ST MW 78 767
SQ SEQUENCE 767 AA; 86823 MW; 8960E253P1F4D41 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 157;
Best Local Similarity 66.7%; Pred. No 65;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9

DB 236 VSSPPFQTS 244

RESULT 27
Q76216

ID Q76216 PRELIMINARY; PRT; 813 AA.
AC Q76216
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE GN5.
GN PCAF OR GN5 OR CG4107.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=99278910; PubMed=9611240;
RA Smith E.R., Belote C.M., Schlotz R.D., Yabu X., Yoon E.A.,
RA Berner S.L., Nakatani Y., Allis C.D.,
RT "Cloning of Drosophila GN5: conserved features among metazoan GN5
family members",
RC Nucleic Acids Res. 26:2948-2954(1998)

DR EMBL: AF029776; AAC39102.1;
DR HSSP: Q03330; 1YGH.
DR FlyBase: FBgn020388; Pcaf.
DR InterPro: IPR001487; Bromodomain.
DR InterPro: IPR000182; GN5acetyltransf.
DR Pfam: PF00583; Acetyltransf; 1.
DR Pfam: PF00439; bromodomain; 1.
DR PRINTS: PROC503; BROMODOMAIN.
DR SMART: SM00297; BROMO; 1.
DR PROSITE: PS50014; BROMODOMAIN_2; 1.
SQ SEQUENCE 813 AA; 92095 MW; 7983E218CB898D93 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 813;
Best Local Similarity 87.5%; Pred. No 65;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPPFET 8

DB 208 LGDPPFET 215

RESULT 28

Q9VTZ1

ID Q9VTZ1 PRELIMINARY; PRT; 813 AA.
AC Q9VTZ1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE PCAF protein (GH11602p).
GN PCAF OR CG4107.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yeandle M.D., Zhang Q., Chen L.X.,
RA Brandon P.C., Rogers Y.H., Blazer V.G., Champe M., Pfeiffer A.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abit C.F., Agbayani A., An H., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bengtson P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.E., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaisli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matter B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Ye R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

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BA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
BA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RF SEQUENCE FROM N.A.
RC STRAIN Berkeley.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Chang M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Murgail C.,
RA Munro J., Paclet J., Paragas V., Park S., Prouncharvong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Gainer S.,
RL Submitted (DEC-2001) to the EMBL/GenBank/CDR databases.
DR EMBL: AEC03541; AAF49904.1;
DR EMBL: AYC69097; AAL39242.1;
DR HSSP: Q03330; IYGH.
DR FlyBase: FBgn020388; Pcaf.
DR InterPro: IPR001487; Bromodomain.
DR InterPro: IPR003182; GCN5acetyltransf.
DR Pfam: PF00583; Acetyltransf.;
DR Pfam: PF00439; Bromodomain;
DR PRINTS: PRO0503; BROMODOMAIN.
DR SMART: SM00297; BROMO;
DR PROSITE: PS0014; BROMODOMAIN_2;
SQ SEQUENCE 813 AA; 92169 MW; 0810E9FFB1BCC02A5 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 813;
Best Local Similarity 87.5%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : LGRPPPFET 8
DB 208 LGRPPPFET 215

RESULT 30
Q95016
ID Q95016 PRELIMINARY; PRT; 171 AA.
AC Q95016;
DT 01-DEC-2001 (TrEMBLrel. 19, Created);
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update);
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update);
DE NADH dehydrogenase subunit 1 (EC 1.6.1.3) (NADH dehydrogenase
DE oxidoreductase chain 1);
GN NAD1.
OS Rhizophidium sp. 136.
OC Mitochondrion.
OC Eukaryota; Fungi; Chytridiomycota; Chytridiales; Chytridiaceae;
OC Rhizophidium.
OX NCBI_TaxID=60187;
RN [1]
RF SEQUENCE FROM N.A.
RC STRAIN=136;
RA Forget L., Ostinova Z., Wang Z., Huss V.A.R., Laroche B.F.;
RT "Hyalaraphidium curvatum: a linear mitochondrial genome, tRNA editing,
RT and an evolutionary link to lower fungi";
RL Mol. Biol. Evol. 01:01(2001).
RN [2]
RF SEQUENCE FROM N.A.
RC STRAIN=136;
RA Wang B.B.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/CDR databases.
CC -||- CATALYTIC ACTIVITY: NADH + URICININE + NAD(+) + URICINOL.
CC -||- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
DR EMBL: AF404306; AAK84292.1;
DR InterPro: IPR001694; Resp_NADH_dhl.
DR Pfam: PF00146; NADHdh;
KW NAD; Oxidoreductase; Transmembrane; (biquinone) Mitochondrion.
SQ SEQUENCE 301 AA; 33286 MW; ED58105053EF41D5 CRC64;

Query Match 75.5%; Score 37; DB 8; Length 301;
Best Local Similarity 85.2%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY : LGRPPFE 7
DB 194 LGRPPFD 200

RESULT 30
Q8JGS8
ID Q8JGS8 PRELIMINARY; PRT; 346 AA.
AC Q8JGS8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created);
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Aurora-like serine/threonine kinase (Fragment).
GN STKA.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RF SEQUENCE FROM N.A.
RX MEDLINE=22035902; PubMed=12006978;
RA Golling G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,
RA Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y., Nissen R.M.,
RA Hopkins N.;
RT "Insertional mutagenesis in zebrafish rapidly identifies genes
RT essential for early vertebrate development.";
RL Nat. Genet. 31:135-140(2002).
DR EMBL: AY099518; AAM28206.1;
DR InterPro: IPR002052; N6_Mtase.
DR InterPro: IPR003719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; pkinase;
DR PRINTS: PRO0109; TYRKINASE.
DR PRODOM: PD000001; Prot_kinase;
DR SMART: SM00220; S_TKc;
DR SMART: SM00219; TYRKc;
DR PROSITE: PS00092; N6_MTASE;
DR PROSITE: PS00107; PROTEIN_KINASE_ATP;
DR PROSITE: PS00011; PROTEIN_KINASE_DOM;
DR PROSITE: PS00108; PROTEIN_KINASE_ST;
KW ATP-binding; Kinase; Transferase.
FT NON TER 1
SQ SEQUENCE 346 AA; 39977 MW; 08A2CEC221C7C2D9 CRC64;

Query Match 75.5%; Score 37; DB 13; Length 346;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY : LGRPPPFET 8
DB 270 VGNPPFET 277

RESULT 31
Q8CIE3
ID Q8CIE3 PRELIMINARY; PRT; 582 AA.
AC Q8CIE3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created);
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RF SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Straussberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/CDR databases.

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DR  BMRB; BC024076; AAH24076.1; ...
KW  Hypothetical protein.
FT  NON_TER
SQ  SEQUENCE 582 AA; 65262 MW; 2A54742V247FAD99 CRC64;

Query Match
Best Local Similarity 75.5%; Score 37; DB 11; Length 582;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGPPPPET 8
DB 305 LGPPPPSET 312

RESULT 32
Q8R311
ID Q8R311 PRELIMINARY; PRT; 779 AA.
AC Q8R311.
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to meningioma expressed antigen 6 (colloid-coil proline-rich).
DE rich).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.
RC Submitted (APR 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024076; AAH26864; 779 AA; 87218 MW; 07F5FC98B3B3D8 CRC64;
SQ SEQUENCE 779 AA; 87218 MW; 07F5FC98B3B3D8 CRC64;

Query Match
Best Local Similarity 75.5%; Score 37; DB 11; Length 582;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGPPPPET 8
DB 502 LGPPPPSET 509

RESULT 33
Q8HAB6
ID Q8HAB6 PRELIMINARY; PRT; 123 AA.
AC Q8HAB6;
DT 01-MAR-2003 (TrEMBLrel. 16, Created)
DT 01-MAR-2003 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homini; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Issige T., Chu T., Hayashi K., Sugiyama T., Otsuki Y., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi F., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara H., Takeuchi K., Arita Y., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto S., Wakamatsu A., Nakamura Y., Nagahara F., Masuda Y., Shimada A.
RC "NEO Human cDNA sequencing project".
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK021912; BAB1934.1; ...
KW Hypothetical protein.
SQ SEQUENCE 123 AA; 13743 MW; 5C4C04E675143D8 CRC64;

Query Match
Best Local Similarity 73.5%; Score 36; DB 16; Length 123;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 LGPPPPET 8
DB 72 LGPPPPSET 79

RESULT 34
Q9PPA6
ID Q9PPA6 PRELIMINARY; PRT; 256 AA.
AC Q9PPA6;
DT 01-OCT-2003 (TrEMBLrel. 15, Created)
DT 01-OCT-2003 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Glutamine-binding periplasmic protein.
DE GLNH OR CJ0817.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales; Campylobacteraceae; Campylobacter.
CX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream V.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences."
RL Nature 403:665-669 (2000)
DR EMBL; AL139076; CAB73082.1; ...
DR HSSP; P10344; IWDN.
DR InterPro; IPR001311; SBP/glu receptor.
DR InterPro; IPR001638; SBP_bac_3.
DR Pfam; PF00497; SBP_bac_3; ...
DR SMART; SMCC062; PBpb; ...
KW Complete proteome.
SQ SEQUENCE 256 AA; 28913 MW; 6CD44DDE6AF019DF CRC64;

Query Match
Best Local Similarity 73.5%; Score 36; DB 16; Length 256;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGPPPPET 8
DB 27 LGPPPPFEMS 35

RESULT 35
Q8HSW2
ID Q8HSW2 PRELIMINARY; PRT; 257 AA.
AC Q8HSW2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE C11123_B01.20 protein.
DE C11123_B01.20.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
CX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC clone:OJ1123_B01.1".
RL Submitted (JUN 2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003745; BAB1925.1; ...
SQ SEQUENCE 257 AA; 26262 MW; 9A5B78473E265DBA CRC64;

Query Match
Best Local Similarity 73.5%; Score 36; DB 10; Length 257;

```


CS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.
RI submitted (SEP-2001) to the EMBL/GenBank/CDR databases.
CC 111 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DE EMBL: ACC13899; AAH13899.1; ...
DE InterPro: IPR000959; POLO_BOX.
DE InterPro: IPR000719; Prot_kinase.
DE InterPro: IPR002290; Ser_thr_kinase.
DE Pfam: PF00669; pkinase; 1.
DE Pfam: PF00659; POLO_box; 2.
DE ProDom: PDC00001; Prot_kinase; 1.
DE SMART: SMC0220; S_TKC; 1.
DE PROSITE: PSS0078; POLO_BOX; 2.
DE PROSITE: PSS0107; PROTEIN_KINASE_ATP; 1.
DE PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
DE PROSITE: PSS0108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase;
SQ SEQUENCE 646 AA; 71628 MW; 1247ALQD9C08655E CDS-4.

Query Match 73.5%; Score 16; DB 4; Length 646;
Best Local Similarity 75.0%; Pred. No. 134-02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPFFTS 9
DB 256 GSPFFETA 263

RESULT 40
QUERY
ID GRPFFTS PRELIMINARY; PRT; 600 AA
AC GRPFFTS
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative serine/threonine protein kinase.
UN CDS-4.
CS Corynebacterium efficiens.
CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
CC Corynebacteriaceae; Corynebacterium; Corynebacterium
CX NPI_TaxID=152794;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-Y5-314 / AJ 12310 / DSM 44547 / JCM 11169.
RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikee K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.
RT "The entire genomic sequence of Corynebacterium efficiens Y5-314."
RI Submitted (MAY-2002) to the EMBL/GenBank/CDR databases.
DE EMBL: APC05214; BAC16843.1; ...
KW Kinase; Complete proteome.
SQ SEQUENCE 660 AA; 69646 MW; D33D197EB02L4451 CDS-4;

Query Match 73.5%; Score 16; DB 16; Length 660;
Best Local Similarity 100.0%; Pred. No. 134-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
DB 210 GRPFFE 215

GenCore version 5.1.6
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OK protein protein search, using sw model

Run on: November 14, 2003, 14:14:16 / Search time 41 Seconds
without alignment
42,568 Million cell updates/sec

Title: US-09-736-076 19
Perfect score: 58
Sequence: 1 MLISSPPPTTS 11

Scoring table: BiGUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 156726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :		A Geneseq 19Jun03:*	
1:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1980.DAT:	1:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1980.DAT:
2:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1981.DAT:	2:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1981.DAT:
3:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1982.DAT:	3:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1982.DAT:
4:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1983.DAT:	4:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1983.DAT:
5:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1984.DAT:	5:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1984.DAT:
6:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1985.DAT:	6:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1985.DAT:
7:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1986.DAT:	7:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1986.DAT:
8:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1987.DAT:	8:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1987.DAT:
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11:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1990.DAT:	11:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1990.DAT:
12:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1991.DAT:	12:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1991.DAT:
13:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1992.DAT:	13:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1992.DAT:
14:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1993.DAT:	14:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1993.DAT:
15:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1994.DAT:	15:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1994.DAT:
16:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1995.DAT:	16:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1995.DAT:
17:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1996.DAT:	17:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1996.DAT:
18:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1997.DAT:	18:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1997.DAT:
19:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1998.DAT:	19:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1998.DAT:
20:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1999.DAT:	20:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA1999.DAT:
21:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA2000.DAT:	21:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA2000.DAT:
22:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA2001.DAT:	22:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA2001.DAT:
23:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA2002.DAT:	23:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA2002.DAT:
24:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA2003.DAT:	24:	/SIDSL/gcgdata/geneseq/geneseq-emb/AA2003.DAT:

Note: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	58	100.0	11	20	AAW74163
2	58	100.0	11	23	AAU98319
3	55	94.8	469	22	AAB94717
4	55	94.8	469	22	AAG67426
5	55	94.8	685	20	AAU98319
6	55	94.8	685	20	AAU98319
7	55	94.8	685	23	ABP61414
8	55	94.8	753	23	ABP41912
9	52	89.7	626	21	AAB15805

10	49	84.5	9	20	AAW74162	HJ loop peptide J-
11	49	84.5	9	20	AAW74159	HJ loop peptide J-
12	49	84.5	9	23	AAU98315	Polo kinase serine
13	49	84.5	9	23	AAU98318	Polo kinase serine
14	49	84.5	10	20	AAW74213	HJ loop peptide KO
15	49	84.5	10	23	AAU98357	Polo kinase SNK se
16	49	84.5	20	20	AAW74173	HJ loop peptide PO
17	49	84.5	20	23	AAU98306	Peptide sequence o
18	49	84.5	229	21	AAB56690	Human prostate can
19	49	84.5	531	23	AAU74656	Mammalian polo-lik
20	49	84.5	603	16	AAU74620	Human lung tumour
21	49	84.5	603	23	AAU79306	Mouse polo-like k:
22	49	84.5	603	23	AAU79308	Mouse polo-like k1
23	49	84.5	603	23	AAU79309	Mouse polo-like k1
24	49	84.5	603	23	AAU79310	Mouse polo-like k1
25	49	84.5	603	23	AAU79311	Mouse polo-like k1
26	49	84.5	603	23	AAU79312	Mouse polo-like k1
27	49	84.5	603	23	AAU79313	Mouse polo-like k1
28	49	84.5	603	23	AAU79314	Mouse polo-like k1
29	49	84.5	603	23	AAU79315	Mouse polo-like k1
30	49	84.5	603	23	AAU79316	Mouse polo-like k1
31	49	84.5	603	23	AAU79317	Mouse polo-like k1
32	49	84.5	603	23	AAU79318	Mouse polo-like k1
33	49	84.5	603	23	AAU79319	Mouse polo-like k1
34	49	84.5	603	23	AAU79320	Mouse polo-like k1
35	49	84.5	603	24	ABR48196	Human bladder canc
36	48	82.8	769	22	ABB63067	Drosophila melanog
37	46	79.3	9	20	AAW74161	HJ loop peptide J-
38	46	79.3	9	23	AAU98317	Polo kinase serine
39	46	79.3	416	17	AAU92176	Sak serine-threoni
40	46	79.3	464	17	AAU92214	SAK-b serine-threo
41	46	79.3	925	17	AAU92177	SAK-a serine-threo
42	46	79.3	925	23	ABB57273	Mouse ischaemic co
43	46	79.3	970	22	AAU78833	Human protein SEQ
44	46	79.3	970	22	AAU79244	Human polypeptide
45	46	79.3	980	22	AAU79817	Human protein SEQ

ALIGNMENTS

RESULT 1
AAW74163
ID AAW74163 standard, peptide: 11 AA.

XX	AC	AAW74163:			
XX	DT	CS-XAY-1999 (first entry)			
XX	XX	HJ loop peptide J-46.			
XX	XX	HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;			
XX	XX	haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;			
XX	XX	inflammatory disorder; central nervous system disease; septic shock;			
XX	XX	Parkinson's disease; hypertension.			
XX	OS	Synthetic.			
XX	XX	Key	Location/Qualifiers		
XX	XX	Modified-site	1		
XX	XX	Modified-site	11	/note= "acetylated"	
XX	XX	Modified-site	11	/note= "amidated"	

XX	PN	W09853050-A2.			
XX	XX	26-NOV-1998.			
XX	XX	20-MAY-1998;	98WG US10319.		
XX	XX	21-MAY-1997;	97US 3861338.		
XX	PA	(CHILD) CHILDRENS MEDICAL CENT.			

PA YISSI : YISSUM RES & DEV CO.
XX
PI Ben Sasson SA;
XX
XX WPI; 1999 070142/06.
XX
XX New peptides for modulating serine/threonine kinase activity -
PI comprise a sequence corresponding to the HJ loop of a
PI serine/threonine kinase, used for treating, e.g. cancers,
PI inflammatory disorders or autoimmune disorders
XX
XX Claim 14; Fig 4; 20pp; English.
XX
XX This sequence represents a peptide of the invention, and is a derivative
XX of the HJ loop of a serine/threonine kinase (STK). The peptides can be
XX used for the treatment of disorders caused by overactivity or
XX underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
XX shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
XX arteriosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and
XX hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
XX psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
XX of organ transplant rejection, multiple sclerosis, inflammatory bowel
XX disease and AIDS), central nervous system diseases (e.g. Alzheimer's
XX disease, stroke and trauma), septic shock, Parkinson's disease or
XX hypertension. The peptides can also be used to produce antibodies which
XX can be used to identify cells expressing the STK and to study the
XX intracellular distribution of the STK. In addition, the peptides can be
XX used to identify and quantitate ligands which bind the HJ loop of the STK
XX from which the peptide was derived
XX
XX Sequence 11 AA;
SQ

Query Match 100.0%; Score 58; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPETS 11
DB |||||
1 MLLGRPPETS 11

RESULT 2
AAB94717
ID AAB94717 standard; Protein: 469 AA.
XX
AC AAB94717;
XX
DT 26-JUN 2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:15726.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI; 2001-318749/34.
XX

PA YISSI : YISSUM RES & DEV CO.
XX
PI Ben Sasson SA;
XX
XX WPI; 1999 070142/06.
XX
XX New peptides for modulating serine/threonine kinase activity -
PI comprise a sequence corresponding to the HJ loop of a
PI serine/threonine kinase, used for treating, e.g. cancers,
PI inflammatory disorders or autoimmune disorders
XX
XX Claim 14; Fig 4; 20pp; English.
XX
XX This sequence represents a peptide of the invention, and is a derivative
XX of the HJ loop of a serine/threonine kinase (STK). The peptides can be
XX used for the treatment of disorders caused by overactivity or
XX underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
XX shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
XX arteriosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and
XX hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
XX psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
XX of organ transplant rejection, multiple sclerosis, inflammatory bowel
XX disease and AIDS), central nervous system diseases (e.g. Alzheimer's
XX disease, stroke and trauma), septic shock, Parkinson's disease or
XX hypertension. The peptides can also be used to produce antibodies which
XX can be used to identify cells expressing the STK and to study the
XX intracellular distribution of the STK. In addition, the peptides can be
XX used to identify and quantitate ligands which bind the HJ loop of the STK
XX from which the peptide was derived
XX
XX Sequence 11 AA;
SQ

Query Match 100.0%; Score 58; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPETS 11
DB |||||
1 MLLGRPPETS 11

RESULT 2
AAB94717
ID AAB94717 standard; Peptide: 11 AA.
XX
AC AAB94717;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human kinase serine-threonine kinase protein; protein: 469.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
XX central nervous system disorder; inflammatory disorder;
XX autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
XX lipid metabolism; cytostatic; antidiabetic; anesthetic; neurological;
XX antiinflammatory; immunosuppressive; cardiac; haemostatic;
XX modulating STK activity; polo kinase; J-46.
XX
CS Unidentified.
CS Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX /note= "N-terminal acetyl"
XX
XX Mismatch-difference 9
XX /note= "Benzyl ester of glutamic acid"
XX
XX Modified-site 11
XX /note= "C-terminal acetyl"
XX
XX OS Homo sapiens.
XX
XX WPI; 2001-318749/34.
XX
XX 25-APR-2002.
XX

as leukemia, solid tumour cancers and metastases, chronic inflammatory proliferative diseases such as psoriasis and rheumatoid arthritis, proliferative cardiovascular diseases such as restenosis, proliferative ocular disorders such as diabetic retinopathy and benign hyperproliferative diseases such as haemangiomas. The polynucleotides can be used as hybridisation probes for cDNA and genomic DNA or as primers for a nucleic acid amplification (PCR) reaction, to isolate full-length cDNAs and genomic clones encoding polypeptides of this invention and to isolate cDNA and genomic clones of other genes which have a high sequence similarity to the SNK coding sequence. The differences between cDNA and genomic sequences can be observed and therefore mutations detected. Any mutations may then be attributed to likely causative agents of disease. The nucleotide sequences are also useful for chromosome identification.

XX Sequence 685 AA;

Query Match 94.8%; Score 55; DB 20; Length 685;
Best Local Similarity 90.9%; Pred. No. 0.11;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFPETS 11
DB 273 MLLGRPPFPET 283

RESULT 6
AAW88412
ID AAW88412 standard; Protein; 685 AA;
XX
AC AAW88412;
XX

24 APR 1999 (first entry)

Disease associated protein kinase (DAPK-1).

DAPK-1; disease associated protein kinase; human; diagnosis; therapy; adult respiratory distress syndrome; allergy; asthma; arteriosclerosis; bronchitis; emphysema; hyper eosinophilia; myocardial inflammation; pericardial inflammation; anaemia; rheumatoid arthritis; Addison's disease; AIDS; atherosclerosis; atopic dermatitis; dermatomyositis; diabetes mellitus; glomerulonephritis; gout; Grave's disease; lupus erythematosus; multiple sclerosis; myasthenia gravis; osteoarthritis; osteoporosis; pancreatitis; polycystic kidney disease; polymyositis; scleroderma; Sjogren's syndrome; autoimmune thyroiditis; cancer; infection; trauma; cell proliferation.

XX Homo sapiens

XX Key Location/Qualifiers

XX Binding site 89..96

XX /note= "potential AIP binding site"

XX Peptide 506..511

XX /note= "presumed regulatory sequence common to

XX polo family protein kinases"

XX W03558052-A2.

XX 13-DEC 1998.

XX 19 JUN 1998; 98WO-US12813.

XX 19 JUN 1997; 97US-0878989.

XX LINAY; INCYTE PHARM. INC.

XX

PI Pindman C., Corley NO., Gell SK., Gougher E., Hillman JG.

PI Pat P., Shah P.

XX

XX WPI, 1999-080952/07.

XX N-PSDB; AAX06831.

PT New disease associated protein kinases - used to stimulate cell proliferation and to treat the immune response and cancer

XX Claim 1; Page 54-56; 93pp; English.

XX This is the amino acid sequence of human disease associated protein kinase DAPK-1, as deduced from a consensus sequence (see AAX06831) of overlapping cDNA clones from libraries which are immortalised or cancerous and show inflammatory or immune responses. DAPK-1 shows 53% homology to human proliferation-related protein kinase PRK (GI 1488263). The invention provides DAPK-1 to DAPK-7 polypeptides (see AAW88432-38) and cDNA clones encoding them (see AAX06831-36 and AAX06882), as well as expression vectors, host cells, agonists, antagonists and antibodies. The invention further provides uses of such products in the diagnosis, prevention and treatment of diseases associated with cell proliferation, especially cancer or an immune response (claimed). Conditions that may be treated include adult respiratory distress syndrome, allergies, asthma, arteriosclerosis, bronchitis, emphysema, hyper eosinophilia, myocardial or pericardial inflammation, rheumatoid arthritis, Addison's disease, AIDS, anaemia, atherosclerosis, various diseases of the digestive system, atopic dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis, gout, Grave's disease, lupus erythematosus, multiple sclerosis, myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis, polycystic kidney disease, polymyositis, scleroderma, Sjogren's syndrome, autoimmune thyroiditis, complications of cancer, extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal and helminthic infections, and trauma (disclosed).

XX Sequence 685 AA;

Query Match 94.8%; Score 55; DB 20; Length 685;
Best Local Similarity 90.9%; Pred. No. 0.11;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFPETS 11
DB 273 MLLGRPPFPET 283

RESULT 7
ABP61474
ID ABP61474 standard; Protein; 685 AA.

XX

AC ABP61474;

XX 30-SEP-2002 (first entry)

XX Human NF-kB activating protein SEQ ID NO 101.

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory; immunomodulator; cytostatic; antiinfective; osteopathic; nootropic; neuroprotective; anti-HIV; autoimmune disease; cancer; infection; bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

XX Homo sapiens.

XX WO200253737-A1.

XX 11-JUL-2002.

XX 25-DEC-2001; 2001WO-JP11389.

XX 28-DEC-2000; 2000JP-0402289.

XX 26-MAR-2001; 2001JP-0088912.

XX 24-AUG-2001; 2001JP-0254018.

XX (ASAH) ASAH KASEI KOGYO KK.

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

XX WPI; 2002 583617/62.

DE N PSDB; ABQ91962.
XX NF approximatelykB activating gene and expressed protein, applicable in
PT diagnosis and screening inhibitors or promoters to control excessive
PT activation or inhibition for treating e.g. inflammations, autoimmune
PT diseases and cancer .
XX
PS Claim 17 Page 449-453; 841pp; Japanese
XX
CC The invention relates to a purified protein (1), comprising one of 30
CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
CC the sequences but with some amino acids deleted, substituted or added and
CC with a NF-kB nuclear factor kappa B activating effect. The protein and
CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
CC inhibitors or promoters to control excessive activation or inhibition
CC and for treating e.g. inflammations, autoimmune diseases, cancers,
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
CC disorders.
XX
SQ Sequence 685 AA;
Query Match 94.8%; Score 55; DB 23; Length 685;
Best Local Similarity 90.9%; Pred.No. 0.12;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy : MLLGRPPFFETS 1;
Db 273 MLLGRPPFFET 283
RESULT 8
ABP41092
ID ABP41092 standard; Protein; 753 AA
XX
AC ABP41092;
XX
DT 22-AUG 2002 (first entry)
XX
DE Human ovarian antigen HAOSMOR, SEQ ID NO:1124.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive system; genome 5.
XX
CS Homo sapiens.
XX
XX
PN WG200200677-A1.
XX
PD 01 JAN 2002.
XX
XX
PF 02-JUN 2001, 2001WG-US:18569.
XX
PR 02-JUN 2000; 2000US-209467P.
XX
PA HUMANA) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
XX
DR WPI; 2002-147878/19.
DR N PSDB; ABQ55069.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases .
XX

PS Claim 11; SEQ ID NO 3124; 2922pp; English.
XX
CC The invention relates to 2175 novel human ovarian antigens (ABP41094-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 753 AA;
Query Match 94.8%; Score 55; DB 23; Length 753;
Best Local Similarity 90.9%; Pred.No. 0.12;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy : MLLGRPPFFETS 1;
Db 341 MLLGRPPFFET 351
RESULT 9
AAB35805
ID AAB35805 standard; Protein; 626 AA.
XX
AC AAB35805;
XX
DT 23-FEB-2001 (first entry)
XX
DE Protein involved in cell cycle regulation SEQ ID 46.
XX
XX
KW Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
KW cotton; rice; barley; millet.
XX
CS Zea mays.
XX
PN WG2000065040-A2.
XX
XX
PD 02-NOV-2000.
XX
PF 13-APR-2000; 2000WG-US:99975.
XX
PR 22-APR-1999; 99JS-0130849.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Heientjaris TG, Habben JE, Sun Y;
XX
DR WPI; 2000-68733/67.
DR N-PSDB; AAC83112.

XX Nucleic acids useful for producing transgenic plants, preferably maize,
PT with increased cell cycle gene activity, preferably activity of cyclin
PT and/or cyclin-dependent kinase -
XX
XX
PS Claim 16: Page 117-118; 122pp; English.
XX
XX Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
CC AAB35806 which are involved in regulating the cell cycle. The protein and
CC DNA sequences have been isolated from Zea mays (corn), and the invention
CC also includes oligonucleotides AAC83114 - AAC83119 which are related to
CC the cell cycle polynucleotides. The cell cycle polynucleotide sequences
CC are useful for producing transgenic plants such as maize, soybean,
CC sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
CC millet with increased levels of cell cycle gene activity, such as
CC activity of cyclin and cyclin-dependent kinases. The DNA sequences are
CC also useful as probes for detecting deficiencies in the level of mRNA in
CC screening for desired transgenic plants, for detecting mutations in the
CC gene, for monitoring upregulation of expression or changes in enzyme
CC activity in screening assays of compounds, for detecting any number of
CC allelic variants, orthologs or paralogues of the gene, and site-directed
CC mutagenesis in eukaryotic cells. The DNA sequences are also useful for
CC recombinant expression of the encoded polypeptides and as immunogens for
CC preparing and screening antibodies. A transgenic plant comprising an
CC expression cassette including a cell cycle regulatory gene is useful for
CC assaying enzyme agonists and antagonists, and as immunogens or antigens
CC to obtain antibodies. The antibodies are useful in assaying expression
CC levels of cell cycle regulatory proteins, for identifying and isolating
CC nucleic acids from expression libraries, for identifying homologues of
CC polypeptides from other species, and for purification of the proteins.
XX
SQ Sequence 476 AA;

Query Match 89.7%; Score 52; DB 21; Length 626;
Best Local Similarity 81.8%; Pred. No. 0.36;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGLRPPFFETS 11
DB 228 LGLRPPFFETS 238
RESULT 11
AAW74159
ID AAW74159 standard; peptide; 9 AA.
XX
AC AAW74159;
XX
DT 05 MAY 1999 (first entry)
XX
DE HJ loop peptide 3-45.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 9 /note= "amidated"
FT Modified-site 9 /note= "benzyl ester of Glu"
XX
PN W09853050-A2.
XX
PD 26 NOV-1998.
XX
PF 20 MAY 1998; 98WC-US10319.
XX
PR 21-MAY-1997; 97US-0861332.
XX

PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX
PI Ben-Sasson SA;
XX
DR WPI; 1999-070142/06.
XX
PT New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
PS Claim 14; Fig 4; 70pp; English.
XX
CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 9 AA;

Query Match 84.5%; Score 49; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGRPPFFETS 11
DB 1 LGRPPFFETS 9
RESULT 11
AAW74159
ID AAW74159 standard; peptide; 9 AA.
XX
AC AAW74159;
XX
DT 05 MAY-1999 (first entry)
XX
DE HJ loop peptide 3-42.
XX
KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 9 /note= "amidated"
FT Modified-site 9 /note= "benzyl ester of Glu"
XX
PN W09853050-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WC-US10319.
XX

PR 21-MAY-1997; 97US-0861338.
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) VISSUM RES & DEV CO.
XX
XX Ben Sasson SA;
XX
PR 21-MAY-1999 070142/06.

XX
XX New peptides for modulating serine/threonine kinase activity
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders

XX Claim 14; Fig 4; 70pp; English.

XX This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosis, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.

XX Sequence 9 AA;

Query Match 84.5%; Score 49; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPPE 9
Db |||||
1 MLGRRPPPE 9

RESULT 13
AAJ98318
ID AAJ98318 standard; Peptide; 9 AA.
XX
AC AAJ98318;
XX
DT 13-AUG-2002 (first entry)

XX
DE Polo kinase serine-threonine kinase HJ loop peptide J-42.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; J-42.

XX Unidentified.
OS Synthetic.

XX Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 9 /note= "Benzyl ester of Glutamic acid"
FT Modified-site 9 /note= "C-terminal amide"

XX US2002049301 A1.

XX

PD 25-APR-2002.

XX 13-DEC-2000; 2000US 0736076.

XX 21-MAY-1997; 97US-0861338.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Ben-Sasson SA;

XX WPI; 2002-462787/49.

XX New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -

XX Disclosure; Fig 4; 41pp; English.

XX The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HJ loop peptide J-42. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.

XX Sequence 9 AA;

Query Match 84.5%; Score 49; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPPE 9
Db |||||
1 MLGRRPPPE 9

RESULT 13
AAJ98318
ID AAJ98318 standard; Peptide; 9 AA.

XX AAJ98318;

XX 13-AUG-2002 (first entry)

XX Polo kinase serine-threonine kinase HJ loop peptide J-45.

XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; J-45.

XX Unidentified.
OS Synthetic.

XX Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Misc-difference 7 /note= "Benzyl ester of Glutamic acid"
FT Modified-site 9 /note= "C-terminal amide"

XX US2002049301-A1.

XX 25-APR-2002.

PC

XX 13 DEC-2000; 2000US-0736076.
XX
XX
XX 21-MAY 1997; 97US-0861338.
XX
XX CHILDRENS MEDICAL CENT.
XX Ben Sasson SA;
XX WPI; 2002-462787/49.
XX
XX New peptide from the HJ loop of serine-threonine kinase, useful for
XX treating e.g. cancer and for producing diagnostic antibodies -
XX
XX Disclosure; Fig 4; 4ipp; English.
XX
XX The present invention relates to new peptides derived from the HJ loop
XX of a serine/threonine kinase (STK). The peptides of the invention are
XX used to modulate STK activity, especially for treating cancer, diabetes,
XX obesity or a wide variety of central nervous system, inflammatory,
XX autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
XX regulating lipid metabolism. The peptides are also used to generate
XX antibodies that bind specifically to the parent STK, used e.g. for
XX identifying STK-expressing cells and to study intracellular distribution
XX of STK, and to identify or quantify ligands that bind to the HJ loop.
XX The present amino acid sequence represents the polo kinase
XX serine-threonine kinase HJ loop peptide J-45. This sequence is one of
XX the short peptides of the invention that selectively modulate the
XX activity of STK.
XX
XX Sequence 9 AA;
SQ
Query Match 84.5%; Score 49; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LGLRPFFTS 11
DB 1 LGLRPFFTS 9
RESULT 14
AAW74213
ID AAW74213 standard; peptide; 10 AA.
XX
XX AAW74213;
AC
XX
XX 06-MAY-1999 (first entry)
DT
XX
XX HJ loop peptide K038H101.
DE
XX
XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
XX haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
XX inflammatory disorder; central nervous system disease; septic shock;
XX Parkinson's disease; hypertension.
XX
XX Synthetic.
CS
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "myristylated"
FT Modified-site 10 /note= "amidated"
FT
XX
XX W09863050-A2.
PN
XX
XX 26 MAY-1999.
PD
XX
XX 20-MAY 1998; 98WO-US10319
PF
XX
XX 21-MAY-1997; 97US-0861338.
PS
XX
XX CHILDRENS MEDICAL CENT.
PA

PA (YISS ; YISSUM RES & DEV CO.
XX Ben Sasson SA;
XX WPI; 1999-070142/06.
XX
XX New peptides for modulating serine/threonine kinase activity -
XX comprise a sequence corresponding to the HJ loop of a
XX serine/threonine kinase, used for treating, e.g. cancers,
XX inflammatory disorders or autoimmune disorders
XX
XX Disclosure; Fig 6; 70pp; English.
XX
XX This sequence represents a peptide of the invention, and is a derivative
XX of the HJ loop of a serine/threonine kinase (STK). The peptides can be
XX used for the treatment of disorders caused by overactivity of
XX underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
XX shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
XX arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
XX hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
XX psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
XX of organ transplant rejection, multiple sclerosis, inflammatory bowel
XX disease and AIDS), central nervous system diseases (e.g. Alzheimer's
XX disease, stroke and trauma), septic shock, Parkinson's disease or
XX hypertension. The peptides can also be used to produce antibodies which
XX can be used to identify cells expressing the STK and to study the
XX intracellular distribution of the STK. In addition, the peptides can be
XX used to identify and quantitate ligands which bind the HJ loop of the STK
XX from which the peptide was derived.
XX
XX Sequence 10 AA;
SQ
Query Match 84.5%; Score 49; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGLRPFFE 9
DB 2 MLGLRPFFE 10
RESULT 15
AAU98357
ID AAU98357 standard; Peptide; 10 AA.
XX
XX AAU98357;
AC
XX
XX 13-AUG-2002 (first entry)
DT
XX
XX Polo kinase SNK serine-threonine kinase HJ loop peptide K038H101.
DE
XX
XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
XX central nervous system disorder; inflammatory disorder;
XX autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
XX lipid metabolist; cytostatic; antidiabetic; anorectic; neurological;
XX antiinflammatory; immunosuppressive; cardiac; haemostatic;
XX modulating STK activity; polo kinase; SNK; K038H101.
XX
XX Unidentified
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal myristyl"
FT Modified-site 10 /note= "Benzy; Ester of Glutamic Acid, C-terminal amide"
FT
XX
XX US2002049301-A1.
PN
XX
XX 25-APR-2002.
PD
XX
XX 13 DEC-2000; 2000US-0736076.
PF
XX

PR 21-MAY-1997; 97US-0861338.
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX Ben-Sasson SA;
PI WPI: 2002-462787/49.
PR New peptide from the HJ loop of serine-threonine kinase, useful for
XX treating e.g. cancer and for producing diagnostic antibodies
PS (disclosure) Fig 6; 41pp; English.
XX The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HJ loop.
CC The present amino acid sequence represents the polo kinase SNK
CC serine-threonine kinase HJ loop peptide K038H101. This sequence is one
CC of the short peptides of the invention that selectively modulate the
CC activity of STK.
XX
SQ Sequence 10 AA;
Query Match 84.5%; Score 49; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 MLGGRPPETS 9
II :|||
DI 2 MLGGRPPETS 10
RESULT 10
AAW74173
ID AAW74173 standard; peptide; 20 AA.
XX
AC AAW74173;
XX
DT 05-MAY-1999 (first entry)
XX
DE HJ loop peptide POLO
XX
KW HJ loop; serine/threonine kinase; cancer; obesity; obesity; therapy;
KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
CS Synthetic.
XX
FN W0964050-A2.
XX
PD 26 NOV 1999.
XX
PE 20-MAY-1999; 98WO-US10319.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX Ben-Sasson SA;
XX WPI: 1999-070142/06.
XX
XX New peptides for modulating serine/threonine kinase activity
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,

PT inflammatory disorders or autoimmune disorders
XX
PS Claim 4i; Fig 3b; 70pp; English.
XX
CC This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
SQ Sequence 20 AA;
Query Match 84.5%; Score 49; DB 20; Length 20;
Best Local Similarity 72.7%; Pred. No. 0.039;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
CY 1 MLGGRPPETS 1;
II :|||
DI 3 LLVGKPPETS 13
RESULT 17
AAU98306
ID AAU98306 standard; Peptide; 20 AA.
XX
AC AAU98306;
XX
DT 13-AUG 2002 (first entry)
XX
DE Peptide sequence of HJ loop of serine-threonine kinase polo kinase.
XX
KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase.
XX
OS Unidentified.
XX
PN US2002049301-A1.
XX
PD 25-APR-2002.
XX
PF 13-DEC-2000; 2000US-0736076.
XX
PR 21-MAY-1997; 97US-0861338.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX Ben-Sasson SA;
XX WPI: 2002-462787/49.
XX New peptide from the HJ loop of serine-threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies -
XX
PS Claim 33; Fig 3; 41pp; English.
XX The present invention relates to new peptides derived from the HJ loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,

CC obesity or a wide variety of central nervous system, inflammatory,
CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the H3 loop.
CC The present amino acid sequence represents the peptide sequence of the H3
CC loop of serine threonine kinase polio. This sequence is one of the
CC short peptides of the invention that selectively modulate the activity
CC of STK.
XX
SQ Sequence 20 AA;

Query Match 84.5% Score 47 DB 21; Length 20;
Best Local Similarity 72.7% Pred. No. 0.039;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY : MLVGKPPFFETS 11
 |||||
DB 3 LLVGKPPFFETS 13

RESULT 18
AAB56690
ID AAB56690 standard; Protein; 120 AA

XX AAB56690;
AC AAB56690;
XX
DT 13 MAR 2001 (first entry)
XX
DE Human prostate cancer antigen protein sequence SEQ ID NO:1268.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW veterinary; gastrointestinal; hepatotropic; antineoplastic; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX

CC Homo sapiens

XX NC_009551:74 A1.

XX 21 SEP 2000.

FF 08 MAR 2000; 3003WQ-US05988.

EE 10 MAR 1997; 58US-0124200.

XX HUMAN-1 HUMAN GENOME SCI INC.

PA (BIOGEN) ROSEN C A.

XX Boston CA, Ruben SM;

XX WPI, 2000-587513/55.

EE N-PSDB; AAB56693.

XX Prostate cancer associated gene sequences, referred to as prostate

XX cancer antigens, useful for treatment, prevention, and diagnosis of
XX disorders such as prostate cancer
PS Claim 11; Page 1691-1692; 233pp; English.
XX
CC AAB56690 to AAB56505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56463 to AAB57302.
CC the prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
CC hepatotropic, antineoplastic, gynaecological and antimicrobial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive.

CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAB56506 to AAB56514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.

XX Sequence 329 AA;

SQ Query Match 84.5% Score 49; DB 21; Length 329;
Best Local Similarity 72.7% Pred. No. 0.68;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLVGKPPFFETS 11
 |||||
DB 260 LLVGKPPFFETS 270

RESULT 19
AAU74656
ID AAU74656 standard; Protein; 531 AA.

XX AAU74656;

AC AAU74656;

XX 09-APR-2002 (first entry)

DE Mammalian polo-like kinase (Plk).

XX Polo-like kinase; PK; polo-box; cytostatic; neoplasm;
KW hyperproliferative disorder; cytokinesis; solid tumour;
KW carcinoma; sarcoma; cancer; small cell carcinoma; adenocarcinoma;
KW Mullerian tumour; squamous cell carcinoma; protein.

OS Mammalia.

XX Key Location/Qualifiers

FF Misc-difference 130 /label= Unknown

FT Misc-difference 131 /label= Unknown

FT Misc-difference 132 /label= Unknown

FT Misc-difference 133 /label= Unknown

FT Misc-difference 134 /label= Unknown

FT Misc-difference 135 /label= Unknown

FT Misc-difference 136 /label= Unknown

FT Misc-difference 137 /label= Unknown

FT Misc-difference 138 /label= Unknown

FT Misc-difference 139 /label= Unknown

FT Misc-difference 140 /label= Unknown

FT Misc-difference 141 /label= Unknown

FT Misc-difference 142 /label= Unknown

FT Misc-difference 143 /label= Unknown

FT Misc-difference 144 /label= Unknown

FT Misc-difference 145 /label= Unknown

FT Misc-difference 146 /label= Unknown

FT Misc-difference 147 /label= Unknown

FT Misc-difference 148 /label= Unknown

FT Misc-difference 149 /label= Unknown

FT /label= Unknown
 FT Misc-difference 355
 FT /label= Unknown
 FT Misc-difference 356
 FT /label= Unknown
 FT Misc-difference 357
 FT /label= Unknown
 FT Misc-difference 358
 FT /label= Unknown
 FT Misc-difference 359
 FT /label= Unknown
 FT Misc-difference 360
 FT /label= Unknown
 FT Misc-difference 361
 FT /label= Unknown
 FT Misc-difference 362
 FT /label= Unknown
 FT Misc-difference 363
 FT /label= Unknown
 FT Misc-difference 364
 FT /label= Unknown
 FT Misc-difference 365
 FT /label= Unknown
 FT Region
 FT 410..439
 FT /label= polo box
 FT /note= "Core polo-box consensus sequence"
 XX
 PN W0200190401-A2.
 XX
 PC 29-NOV-2001.
 XX
 XX 23-MAY-2001; 2001WO-US16903.
 PF
 PR 13-MAY-2000; 2000US-206588P.
 XX
 PA HARVARD HARVARD COLLEGE.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (USSH) US NAT INST OF HEALTH.
 XX
 PI Lee KS, Song S, Erikson R;
 XX WPI: 2002-106210/14.
 DR
 XX
 PT Identifying polo-like kinase modulators by contacting eukaryotic cells
 PT expressing polo-box peptides with test compounds and evaluating changes
 PT in dominant negative cytokinesis-defective growth patterns
 XX
 PS Example at Fig 8; 57pp; English.
 XX
 CC The invention describes a novel method of detecting compounds with
 CC polo-like kinase (PLK) modulating activity. This comprises contacting
 CC eukaryotic cells expressing polo-box or polo-box related peptides,
 CC binding peptides comprising 25 contiguous residues from a polo-like
 CC kinase C-terminal region, with a test compound. Ectopic expression of a
 CC polo box in a eukaryotic cell causes a severe cytokinetic defect in the
 CC cell. These eukaryotic cells can also be tested with the test compound
 CC used in the method of the invention. The polo-box related peptides and
 CC polo-like kinase activity modulatory compounds can be used to inhibit or
 CC enhance cellular proliferation and subsequently for treating
 CC hyper-proliferative disorders including neoplasia, solid tumours,
 CC carcinomas, sarcomas and cancers e.g. small cell carcinoma,
 CC adenocarcinoma, Mullerian tumours and squamous cell carcinomas. This
 CC is the amino acid sequence of a mammalian polo like kinase (Plk),
 CC uncontrolled expression of the Plk family is implicated in the
 CC development of human cancers, discussed in the method of the invention.
 XX
 SQ Sequence 531 AA;

Query Match 84.5%; Score 49; DB 23; Length 511;
 Best Local Similarity 72.7%; Pred. No. 1.1;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGKPPFETS 11
 Db 244 LLVGKPPFETS 254

Db 204 LLVGKPPFETS 214
 RESULT 20
 AAR74620
 ID AAR74620 standard; Protein; 603 AA.
 XX
 AC AAR74620;
 XX 25-MAR-2003 (updated)
 DT 26-OCT-1995 (first entry)
 XX
 DE Human lung tumour Polo-like kinase.
 XX
 KW Polo-like kinase; PLK; serine threonine kinase; human; lung tumour;
 KW autoimmune disease; lymphocyte activity.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Binding-site 60..86
 FT /label= ATP-binding_motif
 FT Region 174..177
 FT /note= "motif that is highly conserved in protein
 FT kinases"
 FT Region 194..196
 FT /note= "motif that is highly conserved in protein
 FT kinases"
 FT
 XX
 PN DE4329177-A1.
 XX
 PD 02-MAR-1995.
 XX
 PF 30-AUG-1993; 93DE 4329177.
 XX
 PR 30-AUG-1993; 93DE-4329177.
 XX
 PA (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.
 XX
 PI Holtrich U, Rubsamen-Waigmann H, Streibhardt K;
 PI Rubsamen-Waigmann H;
 XX
 DR WPI: 1995-099454/14.
 DR N-PSDB; AAQ88155.
 XX
 PT A polo-like serine threonine kinase-protein - isolated from
 PT proliferating human tissue, useful in the determin of lymphocyte
 PT activity, eg in autoimmune diseases
 XX
 PS Claim 1; Page 8-10; lipp; German.
 XX
 CC A human lung tumour-derived cDNA (AAQ88155) was found to have high
 CC homology with sequences from members of the serine/threonine kinase
 CC family. Due to the strong homology with the Drosophila polo gene,
 CC the protein encoded by the new cDNA (AAR74620) was designated a polo-
 CC like kinase (PLK). PLK mRNA is expressed in proliferating cells such
 CC as placenta, colon and tumours of the lung, oesophagus, gut and
 CC intestine. Resting lymphocytes do not express the PLK gene but after
 CC stimulation with phytohaemagglutinin, PLK is expressed and can be
 CC used as an indicator of lymphocyte stimulation.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 603 AA;

Query Match 84.5%; Score 49; DB 16; Length 603;
 Best Local Similarity 72.7%; Pred. No. 1.3;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGKPPFETS 11
 Db 244 LLVGKPPFETS 254

RESULT 21
AAU79306
ID AAU79306 standard; Peptide: 603 AA.
XX
XX
AC
XX AAU79306;
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk).
XX
XX Polo box; PBl; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 210
FT /note= "Wild type Thr substituted by Asp"
XX
PN US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX PF US6358738-B1.
XX
XX PR 19-MAR-2002.
XX
XX PA 19-MAY 1999; 99US-0311311.
XX
XX PF 19-MAY 1998; 98US-085296P.
XX
XX PA HARD ; HARVARD COLLEGE.
XX
XX PI Erikson RL, Lee KS;
XX
XX DR WPI; 2002-314756/35.
XX
XX PT Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections .
XX
XX PS Example 1; Column: 59-64; 47pp; English.
XX
XX CC The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of the polo-like kinase (Plk), a
XX protein from which mitotic protein polo kinase inhibitory peptides are
XX derived.
XX
SQ Sequence 603 AA;
Query Match 84.5%; Score 49; DB 23; Length 603;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
CY : MLGRPPFETS 11
: |||||
DB 144 LLVGKPPFETS 254
RESULT 22
AAU79306
ID AAU79306 standard; Peptide: 603 AA.
XX
XX
AC AAU79306;
XX
XX DT 02-JUL-2002 (first entry)
XX
XX DE Mouse polo-like kinase (Plk).
XX

DE Mouse polo-like kinase (Plk) T210D mutant.
XX
XX Polo box; PBl; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 210
FT /note= "Wild type Thr substituted by Asp"
XX
PN US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX PF 13-MAY-1999; 99US-0311311.
XX
XX PR 13-MAY-1998; 98US-085296P.
XX
XX PA (HARD ; HARVARD COLLEGE.
XX
XX PI Erikson RL, Lee KS;
XX
XX DR WPI; 2002-314756/35.
XX
XX PT Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections .
XX
XX PS Example 1; Page : 47pp; English.
XX
XX CC The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk);
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
SQ Sequence 603 AA;
Query Match 84.5%; Score 49; DB 23; Length 603;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
CY : MLGRPPFETS 11
: |||||
DB 244 LLVGKPPFETS 254
RESULT 23
AAU79309
ID AAU79309 standard; Peptide: 603 AA.
XX
XX
AC AAU79309;
XX
XX DT 02-JUL-2002 (first entry)
XX
XX DE Mouse polo-like kinase (Plk) T210E mutant.
XX

KW Polo box; P81; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
XX
OS Mus musculus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc difference 210 /note= "Wild type Thr substituted by Glu"
FT XX
XX
PN US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 1; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
SQ Sequence 603 AA;

Query Match 84.5%; Score 49; DB 23; Length 603;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLJGRPPFFETS 1;
1111111111
DB 244 LLVGKPPFFETS 254

RESULT 24
AAU79310
ID AAU79310 standard; Peptide; 603 AA.
XX
XX
AC AAU79310;
XX
XX 02-JUL-2002 (first entry)
XX
XX Mouse polo like kinase (Plk) E206V mutant.
XX
XX Polo box; P81; cytostatic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW Polo box; P81; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten;
KW cancer of the uterus; ovarian cancer; cervical cancer;

KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
OS Mus musculus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc difference 210 /note= "Wild type Thr substituted by Val"
FT XX
XX
PN US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 1; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
SQ Sequence 603 AA;

Query Match 84.5%; Score 49; DB 23; Length 603;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLJGRPPFFETS 1;
1111111111
DB 244 LLVGKPPFFETS 254

RESULT 25
AAU79311
ID AAU79311 standard; Peptide; 603 AA.
XX
XX
AC AAU79311;
XX
XX 02-JUL-2002 (first entry)
XX
XX Mouse polo-like kinase (Plk) E206V mutant.
XX
XX Polo box; P81; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;

KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; lichen, Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo like kinase; Plk; mutant; mutain.
XX
CS Mus musculus.
CS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Plk substituted by Val"
FT
XX US6358738-B1.
XX 19 MAR-2002.
XX 13 MAY-1999, 99US-0311311.
XX 13-MAY-1998, 98US-085296P.
XX (HARD) HARVARD COLLEGE.
PA Erikson RL, Lee KS;
XX
PI WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections .
XX
XX Example 1; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
SQ Sequence 603 AA;

Query Match 64.5%; Score 49; DB 23; Length 603;
Best Local Similarity 72.7%; Pred. No. 103;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLIGRPPFFETS 11
||| ||| ||
DB 244 LLVGRPPFFETS 254

RESULT 26
AAU79312
ID AAU79312 standard; Peptide; 603 AA
XX
AC AAU79312;
XX
CT 02 JUL 2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) E236V mutant.
XX
KW Polo box; PB1; cytosolic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo like kinase; Plk; mutant; mutain.

KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
XX
CS Mus musculus.
CS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Glu substituted by Asn"
FT
XX US6358738-B1.
XX 19 MAR-2002.
XX 13-MAY-1999, 99US-0311311.
XX 13-MAY-1998, 98US-085296P.
XX (HARD) HARVARD COLLEGE.
PA Erikson RL, Lee KS;
XX
PI WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections .
XX
XX Example 1; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
SQ Sequence 603 AA;

Query Match 84.5%; Score 49; DB 23; Length 603;
Best Local Similarity 72.7%; Pred. No. 103;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLIGRPPFFETS 11
||| ||| ||
DB 244 LLVGRPPFFETS 254

RESULT 27
AAU79313
ID AAU79313 standard; Peptide; 603 AA
XX
AC AAU79313;
XX
CT 02 JUL 2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) E236V/T210V mutant.
XX
KW Polo box; PB1; cytosolic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo like kinase; Plk; mutant; mutain.

XX Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Glu substituted by Val"
FT Misc difference 210 /note= "Wild type Thr substituted by Val"
FT
XX
PN US6358738-B1.
XX
PC 19-MAR-2002.
XX
PF 13-MAY-1999; 99JUS-03111311.
XX
PR 13-MAY-1998; 98JUS-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
XX
DR WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections
XX
XX
PS Example 1; Page -; 47pp; English.

XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.

XX Sequence 603 AA;
SQ
Query Match 84.5%; Score 49; DB 23; Length 603;
Best Local Similarity 72.7%; Pred. No. 113;
Matches 8; Conservative 3; Mismatches 0; Gaps 0;

QY 1 MLLGRPPPPETS 11
:|:|:|:|:
DB 244 LLVGKPPPPETS 254

RESULT 29
AAU79315
ID AAU79315 standard; Peptide; 603 AA.
XX
AC AAU79315;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) D194N mutant.

XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.

XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 194 /note= "Wild type Asp substituted by Asn"
FT
XX
PN US6358738-B1.
XX
PC 19-MAR-2002.
XX
PF 13-MAY-1999; 99JUS-03111311.
XX
PR 13-MAY-1998; 98JUS-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
XX
DR WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections
XX
XX
PS Example 1; Page -; 47pp; English.

XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.

XX Sequence 603 AA;
SQ

Query Match 84.5%; Score 49; DB 23; Length 603;
Best Local Similarity 72.7%; Pred. No. 113;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPPETS 11
:|:|:|:|:
DB 244 LLVGKPPPPETS 254

RESULT 29
AAU79315
ID AAU79315 standard; Peptide; 603 AA.
XX
AC AAU79315;
XX
DT 02-JUL-2002 (first entry)
XX
DE Mouse polo-like kinase (Plk) D194R mutant.

XX
KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX
OS Mus musculus.

PT /note= "Wild type Val substituted by Ala"
 XX
 PN US6358738-B1
 PD 19-MAR-2002
 XX
 PF 13-MAY-1999; 99US-0311311
 XX
 PR 13-MAY-1998; 98US-085296P
 XX
 PA (HARD) HARVARD COLLEGE
 XX
 PI Erikson RL, Lee KS;
 XX
 DR WPI, 2002-314756/35
 XX
 PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections
 XX
 PS Example 7; Page : 47pp; English
 XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79319 using information
 CC given in the invention.
 XX
 SQ Sequence 603 AA

 Query Match: 84.5%; Score 49; DB 23; Length 603;
 Best Local Similarity 72.7%; Pred. No. 13;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MLLGRPPETS 11
 : : : : :
 Db 244 LLVGKPPETS 254

 RESULT 12
 AAU79319
 CD AAU79319 standard; Peptide: 603 AA
 XX
 AC AAU79319;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) L427A mutant.
 XX
 KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
 XX
 CS Mus musculus.
 CS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Misc difference 427
 FT /note= "Wild type Lys substituted by Ala"
 XX

PN US6358738-B1
 XX
 PD 19-MAR-2002
 XX
 PF 13-MAY-1999; 99US-0311311
 XX
 PR 13-MAY-1998; 98US-085296P
 XX
 PA (HARD) HARVARD COLLEGE
 XX
 PI Erikson RL, Lee KS;
 XX
 DR WPI, 2002-314756/35
 XX
 PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections
 XX
 PS Example 7; Page : 47pp; English
 XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.
 XX
 SQ Sequence 603 AA

 Query Match: 84.5%; Score 49; DB 23; Length 603;
 Best Local Similarity 72.7%; Pred. No. 13;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MLLGRPPETS 11
 : : : : :
 Db 244 LLVGKPPETS 254

 RESULT 33
 AAU79319
 CD AAU79319 standard; Peptide: 603 AA
 XX
 AC AAU79319;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) N437I mutant.
 XX
 KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
 XX
 CS Mus musculus.
 CS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Misc difference 437
 FT /note= "Wild type Asn substituted by Ile"
 XX
 PN US6358738-B1
 XX

PD 10 MAR-2002.
XX
PF 13 MAY-1999; 99US-0311311.
XX
PR 13 MAY-1998; 98US 085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections
XX
PS Example 7; Page : 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (pik)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match 84.5%; Score 49; DB 23; Length 603;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
Db : : : : :
244 LLVGKPPFFETS 254

RESULT 14
AAU79306
ID AAU79306 standard; Peptide; 603 AA
XX
AC AAV79306
XX
PF 10 APR-2002 (first entry)
XX
DE Mouse polo like kinase (pik); W414P/TAL 0 mar 03
XX
KW Polo box; FRL; cytostatic; fungicide; proteasomide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; pik; mutant; mutetin.
XX
OS Mus musculus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc difference 414 /note= "Wild type Trp substituted by Phe"
FT /note= "Wild type Trp substituted by Phe"
FT Misc-difference 210 /note= "Wild type Thr substituted by Asp"
XX
XX
PN US6358738-B1.
XX

PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US 085296P.
XX
PA (HARD) HARVARD COLLEGE
XX
PI Erikson RL, Lee KS;
XX
DR WPI; 2002-314756/35.
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections
XX
PS Example 10; Page : 43pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (pik)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match 84.5%; Score 49; DB 23; Length 603;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
Db : : : : :
244 LLVGKPPFFETS 254

RESULT 35
ABR48196
ID ABR48196 standard; Protein; 603 AA.
XX
AC ABR48196;
XX
PF 12 JUN-2003 (first entry)
XX
DE Human bladder cancer associated protein sequence SEQ ID NO:110
XX
KW Human; bladder cancer; cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO2003003906-A2.
XX
PD 16-JAN-2003.
XX
PF 03-JUL-2002; 2002WO-US21338.
XX
PR 03-JUL-2001; 2001US-302814P.
PR 03-AUG-2001; 2001US-310099P.
PR 08-NOV-2001; 2001US-343705P.
PR 13-NOV-2001; 2001US-350666P.
PR 12-APR-2002; 2002US-372246P.
XX
PA (ECOB-) EOS BIOTECHNOLOGY INC.
XX
PI Yack DH, Aziz N;
XX

CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HC loop of the STK
CC from which the peptide was derived.

XX
SQ Sequence 9 AA;
Query Match 79.3%, Score 46, DB 23, Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 1 MLLGRPPPE 9

RESULT 38
AAC98317
ID AAC98317 standard; Peptide; 9 AA;
XX
AC AAC98317;
XX
DT 14 AUG 2002 (first entry)
XX
DE Polo kinase serine-threonine kinase HC loop peptide J-431.
XX
KW HC loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytoskeletal disorder; anorectic; neurological;
KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase, J 431.

XX
OS Patient identified.
XX
OS Synonymous.

PE Key Location/Qualifiers
PT Modified site 1 /note= "N-terminal acetyl"
PT Modified-site 9 /note= "Benzyl ester of glutamine and N-terminal amide"

XX
PN US2002049301-A1;
XX
PD 16 APR-2002.
XX
PP 14 DEC 2000; 2000US-0736076.
XX
PS 21 MAY-1997; 97US-0861338.
XX
PA CHIL-1 CHILDRENS MEDICAL CENT.
XX
PT Ben Sasson SA;
XX
PP WPI; 2002-462787/49.

XX
PT New peptide from the HC loop of serine threonine kinase, useful for
PT treating e.g. cancer and for producing diagnostic antibodies.
XX
PS Disclosure; Fig 4; 41pp; English.

XX
CC the present invention relates to new peptides derived from the HC loop
CC of a serine/threonine kinase (STK). The peptides of the invention are
CC used to modulate STK activity, especially for treating cancer, diabetes,
CC obesity or a wide variety of central nervous system, inflammatory,
CC and immune or cardiovascular disorders, also haemorrhagic shock, and for

CC regulating lipid metabolism. The peptides are also used to generate
CC antibodies that bind specifically to the parent STK, used e.g. for
CC identifying STK-expressing cells and to study intracellular distribution
CC of STK, and to identify or quantify ligands that bind to the HC loop.
CC The present amino acid sequence represents the polo kinase
CC serine-threonine kinase HC loop peptide J-431. This sequence is one of
CC the short peptides of the invention that selectively modulate the
CC activity of STK.

XX
SQ Sequence 9 AA;

Query Match 79.3%, Score 46, DB 23, Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 1 MLLGRPPPE 9

RESULT 39
AAR92176
ID AAR92176 standard; Protein; 416 AA;
XX
AC AAR92176;
XX
DT 25-MAY-1996 (first entry)
XX
DE Sak serine-threonine kinase N-terminus.

XX
KW Sak; serine-threonine kinase; STK; agonist; antagonist;
KW proliferative disease; cancer; tumour; antisense; transgenic animal;
KW therapy.

XX
OS Mus musculus.
XX
PN CA2150789-A.
XX
PD C3-DEC-1995.
XX
PP 01-JUN-1995; 95CA-2150789.
XX
PR 02-JUN-1994; 94US-0252995.

XX
PA (MOUN; MOUNT SINAI HOSPITAL CORP.
XX
PI Dennis JW, Fode C, Heffernan M;
XX
DR WPI; 1996-129812/14.
XX
DR N-PS99; AAT08710.

XX
PT Nucleic acid encoding Sak serine-threonine kinase - useful for
PT identifying modulators potentially useful in treatment or prevention
PT of proliferative disease.

XX
PS Claim 3; Page 46-48; 73pp; English.
XX
CC 2 isoforms, sak a and sak-b, of a novel serine/threonine kinase
CC have an identical N-terminal sequence (AAR92176) that contains the
CC kinase domain and that shows significant homology to the poic
CC subfamily. The C-terminal sequences (each contg. 3 PEST regions)
CC of the 2 isoforms differ (see AAR92177 and AAR92214). Sak-a and Sak-b
CC are associated with mitotic and meiotic cell division, and may be
CC involved in cell proliferation. They can be obtd. in recombinant
CC form by expression of encoding sequences (see AAT08710-12) and used
CC to test for inhibitory or stimulatory cpds. that may be useful
CC in the treatment/diagnosis of proliferative disorders, such as
CC cancer and viral (esp. HIV) infection.

XX
SQ Sequence 416 AA;

Query Match 79.3%; Score 46; DB 17; Length 416;
Best Local Similarity 70.6%; Pred. No. 3.1;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Search completed: November 14, 2003, 14:35:32
Job time : 41 secs

QY 1 MLIGRPPPFET 10
||| |
DB 204 LLIGRPPPFDT 213

RESULT 4:
AAR92014
ID AAR9214 standard; Protein; 464 AA.
XX
AC AAR9214;
XX
ET 25 MAY-1996 (first entry)
XX
DE SAK-1 serine-threonine kinase.
XX
KW SAK b, serine-threonine kinase; STK; agonist; antagonist;
KW proliferative disease; cancer; tumour; antisense; transgenic animal;
KW therapy.
XX
CS Mus musculus.
XX
FH Key location/Qualifiers
FT Domain 1..416
FT /label= N-terminal domain
FT /note= "contains the kinase domain"
FT Domain 417..464
FT /label= C-terminal domain
FT /note= "contains 3 PEST regions"
XX
EV CA1-1289-A;
XX
ZC 31 PEC-1995;
XX
PF 0. JUN-1995; 95CA-2150759.
PE 02 JUN-1994; 94JUS-0252995.
XX
PA (MONT) MOUNT SINAI HOSPITAL CORP
XX
ZI Dennis JW, Fode G, Heffernan M;
XX
ER WPI, 1996 129617/14.
XX M PSH; AAT08912.
XX
XX Nucleic acid encoding Sak serine/threonine kinase. Used for
XX identifying modulators potentially useful in treatment or prevention
XX of proliferative disease.
PS Pfam 6; Page 53-61; 73pp; English
XX
CC 2 isoforms, SAK-a (AAR92177) and SAK-b (AAR92141), of a novel
CC serine/threonine kinase are associated with mitotic and meiotic cell
CC division and are characterized by having a kinase domain at the
CC N-terminus and 3 PEST sequences (rich in Pro, Ser, Thr, Asp, Glu) at
CC the C-terminus. The N-terminal regions of the 2 isoforms are
CC identical (see AAR92176). SAK-a and SAK-b can be used, in recombinant
CC form, by expression of encoding sequences (see AAT08911-12), and used
CC to test for inhibitory or stimulatory cpds. useful in the
CC treatment/diagnosis of proliferative disorders such as cancer and
CC and viral (esp. HIV) infection, or used to raise antibodies.
XX
SC Sequence 464 AA;

Query Match 79.3%; Score 467; DB 10; Length 464;
Best Local Similarity 70.0%; Pred. No. 104;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLIGRPPPFET 10
||| |
DB 204 LLIGRPPPFDT 213

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CM protein - protein search, using sw tool.

Run on: November 14, 2003, 14:24:43 / Search time 22 seconds
(without alignments)
20155 Million cell updates/sec

Title: US-09-736-076 19
Perfect score: 58
Sequence: 1 MAAAPPPFETS 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 3
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database Issued Patents_AA:
1: /cgn2_6/ptodata/1/aa/5A_CCM3.pept
2: /cgn2_6/ptodata/1/aa/5B_CCM3.pept
3: /cgn2_6/ptodata/1/aa/5A_CCM3.pept
4: /cgn2_6/ptodata/1/aa/5B_CCM3.pept
5: /cgn2_6/ptodata/1/aa/5A_CCM3.pept
6: /cgn2_6/ptodata/1/aa/5B_CCM3.pept

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	21	US-08-861-338-19	Sequence 19, Appl
2	55	94.8	272	US-08-861-338-19	Sequence 12, Appl
3	55	94.8	272	US-08-861-338-19	Sequence 12, Appl
4	55	94.8	685	US-08-861-338-19	Sequence 1, Appl
5	55	94.8	685	US-08-861-338-19	Sequence 2, Appl
6	55	94.8	685	US-08-861-338-19	Sequence 1, Appl
7	55	94.8	685	US-08-861-338-19	Sequence 2, Appl
8	49	84.5	9	US-08-861-338-19	Sequence 15, Appl
9	49	84.5	9	US-08-861-338-19	Sequence 18, Appl
10	49	84.5	20	US-08-861-338-19	Sequence 6, Appl
11	49	84.5	272	US-08-252-995D-14	Sequence 14, Appl
12	49	84.5	272	US-08-834-108-14	Sequence 14, Appl
13	49	84.5	603	US-09-398-122-2	Sequence 2, Appl
14	49	84.5	603	US-09-398-122-2	Sequence 25, Appl
15	46	79.3	9	US-08-861-338-19	Sequence 17, Appl
16	46	79.3	273	US-08-252-995D-10	Sequence 10, Appl
17	46	79.3	273	US-08-834-108-10	Sequence 10, Appl
18	46	79.3	416	US-08-252-995D-2	Sequence 2, Appl
19	46	79.3	416	US-08-834-108-2	Sequence 2, Appl
20	46	79.3	464	US-08-252-995D-6	Sequence 6, Appl
21	46	79.3	464	US-08-834-108-6	Sequence 6, Appl
22	46	79.3	925	US-08-252-995D-4	Sequence 4, Appl
23	46	79.3	925	US-08-834-108-4	Sequence 4, Appl
24	44	75.9	271	US-08-252-995D-11	Sequence 11, Appl
25	44	75.9	271	US-08-834-108-11	Sequence 11, Appl
26	41	70.7	8	US-08-861-338-19	Sequence 16, Appl
27	41	70.7	607	US-08-878-939-15	Sequence 15, Appl

28	41	70.7	607	3	US-09-272-796-15	Sequence 15, Appl
29	40	69.0	344	2	US-08-755-728-3	Sequence 3, Appl
30	40	69.0	344	2	US-08-974-655-3	Sequence 3, Appl
31	40	69.0	344	3	US-09-283-011-3	Sequence 3, Appl
32	40	69.0	347	2	US-09-316-000-1	Sequence 1, Appl
33	39	67.2	264	2	US-07-857-224B-17	Sequence 17, Appl
34	39	67.2	303	4	US-09-739-455-12	Sequence 12, Appl
35	39	67.2	303	4	US-09-739-455-22	Sequence 22, Appl
36	39	67.2	403	2	US-08-755-728-4	Sequence 4, Appl
37	39	67.2	403	2	US-08-974-655-4	Sequence 4, Appl
38	39	67.2	403	3	US-09-283-011-4	Sequence 4, Appl
39	38	65.5	259	4	US-09-252-991A-28679	Sequence 28679, A
40	38	65.5	275	1	US-08-252-995D-13	Sequence 13, Appl
41	38	65.5	275	2	US-08-834-108-13	Sequence 13, Appl
42	38	65.5	737	4	US-09-772-647-4	Sequence 4, Appl
43	37	63.8	20	3	US-08-861-338-3	Sequence 3, Appl
44	37	63.8	182	4	US-09-134-001C-3742	Sequence 3742, Ap
45	37	63.8	220	1	US-08-233-146-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-861-338-19
; Sequence 19, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brock, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11

APPLICATION NUMBER: US/08/878,989
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0321 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 685 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: HUVENOR01
 CLONE: 39043
 US-08 PRT 989-1

Query Match: 94.8%; Score 55; DB 2; Length 685;
 Best Local Similarity 90.9%; Pred. No. 0.027;
 Matches 10; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
 I: |||||
 DP 173 MLLGRPPFFET 293

RESULT 4

US-09-136-292-2
 Sequence 2, Application US/09136292
 Patent No. 6063609

GENERAL INFORMATION:

APPLICANT: ANDERSON, KAREN
 APPLICANT: JACKSON, JEFFREY
 APPLICANT: HANSBURY, MICHAEL
 APPLICANT: NERURKAR, SANDHYA
 APPLICANT: ROSHAK, AMY
 APPLICANT: BOUZYK, MARK
 TITLE OF INVENTION: HUMAN SERUM INHIBIBLE KINASE GENE
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ratner & Priestly
 STREET: P.O. Box 980
 CITY: Valley Forge
 STATE: PA
 COUNTRY: USA
 ZIP: 19482
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,292
 FILING DATE: 20-AUG-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/056,112
 FILING DATE: 20-AUG-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F
 REGISTRATION NUMBER: 23,041
 REFERENCE/DOCKET NUMBER: GH 70231
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0700

TELEX: 846169
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 685 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-136-282 2

Query Match: 94.8%; Score 55; DB 3; Length 685;
 Best Local Similarity 90.9%; Pred. No. 0.027;
 Matches 10; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
 I: |||||
 DB 273 MLLGRPPFFET 293

RESULT 6

US-09-272-796-1
 Sequence 1, Application US/09272796
 Patent No. 6207148

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Corley, Neil C.
 APPLICANT: Guegler, Karl G.
 APPLICANT: Lal, Preeti
 APPLICANT: Goli, Surya K.
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/272,796
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/878,989
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0321 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 685 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: HUVENOR01
 CLONE: 39043
 US-09-272 796-1

Query Match: 94.8%; Score 55; DB 3; Length 685;


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Best Local Similarity 90.9%; Pred. No. 0.027;
Variables: 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPETS 11
      11111
DB      23 MLLGRPPETT 293

RESULT
US 09 505 744 2
Sequence 2, Application US/09505744
Patent No. 6245544
GENERAL INFORMATION:
APPLICANT: Karen M. Anderson
APPLICANT: Mark W. Bonzyk
APPLICANT: Michael C. Hansbury
APPLICANT: Jeffrey R. Jackson
APPLICANT: Sandhya S. Nerurkar
APPLICANT: Aty K. Rosnak
TITLE OF INVENTION: HUMAN SERUM INHIBITABLE KINASE (HSK)
FILE REFERENCE: GH-70231-C1
CURRENT APPLICATION NUMBER: US/09505744
EARLIER APPLICATION NUMBER: 09/236,081
EARLIER FILING DATE: 1998-08-20
EARLIER APPLICATION NUMBER: 60/056,112
EARLIER FILING DATE: 1997-09-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 1.2
SEQ ID NO 2
LENGTH: 865
TYPE: CRT
ORGANISM: HOMO SAPIENS
US 09 505 744 2

Query Match 94.8%; Score 49; DP 3; Length 9;
Best Local Similarity 90.9%; Pred. No. 0.027;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPETS 11
      11111
DB      23 MLLGRPPETT 293

RESULT
US 09 505 744 2
Sequence 2, Application US/09505744
Patent No. 6245544
GENERAL INFORMATION:
APPLICANT: Karen M. Anderson, Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,338
FILING DATE: 21-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC-590
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION:
OTHER INFORMATION: (note= "N-Acetyl Methionine"
```

FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "Serine NH2"
US-08-861-338-18

Query Match 84.5%; Score 49; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2,560,950;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGRPPFFETS 11
|||
DB : LGRPPFFETS 9

RESULT 10
US-08-861-338-6
Sequence 6, Application US/08861-39
Patent No. 6174993
GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brock, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,338
FILING DATE: 21 MAY 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brock, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC 592
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-861-338-6

Query Match 84.5%; Score 49; DB 3; Length 20;
Best Local Similarity 72.7%; Pred. No. 3,660,950;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
|||
DB 3 LLVGKPPFFETS 13

RESULT 11
US-08-252-995D-14
Sequence 14, Application US/082520945D
Patent No. 5650551

GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02 JUN 1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-252-995D-14

Query Match 84.5%; Score 49; DB 1; Length 272;
Best Local Similarity 72.7%; Pred. No. 3,13;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
|||
DB 199 LLVGKPPFFETS 209

RESULT 12
US-08-834-108-14
Sequence 14, Application US/08934108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108

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; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 14
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-09-736-108-14
;
; Query Match: 84.5%; Score 49; DB 2; Length 272
; Best Local Similarity 72.7%; Pred. No. 0.31;
; Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 MLLGRPPPTS 11
DB 199 LLVGKPPPTS 209
;
; RESULT 13
US-09-198-122-2
; Sequence 2, Application US/09198122
; Patent No. 6180380
; GENERAL INFORMATION:
; APPLICANT: Strebhardt, Klaus; Ruesamen-Waigmann, Heiga;
; APPLICANT: Heitrich, Uwe
; TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE
; TITLE OF INVENTION: THREONINE-KINASE FAMILY
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: SPRING HORN KRAEMER & NORDS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: Net Powermate SX 40
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09198122
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/601,014
; FILING DATE: 23-FEB-1996
; APPLICATION NUMBER: PCT/EP94/02871
; FILING DATE: 30-AUG-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: DE 432917-
; FILING DATE: 30-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 9510 KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-09-198-122-2
;
; Query Match: 84.5%; Score 49; DB 3; Length 603
; Best Local Similarity 72.7%; Pred. No. 0.31;
; Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 MLLGRPPPTS 11
DB 244 LLVGKPPPTS 254
;
; RESULT 14
US-09-311-311C-26
; Sequence 26, Application US/09311311C
; Patent No. 6358738
; GENERAL INFORMATION:
; APPLICANT: Erikson, et al.
; TITLE OF INVENTION: POLC BOX THERAPEUTIC COMPOSITIONS,
; TITLE OF INVENTION: METHODS, AND USES THEREFOR
; FILE REFERENCE: 1874/117
; CURRENT APPLICATION NUMBER: US/09/311,311C
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,296
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 603
; TYPE: PPT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: 11...1603
; OTHER INFORMATION: Plk protein
US-09-311-311C-26
;
; Query Match: 84.5%; Score 49; DB 4; Length 603
; Best Local Similarity 72.7%; Pred. No. 0.31;
; Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 MLLGRPPPTS 11
DB 244 LLVGKPPPTS 254
;
; RESULT 15
US-08-961-338-17
; Sequence 17, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338

```

```

; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CXCC-993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; OTHER INFORMATION: Glutamine Acid-NH2"
US 08-252-995D-10
; Query Match 79.3% Score 46; DB 1; Length 9;
; Best Local Similarity 88.9% Pred. No. 2,5e-05;
; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY : MLLGRPPPE 9
; DB : MLLGRPPPE 9
;
; RESULT 16
; US 08-252-995D-10
; Sequence 10, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdýdyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-834-108-10
; Query Match 79.3% Score 46; DB 2; Length 273;
; Best Local Similarity 70.0% Pred. No. 0.48;
; Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
;
; QY : MLLGRPPPE 10
; DB : MLLGRPPPE 209
;
; RESULT 18
; US-08-252-995D-2
; Sequence 2, Application US/08252995D
; Patent No. 5650501
```

```

GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252-995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-995D-2

```

```

Query Match          79.3%   Score 46;   DB 1;   Length 416;
Best Local Similarity 70.0%   Pred. No. 0.75;
Matches 7;   Conservative 3;   Mismatches 0;   Indels 0;   Gaps 0;

```

```

CY          1  MLLGRPPPET 10
          :|||  |||
DB          204  LLIGRPPPT 213

```

```

RESULT 10
US-08-814-108-2
Sequence 2: Application US/08-416-6
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-814-108-2
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

```

```

NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-834-108-2

```

```

Query Match          79.3%   Score 46;   DB 2;   Length 416;
Best Local Similarity 70.0%   Pred. No. 0.75;
Matches 7;   Conservative 3;   Mismatches 0;   Indels 0;   Gaps 0;

```

```

CY          1  MLLGRPPPET 10
          :|||  |||
DB          204  LLIGRPPPT 213

```

```

RESULT 20
US-08-252-995D-6
Sequence 6: Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-995D-6

```

```

Query Match          79.3%   Score 46;   DB 1;   Length 464;
Best Local Similarity 70.0%   Pred. No. 0.84;
Matches 7;   Conservative 3;   Mismatches 0;   Indels 0;   Gaps 0;

```

```

CY          1  MLLGRPPPET 10
          :|||  |||
DB          204  LLIGRPPPT 213

```


RESULT 21
US-08-834-108-6
Sequence 5, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-834-108-6

Query Match 79.3%; Score 46; DB 2; Length 464;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFET 10
DB 204 LLIGRPPFDT 213

RESULT 22
US-08-252-995D-4
Sequence 4, Application US/08252995D
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-995D-4

Query Match 79.3%; Score 46; DB 1; Length 925;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFET 10
DB 204 LLIGRPPFDT 213

RESULT 23
US-08-834-108-4
Sequence 4, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-834-108-4

Query Match 79.3%; Score 46; DB 2; Length 925;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFET 10

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DB          204 LLGQPPFT 213
          11: 111
RESULT 24
US-08-954 995D-11
: Sequence 11, Application US/08252995D
: Patent No. 5976893
: GENERAL INFORMATION:
: APPLICANT: Dennis, James W
: APPLICANT: Heffernan, Mike
: APPLICANT: Fode, Carol
: TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BERESKIN & PARR
: STREET: 40 King Street West
: CITY: Toronto
: STATE: Ontario
: COUNTRY: Canada
: ZIP: M5H 3Y2
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/252-995D
: FILING DATE: 02 JUN-1994
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Kurdydyk, Linda M
: REGISTRATION NUMBER: 34,971
: REFERENCE/DOCKET NUMBER: 3153-94
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (416) 364-7311
: TELEFAX: (416) 361-1398
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 271 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Drosophila melanogaster
: US-08-954 995D-11
Query Match 75.9% Score 44 DB 11 Length 271
Best Local Similarity 70.0% Pred. No. 111
Matches 77 Conservative 0 Mismatches 0 Gaps 0
QY 1 MLGQPPFT 10
11: 111
DB 198 LLVGQPPFT 207
RESULT 25
US-08-934 108-11
: Sequence 11, Application US/08934108
: Patent No. 5976893
: GENERAL INFORMATION:
: APPLICANT: Dennis, James W
: APPLICANT: Heffernan, Mike
: APPLICANT: Fode, Carol
: TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BERESKIN & PARR
: STREET: 40 King Street West
: CITY: Toronto
: STATE: Ontario
: COUNTRY: Canada
```

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ZIP: M5H 3Y2
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/814-108
: FILING DATE:
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Kurdydyk, Linda M
: REGISTRATION NUMBER: 34,971
: REFERENCE/DOCKET NUMBER: 3153-210
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (416) 364-7311
: TELEFAX: (416) 361-1398
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 271 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Drosophila melanogaster
: US-08-814-108-11
Query Match 75.9% Score 44 DB 2 Length 271
Best Local Similarity 70.0% Pred. No. 111
Matches 77 Conservative 3 Mismatches 0 Indels 0 Gaps 0
QY 1 MLGQPPFT 10
11: 111
DB 198 LLVGQPPFT 207
RESULT 26
US-08-861-338-16
: Sequence 16, Application US/08861338
: Patent No. 6174993
: GENERAL INFORMATION:
: APPLICANT: Ben-Sasson, Shmuel A.
: TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
: TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Millia Drive
: CITY: Lexington
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/861,338
: FILING DATE: 21-MAY-1997
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Brook, David E.
: REGISTRATION NUMBER: 22,592
: REFERENCE/DOCKET NUMBER: CMCC-590
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (781) 861-6240
: TELEFAX: (781) 861-9540
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
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STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /note= "N Acetyl Methionides"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 8
 OTHER INFORMATION: /note= "Phenylalanine NR2"
 US-09-867-339-16

Query Match: 20.7%; Score 41; DB 3; Length 607;
 Best Local Similarity: 63.6%; Pred. No. 9.5;
 Matches: 7; Conservative: 2; Mismatches: 2; Indels: 0; Gaps: 0;

QY 1 MLLGRPPETS 11
 |||||
 DB 1 MLLGRPPETS 11

RESULT 27
 US-09-878-989-15
 ; Sequence 15, Application US/08872989
 ; Patent No. 5885803
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil G.
 ; APPLICANT: Guegler, Karl G.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 ; TITLE OF INVENTION: KINASES
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Inocyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/878,989
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J C
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0321 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 607 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1827450

US-08-878-989-15
 Query Match: 20.7%; Score 41; DB 2; Length 607;
 Best Local Similarity: 63.6%; Pred. No. 9.5;
 Matches: 7; Conservative: 2; Mismatches: 2; Indels: 0; Gaps: 0;

QY 1 MLLGRPPETS 11
 |||||
 DB 214 LLCSPPPETA 224

RESULT 28
 US-09-272-796-15
 ; Sequence 15, Application US/09272796
 ; Patent No. 6207148
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil G.
 ; APPLICANT: Guegler, Karl G.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 ; TITLE OF INVENTION: KINASES
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Inocyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/272,796
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/878,989
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J C
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0321 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 607 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1827450

US-09-272-796-15
 Query Match: 20.7%; Score 41; DB 3; Length 607;
 Best Local Similarity: 63.6%; Pred. No. 9.5;
 Matches: 7; Conservative: 2; Mismatches: 2; Indels: 0; Gaps: 0;

QY 1 MLLGRPPETS 11
 |||||
 DB 214 LLCSPPPETA 224

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RESULT 29
US-08 755-728-3
; Sequence 3, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,728
; FILING DATE: No. 5962312 October 25, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; US-09 904-655-3
;
Query Match 69.0%; Score 40; DB 1; Length 344;
Best Local Similarity 54.5%; Pred. No. 8;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 0;

QY 1 MLLGRFPFETS 11
||| |||
DB 266 LLYGNPFESA 276

RESULT 30
US-08 904-655-3
; Sequence 3, Application US/08974655
; Patent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

```

```

; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 5972676 December 25, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEtical: NO
; ANTI-SENSE: NO
; US-08-974-655-3
;
Query Match 69.0%; Score 40; DB 2; Length 344;
Best Local Similarity 54.5%; Pred. No. 8;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRFPFETS 11
||| |||
DB 266 LLYGNPFESA 276

RESULT 31
US-09-283-011-3
; Sequence 3, Application US/09283011
; Patent No. 6207401
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible

```


1 / AUTHORS: Quinn, A. M.
2 / AUTHORS: Hunter, T.
3 / TITLE: The protein kinase family
4 / JOURNAL: Science
5 / VOLUME: 241
6 / PAGES: 42-52
7 / DATE: 1989
8 / US 09 736-076-19
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DB 207 MLGRPLFE 215
RESULT 36
US-08-755-728-4
1 / Sequence 4, Application: US/08755728
2 / Patent No. 5962312
3 / GENERAL INFORMATION:
4 / APPLICANT: Plowman, Gregory
5 / APPLICANT: Mossie, Kevin
6 / TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
7 / TITLE OF INVENTION: AND/OR AUR 2 RELATED DISORDERS
8 / NUMBER OF SEQUENCES: 29
9 / CORRESPONDENCE ADDRESS:
10 / ADDRESSEE: Lyon & Lyon
11 / STREET: 633 West Fifth Street
12 / CITY: Los Angeles
13 / STATE: California
14 / COUNTRY: U.S.A.
15 / ZIP: 90071-2066
16 / COMPUTER READABLE FORM:
17 / MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
18 / MEDIUM TYPE: storage
19 / COMPUTER: IBM compatible
20 / OPERATING SYSTEM: IBM P.C. DOS 5.0
21 / SOFTWARE: FastSeq for Windows 2.0
22 / CURRENT APPLICATION DATA:
23 / APPLICATION NUMBER: US/08/755,728
24 / FILING DATE: No. 5962312ember 25, 1996
25 / CLASSIFICATION: 540
26 / PRIOR APPLICATION DATA:
27 / APPLICATION NUMBER: 60/008,809
28 / FILING DATE: December 18, 1995
29 / APPLICATION NUMBER: 60/023,943
30 / FILING DATE: August 14, 1996
31 / ATTORNEY/AGENT INFORMATION:
32 / NAME: Warburg, Richard J.
33 / REGISTRATION NUMBER: 32,327
34 / REFERENCE/DOCKET NUMBER: 223/113
35 / TELECOMMUNICATION INFORMATION:
36 / TELEPHONE: (213) 489-1600
37 / TELEFAX: (213) 955 0440
38 / TELEX: 67-3510
39 / INFORMATION FOR SEQ ID NO: 4:
40 / SEQUENCE CHARACTERISTICS:
41 / LENGTH: 403 amino acids
42 / TYPE: amino acid
43 / STRANDEDNESS: single
44 / TOPOLOGY: linear
45 / MOLECULE TYPE: protein
46 / HYPOTHETICAL: NO
47 / ANTI-SENSE: NO
48 / US-08-755-728-4
Query Match 67.2% Score 39; DB 2; Length 403;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
CY 2 LGRRPPETS 11
DB 323 LVGKPPPEAN 332
RESULT 37
US-08-974-655-4
1 / Sequence 4, Application: US/08974655
2 / Patent No. 5972676
3 / GENERAL INFORMATION:
4 / APPLICANT: Plowman, Gregory
5 / APPLICANT: Mossie, Kevin
6 / TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
7 / TITLE OF INVENTION: AND/OR AUR 2 RELATED DISORDERS

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/074,655
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/755,728
FILING DATE: November 25, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-074-655 4

Query Match 67.2%; Score 39; DB 4; Length 403;
Best local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY 2 LIGRPPPTS 1:
|:|:|:|:|:
DT 123 LVGKPPFEAN 332

RESULT 38
US-09-283-011 4
Sequence 4, Application US/09283011
Patent No. 6207401
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR
AND/OR AUR-2 RELATED DISORDERS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/283,011
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/012,135
FILING DATE: January 22, 1998
APPLICATION NUMBER: 08/755,728
FILING DATE: No. 6207401ember 25, 1996
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-283-011-4

Query Match 67.2%; Score 39; DB 3; Length 403;
Best local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIGRPPPTS 1:
|:|:|:|:|:
DB 323 LVGKPPFEAN 332

RESULT 39
US-09-252-991A 28679
Sequence 28679, Application US/0925291A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc C. Rubenfield et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 197196136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28679
LENGTH: 259
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28679

Query Match 65.5%; Score 38; DB 4; Length 259;
Best local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLIGRPP 7

DB 152 M52GRPP 158

RESULT 40
US-09-252 995D-13
Sequence 13, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent: Release #100, Version #1.00
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/252.9450
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US 08-252 995D 13

Query Match 56.8% Score 100.00 E-00.00
Best local similarity 55.6% Prob 0.0001
Matches 31 Conservative 41 Mismatches 10 Gaps 07
CY 1 M52GRPP 9
LD 200 M52GRPP 209

Search Completed: November 14, 2003, 14:57:51
Job time: 1:22 secs

GenCore version 5.1.6
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QW protein - protein search, using sw model

Run on: November 14, 2003, 14:36:48 ; Search time 29 seconds
without alignments.
69,247 Million cell updates/sec

Query: US-09-736-076-19
RefSeq score: 58
Sequence: 1 MLLGRPPFFETS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searches: 666186 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pept.
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pept.
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCMB.pept.
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCMB.pept.
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15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCMB.pept.
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pept.
17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCMB.pept.
18: /cgn2_6/ptodata/1/pubpaa/US10_PUBCMB.pept.

Pred. No. is the number of results predicted by uscore to have a score greater than or equal to the one of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	11	9	US-09-736-076-19
2	55	94.8	400	15	US-10-026-021-5
3	55	94.8	469	15	US-10-059-585-14
4	55	94.8	685	10	US-09-771-161A-249
5	55	94.8	685	10	US-09-771-161A-250
6	55	94.8	685	10	US-09-771-161A-251
7	55	94.8	685	12	US-10-024-298A-101
8	55	94.8	685	12	US-09-769-970-11
9	55	94.8	685	12	US-10-042-211A-101
10	49	84.5	9	9	US-09-736-076-19
11	49	84.5	9	9	US-09-736-076-19
12	49	84.5	10	9	US-09-736-076-57
13	49	84.5	20	9	US-09-736-076-6
14	49	84.5	329	10	US-09-725-100-1268
15	49	84.5	367	15	US-10-026-021-6

16	49	84.5	516	10	US-09-771-161A-123	Sequence 123, App
17	49	84.5	603	10	US-09-771-161A-214	Sequence 214, App
18	49	84.5	603	15	US-10-171-311-186	Sequence 186, App
19	46	79.3	9	9	US-09-736-076-17	Sequence 17, Appl
20	46	79.3	379	15	US-10-026-021-3	Sequence 3, Appl
21	46	79.3	970	15	US-10-026-021-2	Sequence 2, Appl
22	41	70.7	8	9	US-09-736-076-16	Sequence 16, Appl
23	41	70.7	373	15	US-10-026-021-4	Sequence 4, Appl
24	41	70.7	607	12	US-09-769-970-15	Sequence 15, Appl
25	41	70.7	607	12	US-10-024-041-16	Sequence 16, Appl
26	41	70.7	607	15	US-10-138-580-2	Sequence 2, Appl
27	40	69.0	344	9	US-09-012-135A-3	Sequence 3, Appl
28	40	69.0	344	15	US-10-059-585-34	Sequence 34, Appl
29	40	69.0	344	15	US-10-171-311-214	Sequence 214, App
30	40	69.0	347	10	US-09-974-298-136	Sequence 136, App
31	40	69.0	528	12	US-10-032-585-7571	Sequence 7571, Ap
32	39	67.2	303	12	US-10-153-919-12	Sequence 12, Appl
33	39	67.2	303	12	US-10-153-919-22	Sequence 22, Appl
34	39	67.2	403	9	US-09-012-135A-4	Sequence 4, Appl
35	39	67.2	403	15	US-10-026-021-7	Sequence 7, Appl
36	39	67.2	403	15	US-10-059-585-33	Sequence 33, Appl
37	39	67.2	403	15	US-10-209-324-2	Sequence 2, Appl
38	38	65.5	8	9	US-09-736-076-58	Sequence 58, Appl
39	38	65.5	256	11	US-09-898-837A-32	Sequence 32, Appl
40	38	65.5	348	12	US-10-291-253A-16	Sequence 16, Appl
41	38	65.5	737	10	US-09-771-161A-195	Sequence 195, App
42	38	65.5	737	15	US-10-228-931-4	Sequence 4, Appl
43	37	63.8	20	9	US-09-736-076-3	Sequence 3, Appl
44	37	63.8	347	10	US-09-801-876B-8	Sequence 8, Appl
45	37	63.8	347	15	US-10-254-869-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-736-076 19
; Sequence 19, Application US/09736076
; Patent No. US20020049301A;
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(0)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (0)...(11)
; OTHER INFORMATION: J46
US-09-736-076-19

Query Match 100.0%; Score 58; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11

|||
Cb 1 MLLGRPPFFETS 11

RESULT 2

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US 10 026-021 8
; Sequence 5, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Genkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAKI Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026-001
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,412
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: 111..1400
; OTHER INFORMATION: human SNK mitotic kinase Kinase domain
US-10-026-021-5
Query Match 94.8% Score 55; DB 15; Length 400;
Best Local Similarity 90.9% Pred. No. 0.15;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
| ||| |||
DB 203 MLLGRPPFFET 293

RESULT 3
US-10-026-021-5
; Sequence 14, Application US/10050585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaori
; APPLICANT: Yamaguchi, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sakiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/050-585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JPO00/04100
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/193,141
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,100
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000 119104
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000 191000
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248000
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-595-14
Query Match 94.8% Score 55; DB 15; Length 469;
Best Local Similarity 90.9% Pred. No. 0.17;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
| ||| |||
DB 57 MLLGRPPFFET 67

RESULT 4
US-09-771-161A-249
; Sequence 249, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 249
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-249
Query Match 94.8% Score 55; DB 10; Length 685;
Best Local Similarity 90.9% Pred. No. 0.25;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
| ||| |||
DB 203 MLLGRPPFFET 283

RESULT 5
US-09-771-161A-250
; Sequence 250, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-250
```



```
Query Match      94.8% Score 55; DB 10; Length 685;
Best Local Similarity 90.9% Pred. No. 0.25;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGRRPPFFTS 11
      : |||||
DB      273 MLGRRPPFFTT 283

RESULT 4
US 09-771 161A-251
; Sequence 283, Application US/09771161A
; Patent No. US2002010811A;
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent in version 2.0
; SEQ ID NO 251:
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US 09 771 161A-251

Query Match      94.8% Score 55; DB 10; Length 685;
Best Local Similarity 90.9% Pred. No. 0.25;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGRRPPFFTS 11
      : |||||
DB      273 MLGRRPPFFTT 283

RESULT 7
US-10-024 298A-101
; Sequence 101, Application US/10014298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHU KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SEIJI MURAYATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Inhib
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 101
; LENGTH: 685
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-024-298A-101

Query Match      94.8% Score 55; DB 12; Length 685;
Best Local Similarity 90.9% Pred. No. 0.25;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGRRPPFFTS 11
      : |||||
DB      273 MLGRRPPFFTT 283

RESULT 8
US-09-769-970-1
; Sequence 1, Application US/09769970
; Publication No. US20030170219A;
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Corley, Neil C.
; Guegler, Karl G.
; Lai, Preeti
; Goli, Surya K.
; Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/769,970
; FILING DATE: 24-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/272,796
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/LOCKET NUMBER: PF-0921 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENOB01
; CCONE: 39043
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-769-970-1

Query Match      94.8% Score 55; DB 12; Length 685;
Best Local Similarity 90.9% Pred. No. 0.25;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGRRPPFFTS 11
      : |||||
DB      273 MLGRRPPFFTT 283
```

<p> RESULT 11 US-09-736-076-18 : Sequence 18, Application US/09736076 : Patent No. US20020049101A1 : GENERAL INFORMATION: : APPLICANT: Ben-Sasson Shmuel A. : TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY : TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES : FILE REFERENCE: 12421315-039 : CURRENT APPLICATION NUMBER: US/09/736,076 : CURRENT FILING DATE: 2000-12-13 : PRIOR APPLICATION NUMBER: US 08/861,338 : PRIOR FILING DATE: 1997-05-21 : NUMBER OF SEQ ID NOS: 68 : SOFTWARE: FastSeq for Windows Version 4.0 : SEQ ID NO 18 : LENGTH: 9 : TYPE: PRT : ORGANISM: Artificial Sequence : FEATURE: : NAME/KEY: ACETYLATION : LOCATION: (1)...(9) : OTHER INFORMATION: position 7 is benzylester : NAME/KEY: AMIDATION : LOCATION: (0)...(9) : OTHER INFORMATION: 145 US-09-736-076-18 </p>	<p> Query Match 94.5%; Score 49; DB 9; Length 9; Best Local Similarity 100.0%; Pred. No. 5.9e+05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; </p>
<p> RESULT 12 US-09-736-076-57 : Sequence 57, Application US/09736076 : Patent No. US20020049101A1 : GENERAL INFORMATION: : APPLICANT: Ben-Sasson Shmuel A. : TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY : TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES : FILE REFERENCE: 12421315-039 : CURRENT APPLICATION NUMBER: US/09/736,076 : CURRENT FILING DATE: 2000-12-13 : PRIOR APPLICATION NUMBER: US 08/861,338 : PRIOR FILING DATE: 1997-05-21 : NUMBER OF SEQ ID NOS: 68 : SOFTWARE: FastSeq for Windows Version 4.0 : SEQ ID NO 57 : LENGTH: 10 : TYPE: PRT : ORGANISM: Artificial Sequence : FEATURE: : NAME/KEY: MYRISTATE : LOCATION: (1)...(10) : OTHER INFORMATION: position 10 is benzylester : NAME/KEY: AMIDATION : LOCATION: (0)...(10) : OTHER INFORMATION: 5NK US-09-736-076-57 </p>	<p> Query Match 94.5%; Score 49; DB 9; Length 10; Best Local Similarity 100.0%; Pred. No. 0.041; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; </p>

```
QY      1 MLLGRPPFFS 9
      ||||| |||
DB      2 MLLGRPPFE 10

RESULT 13
US-09-736-076-6
; Sequence 6, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Samuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015 009
; CURRENT APPLICATION NUMBER: US/09/736-076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,138
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PCLO
US-09-736-076-6

Query Match      84.5%; Score 49; DB 9; Length 20;
Best Local Similarity 72.7%; Pred. No. 0.082;
Matches      8; Conservative      3; Mismatches      0; Indels      0; Gaps      0;

QY      1 MLLGRPPFFS 11
      ||||| |||
DB      3 LLVGKPPFFS 13

RESULT 14
US-09-925-300-1268
; Sequence 1268, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/05498
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/114,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (307)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (1308)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
```

```
; LOCATION: (314)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (317)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (323)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (327)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (329)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1268
```

Query Match 84.5%; Score 49; DB 10; Length 329;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 MLLGRPPFFS 11
      ||||| |||
DB      260 LLVGKPPFFS 270
```

```
RESULT 15
US-10-026-021-6
; Sequence 6, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Vonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-501210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1) (367)
; OTHER INFORMATION: human p13cas mitotic kinase kinase domain
US 10-026-021-6
```

Query Match 84.5%; Score 49; DB 15; Length 367;
Best Local Similarity 72.7%; Pred. No. 1.4;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 MLLGRPPFFS 11
      ||||| |||
DB      244 LLVGKPPFFS 254
```

```
RESULT 16
US-09-771-161A-123
; Sequence 123, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
```

```

; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136,776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135,619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent version 3.0
; SEQ ID NO 123
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-123

```

```

Query Match      84.5%; Score 49; DB 10; Length 516;
Best Local Similarity 72.7%; Pred. No. 27;
Matches      8; Conservative      3; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      1 MLLGRPPFETS 11
      : : : : :
Db      157 LLVGKPPFETS 167

```

```

RESULT 17
US-09-771-161A-214
; Sequence 214, Application US/09/771,161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 902620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136,776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135,619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent version 3.0
; SEQ ID NO 214
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-214

```

```

Query Match      84.5%; Score 49; DB 10; Length 516;
Best Local Similarity 72.7%; Pred. No. 27;
Matches      8; Conservative      3; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      1 MLLGRPPFETS 11
      : : : : :
Db      244 LLVGKPPFETS 254

```

```

RESULT 18
US-10-171-311-186
; Sequence 186, Application US/10/171,311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhang
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY

```

```

; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-186

```

```

Query Match      84.5%; Score 49; DB 15; Length 603;
Best Local Similarity 72.7%; Pred. No. 23;
Matches      8; Conservative      3; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      1 MLLGRPPFETS 11
      : : : : :
Db      244 LLVGKPPFETS 254

```

```

RESULT 19
US-09-736-076-17
; Sequence 17, Application US/09/736,076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(6)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (1)...(19)
; OTHER INFORMATION: 145.1
US-09-736-076-17

```

```

Query Match      79.3%; Score 46; DB 9; Length 9;
Best Local Similarity 68.9%; Pred. No. 5.9e+05;
Matches      8; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      1 MLLGRPPFE 9
      : : : : :
Db      1 MLLGKPPFE 9

```

```

RESULT 20
US-10-026-021-3
; Sequence 3, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demco, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.

```

; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 ; FILE REFERENCE: 021044-001210US
 ; CURRENT APPLICATION NUMBER: US/10/026,021
 ; CURRENT FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/309,632
 ; PRIOR FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 373
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (1)...(373)
 ; OTHER INFORMATION: SAK serine/threonine kinase kinase domain
 US-10-026-021-3

Query Match 79.3%; Score 46; DB 15; Length 373;
 Best Local Similarity 70.0%; Pred. No. 4.9;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPT 10
 DB 204 MLLGRPPPT 213

RESULT 21
 US-10-026-021-2
 ; Sequence 2, Application US/1002602;
 ; Publication No. US2003027756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hitoshi, Yasumichi;
 ; APPLICANT: Detsu, Susan
 ; APPLICANT: Jenkins, Yonchu
 ; APPLICANT: Rigel Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 ; FILE REFERENCE: 021044-001210US
 ; CURRENT APPLICATION NUMBER: US/10/026,021
 ; CURRENT FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/309,632
 ; PRIOR FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 373
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (1)...(373)
 ; OTHER INFORMATION: human SAK serine/threonine kinase
 US-10-026-021-2

Query Match 79.3%; Score 46; DB 15; Length 373;
 Best Local Similarity 70.0%; Pred. No. 4.9;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPT 10
 DB 204 MLLGRPPPT 213

RESULT 22
 US-09-736-076-16
 ; Sequence 16, Application US/09736076
 ; Patent No. US2002049301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; FILE REFERENCE: 12421015-009
 ; CURRENT APPLICATION NUMBER: US/09/736,076

; CURRENT FILING DATE: 2003-12-13
 ; PRIOR APPLICATION NUMBER: US 08/861,338
 ; PRIOR FILING DATE: 1997-05-21
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: ACETYLATION
 ; LOCATION: (1)...(8)
 ; NAME/KEY: AMIDATION
 ; LOCATION: (3)...(8)
 ; OTHER INFORMATION: J43
 US-09-736-076-16

Query Match 70.7%; Score 41; DB 9; Length 8;
 Best Local Similarity 87.5%; Pred. No. 5.9e+05;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPT 8
 DB 1 MLLGRPPPT 8

RESULT 23
 US-10-026-021-4
 ; Sequence 4, Application US/1002602;
 ; Publication No. US2003027756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hitoshi, Yasumichi;
 ; APPLICANT: Detsu, Susan
 ; APPLICANT: Jenkins, Yonchu
 ; APPLICANT: Rigel Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 ; FILE REFERENCE: 021044-001210US
 ; CURRENT APPLICATION NUMBER: US/10/026,021
 ; CURRENT FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/309,632
 ; PRIOR FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 373
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (1)...(373)
 ; OTHER INFORMATION: human FNK mitotic kinase kinase domain
 US-10-026-021-4

Query Match 70.7%; Score 41; DB 15; Length 373;
 Best Local Similarity 63.6%; Pred. No. 35;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLGRPPPT 11
 DB 253 MLLGRPPPT 263

RESULT 24
 US-09-769-970-15
 ; Sequence 15, Application US/09769970
 ; Publication No. US20030179219A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bardran, Olga
 ; TITLE OF INVENTION: HILLMAN, Jennifer L.
 ; FILE REFERENCE: Corley, Neil C.
 ; CURRENT APPLICATION NUMBER: Guegler, Karl G.
 ; LAI, Preeti

1 Goli, Surya K.
2 Shah, Purvi
3 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
4 KINASES
5
6 NUMBER OF SEQUENCES: 2;
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Inocyte Pharmaceuticals, Inc.
9 STREET: 3174 Porter Drive
10 CITY: Palo Alto
11 STATE: CA
12 COUNTRY: USA
13 ZIP: 94304
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Diskette
17 COMPUTER: IBM Compatible
18 OPERATING SYSTEM: DOS
19 SOFTWARE: FASTSEQ for Windows Version 2.0
20
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/769,070
23 FILING DATE: 24-Jan-2001
24 CLASSIFICATION: <Unknown>
25
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 09/272,796
28 FILING DATE: <Unknown>
29
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Billings, Lucy J.
32 REGISTRATION NUMBER: 367749
33 REFERENCE/DOCKET NUMBER: EP 0321 US
34
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 415-855-0555
37 TELEFAX: 415-845-4166
38
39 TEXT: <Unknown>
40
41 INFORMATION FOR SEQ ID NO: 15:
42 SEQUENCE CHARACTERISTICS:
43 LENGTH: 607 amino acids
44 TYPE: a-150 acid
45 STRANDEDNESS: single
46 TOPOLOGY: linear
47
48 IMMEDIATE SOURCE:
49 LIBRARY: GenBank
50 ACCION: 1827450
51
52 SEQUENCE DESCRIPTION: SEQ ID NO: 15:
53 US 09 769070-15

Query Match 70.7% Score 41; DB 12; Length 607;
Best Local Similarity 63.6% Pred. No. 56;
Matches 7; Conservative 2; Mismatches 2; Indels 0;

QY 1 MLGRRPPETS 11
DB 214 LLOGSPPEFA 224

RESULT 26
US 10-204 041 16
Sequence 16, Application US/1027404;
Publication No. US20030176443A1
GENERAL INFORMATION:
APPLICANT: STEIN GERLACH, MATTHEIAS
APPLICANT: SALASSIDIS, KONSTANTINOS
APPLICANT: BACHER, GERALD
APPLICANT: MULLER, STEFAN
TITLE OF INVENTION: Pyridylpyrimidine Derivatives and Methods of Use
TITLE OF INVENTION: Infections and Related Disorders
FILE REFERENCE: AXM-007.1P US
CURRENT APPLICATION NUMBER: US/10/204,041
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: EP 01111489
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: PCT/EP02 000,000
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1

SEQ ID NO 16
LENGTH: 607
TYPE: PRT
ORGANISM: Homo sapiens
US-10-204-041-16

Query Match 70.7% Score 41; DB 12; Length 607;
Best Local Similarity 63.6% Pred. No. 56;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLGRRPPETS 11
DB 214 LLOGSPPEFA 224

RESULT 26
US-10-108-580-2
Sequence 2, Application US/10108580
Publication No. US20030077681A1
GENERAL INFORMATION:
APPLICANT: Cogswell, John
TITLE OF INVENTION: PKC PROTEIN-PROTEIN INTERACTIONS
FILE REFERENCE: PU4458
CURRENT APPLICATION NUMBER: US/10/108,580
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 607
TYPE: PRT
ORGANISM: homo sapiens
US-10-108-580-2

Query Match 70.7% Score 41; DB 15; Length 607;
Best Local Similarity 63.6% Pred. No. 56;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLGRRPPETS 11
DB 214 LLOGSPPEFA 224

RESULT 27
US-09-012-135A-3
Sequence 3, Application US/09012135A
Patent No. US20020081578A1
GENERAL INFORMATION:
APPLICANT: Florman, Gregory
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
TITLE OF INVENTION: AND/OR AUR 2 RELATED DISORDERS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,135A
FILING DATE: January 22, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,266
FILING DATE: January 9, 1999

APPLICATION NUMBER: 08/755,728
FILING DATE: No. US20020081578A1ember 25, 1996
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard C.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US 09-012-135A-3

Query Match 69.0% Score 40; DB 9; Length 344;
Best Local Similarity 54.5% Pred. No. 47;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
DB 266 LLVGNPPFESA 276

RESULT 28
US 10-059-585-34
Sequence 34, Application US/10059585
Publication No. US20030082776A1
GENERAL INFORMATION:
APPLICANT: Ota, Toshio
APPLICANT: Isegai, Takao
APPLICANT: Nishikawa, Tetsuo
APPLICANT: Hayashi, Koji
APPLICANT: Otsuka, Kaoru
APPLICANT: Yamamoto, Jun-ichi
APPLICANT: Ichii, Shizuko
APPLICANT: Sugiyama, Tomoyasu
APPLICANT: Wakatsuki, Ai
APPLICANT: Nagai, Keiichi
APPLICANT: Otsuki, Tetsu
APPLICANT: Furumasa, Shin-ichi
APPLICANT: Senoo, Chiaki
APPLICANT: Naga, Jun-ichi
TITLE OF INVENTION: NOVEL GENES ENCODED IN HUMAN
TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-098001
CURRENT APPLICATION NUMBER: US/10/059,585
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/JP00/05160
PRIOR FILING DATE: 2000-07-29
PRIOR APPLICATION NUMBER: US 60/183,320
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: US 60/159,597
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: JP 2000-118704
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183367
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 11-248034
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34

LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens
US-10-059-585-34

Query Match 69.0% Score 40; DB 15; Length 344;
Best Local Similarity 54.5% Pred. No. 47;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
DB 266 LLVGNPPFESA 276

RESULT 29
US-10-171-311-214
Sequence 214, Application US/10171311
Publication No. US20030082727CA1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Giatt, Karen
APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoerth, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,915
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 214
LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens
US-10-171-311-214

Query Match 69.0% Score 40; DB 15; Length 344;
Best Local Similarity 54.5% Pred. No. 47;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
DB 266 LLVGNPPFESA 276

RESULT 30
US-09-974-298-136
Sequence 136, Application US/09974298
Patent No. US20020156253A1
GENERAL INFORMATION:
APPLICANT: Chen, Huei-Mei
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 136
LENGTH: 347
TYPE: PRT

ORGANISM: Homo sapiens
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20030166263A; C 2940001
 US-09-736-076-19

Query Match 69.0% Score 407 DB 127 Length 303
 Best Local Similarity 54.5% Pred. No. 48
 Matches 67 Conservative 47 Mismatches 17 Indels 0 Gaps 0

QY 1 MLGKPPPE 11
 |||||
 DB 269 LVGNPPESA 279

RESULT 31
 US-10-032-585-7571
 Sequence 7571, Application US/10032585
 Publication No. US20030180933A1
 GENERAL INFORMATION:
 APPLICANT: Terry, Roeder D.
 APPLICANT: Bo, Giang
 APPLICANT: Charles, Boone
 APPLICANT: Howard, Bussey
 TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
 FILE REFERENCE: 10182-005-999
 CURRENT APPLICATION NUMBER: US/10/032-585
 CURRENT FILING DATE: 2001-12-20
 NUMBER OF SEQ ID NOS: 2000
 SOFTWARE: Patent in version 3.1
 SEQ ID NO 7571
 LENGTH: 528
 TYPE: PRT
 ORGANISM: Candida albicans
 US 10-032-585-7571

Query Match 69.0% Score 407 DB 127 Length 303
 Best Local Similarity 54.5% Pred. No. 48
 Matches 67 Conservative 47 Mismatches 17 Indels 0 Gaps 0

QY 1 MLGKPPPE 9
 |||||
 DB 454 LVGNPPPE 462

RESULT 32
 US-10-153-919-12
 Sequence 12, Application US/10153919
 Publication No. US20030166219A1
 GENERAL INFORMATION:
 APPLICANT: VAN, Chunhua et al.
 TITLE OF INVENTION: ISOLATED HUMAN KINASE ENCODING HUMAN KINASE PROTEINS, AND USES
 TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: CLOC0653D1V
 CURRENT APPLICATION NUMBER: US/10/153-919
 CURRENT FILING DATE: 2002-05-24
 PRIOR APPLICATION NUMBER: 60/209,585
 PRIOR FILING DATE: 2000-06-06
 PRIOR APPLICATION NUMBER: 09/739,455
 PRIOR FILING DATE: 2000-12-19
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 12
 LENGTH: 303
 TYPE: PRT
 ORGANISM: Leishmania mexicana
 US-10-153-919-12

Query Match 67.2% Score 397 DB 127 Length 303
 Best Local Similarity 58.9% Pred. No. 62
 Matches 87 Conservative 0 Mismatches 17 Indels 0 Gaps 0

QY 1 MLGKPPPE 9
 |||||
 DB 207 MLGKPPPE 215

RESULT 33
 US-10-153-919-22
 Sequence 22, Application US/10153919
 Publication No. US20030166219A1
 GENERAL INFORMATION:
 APPLICANT: VAN, Chunhua et al.
 TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: CLOC0653D1V
 CURRENT APPLICATION NUMBER: US/10/153-919
 CURRENT FILING DATE: 2002-05-24
 PRIOR APPLICATION NUMBER: 60/209,585
 PRIOR FILING DATE: 2000-06-06
 PRIOR APPLICATION NUMBER: 09/739,455
 PRIOR FILING DATE: 2000-12-19
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 22
 LENGTH: 303
 TYPE: PRT
 ORGANISM: Leishmania mexicana
 US-10-153-919-22

Query Match 67.2% Score 397 DB 127 Length 303
 Best Local Similarity 58.9% Pred. No. 62
 Matches 87 Conservative 0 Mismatches 17 Indels 0 Gaps 0

QY 1 MLGKPPPE 9
 |||||
 DB 207 MLGKPPPE 215

RESULT 34
 US-09-012-135A-4
 Sequence 4, Application US/09012135A
 Patent No. US20020381578A1
 GENERAL INFORMATION:
 APPLICANT: Plovman, Gregory
 APPLICANT: Mossie, Kevin
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
 TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 533 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2566
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/012,135A
 FILING DATE: January 22, 1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/005,268
 FILING DATE: January 9, 1998
 APPLICATION NUMBER: 08/755,728
 FILING DATE: No. US20020381578A1
 APPLICATION NUMBER: 60/023,943
 FILING DATE: August 14, 1996

```

: APPLICATION NUMBER: 60/008,809
: FILING DATE: December 18, 1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Wardlaw, Richard G.
: REGISTRATION NUMBER: 32,327
: REFERENCE/DOCKET NUMBER: 231/282
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 403 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US 09-012-135A-4

Query Match      67.2%  Score 39;  DB 9;  Length 403;
Best Local Similarity 60.0%;  Pred. No. 82;
Matches 6;  Conservative 3;  Mismatches 1;  Indels 0;  Gaps 0;

QY      2  LLGRPPFFETS 11
DB      323  LVGKPPFEAN 332

RESULT 35
US-10-026-021-7
: Sequence 7, Application US/10026021
: Publication No. US20030027756A1
: GENERAL INFORMATION:
: APPLICANT: Hitoshi, Yasumichi;
: APPLICANT: Kero, Susan
: APPLICANT: Jenkins, Yonchu
: APPLICANT: Rigol Pharmaceuticals, Inc
: TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
: TITLE OF INVENTION: Treatment of Cancer
: FILE REFERENCE: 021044-001210US
: CURRENT APPLICATION NUMBER: US/10/026,021
: CURRENT FILING DATE: 2002-06-25
: PRIOR APPLICATION NUMBER: US 60/309,612
: PRIOR FILING DATE: 2001-08-01
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 7
: LENGTH: 403
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: human ARK mitotic kinase
: US-10-026-021-7

Query Match      67.2%  Score 39;  DB 15;  Length 403;
Best Local Similarity 60.0%;  Pred. No. 82;
Matches 6;  Conservative 3;  Mismatches 1;  Indels 0;  Gaps 0;

QY      2  LLGRPPFFETS 11
DB      323  LVGKPPFEAN 332

RESULT 36
US-10-059 585-33
: Sequence 33, Application US/10059585
: Publication No. US20030082776A1
: GENERAL INFORMATION:
: APPLICANT: Ota, Toshio
: APPLICANT: Isogai, Takao
: APPLICANT: Nishikawa, Tetsuo

```

```

: APPLICANT: Hayashi, Koji
: APPLICANT: Otsuka, Kaoru
: APPLICANT: Yamamoto, Jun-ichi
: APPLICANT: Ishii, Shizuko
: APPLICANT: Sugiyama, Tomoyasu
: APPLICANT: Wakamatsu, A.
: APPLICANT: Nagai, Keiichi
: APPLICANT: Otsuki, Tetsuji
: APPLICANT: Funahashi, Shin-ichi
: APPLICANT: Senoo, Chiaki
: APPLICANT: Nezu, Jun-ichi
: TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
: TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
: FILE REFERENCE: 06501-098001
: CURRENT APPLICATION NUMBER: US/10/059,585
: CURRENT FILING DATE: 2002-01-29
: PRIOR APPLICATION NUMBER: PCT/JP00/05060
: PRIOR FILING DATE: 2000-07-28
: PRIOR APPLICATION NUMBER: US 60/183,322
: PRIOR FILING DATE: 2000-02-17
: PRIOR APPLICATION NUMBER: US 60/159,590
: PRIOR FILING DATE: 1999-10-18
: PRIOR APPLICATION NUMBER: JP 2000-118776
: PRIOR FILING DATE: 2000-01-11
: PRIOR APPLICATION NUMBER: JP 2000-183767
: PRIOR FILING DATE: 2000-05-02
: PRIOR APPLICATION NUMBER: JP 11-248036
: PRIOR FILING DATE: 1999-07-29
: NUMBER OF SEQ ID NOS: 64
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 33
: LENGTH: 403
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-059-585-33

Query Match      67.2%  Score 39;  DB 15;  Length 403;
Best Local Similarity 60.0%;  Pred. No. 82;
Matches 6;  Conservative 3;  Mismatches 1;  Indels 0;  Gaps 0;

QY      2  LLGRPPFFETS 11
DB      323  LVGKPPFEAN 332

RESULT 37
US-10-209-324-2
: Sequence 2, Application US/10209324
: Publication No. US2003010910A1
: GENERAL INFORMATION:
: APPLICANT: UNIVERSITY OF CALIFORNIA SAN FRANCISCO
: APPLICANT: Toland, Amanda E.
: APPLICANT: BALMAIN, Allan
: TITLE OF INVENTION: STK15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANC
: FILE REFERENCE: UCSF1120-2
: CURRENT APPLICATION NUMBER: US/10/209,324
: CURRENT FILING DATE: 2002-07-29
: PRIOR APPLICATION NUMBER: US 60/334,146
: PRIOR FILING DATE: 2001-11-28
: PRIOR APPLICATION NUMBER: US 60/308,911
: PRIOR FILING DATE: 2001-07-27
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 403
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: MISC FEATURE
: LOCATION: (31)...(31)
: OTHER INFORMATION: Xaa is Ile or Phe
: US-10-209-324-2

```

Query Match 67.2% Score 39; DB 15; Length 403;
 Best Local Similarity 60.0%; Pred. No. 82;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRPPFFS 1;
 DB 23 LVGRPPFFAN 332

RESULT 38

US-09-736-076-58
 ; Sequence 58, Application US/09736076
 ; Patent No. US2003049301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Res Sasson Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; FILE REFERENCE: 1242.1015-003
 ; CURRENT APPLICATION NUMBER: US/09736076
 ; PRIOR FILING DATE: 2000-12-13
 ; PRIOR APPLICATION NUMBER: US 08/861,338
 ; PRIOR FILING DATE: 1997-05-21
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 58
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: MYRISTATE
 ; LOCATION: (1)...(10)
 ; NAME/KEY: AMIDATION
 ; LOCATION: (1)...(18)
 ; OTHER INFORMATION: SNK
 US-09-736-076-58

Query Match 65.5% Score 38; DB 15; Length 80;
 Best Local Similarity 100.0%; Pred. No. 5,92e+07
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRPP 7
 DB 3 MLGRPP 5

RESULT 39

US-09-898-837A-32
 ; Sequence 32, Application US/09898837A
 ; Publication No. US2003007697A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Quinn, Kerry E.
 ; APPLICANT: Soyter, Kimberly A.
 ; APPLICANT: Majumder, Kumar
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Herrmann, John L.
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Fernandes, Eima
 ; APPLICANT: Taupier Jr., Raymond
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Curagen Corporation
 ; APPLICANT: Gerlach, Valerie L.
 ; APPLICANT: MacDougall, John R.
 ; TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
 ; FILE REFERENCE: 15966-S98 CIP
 ; CURRENT APPLICATION NUMBER: US/09898837A
 ; CURRENT FILING DATE: 2001-07-03
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
 ; PRIOR FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839
 ; PRIOR FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
 ; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
 ; PRIOR FILING DATE: 2000-04-13
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
 ; PRIOR FILING DATE: 2000-04-03
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
 ; PRIOR FILING DATE: 2000-07-03
 ; PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 32
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 US-09-898-837A-32

Query Match 65.5% Score 38; DB 12; Length 256;
 Best Local Similarity 55.6%; Pred. No. 78;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRPPFE 9
 DB 193 LLIGKPPFQ 201

RESULT 40

US-10-291-253A-16
 ; Sequence 16, Application US/10291253A
 ; Publication No. US20030150017A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Botella, Jose
 ; APPLICANT: Graham, Michael
 ; TITLE OF INVENTION: A Method for Facilitating Pathogen Resistance
 ; FILE REFERENCE: nematode
 ; CURRENT APPLICATION NUMBER: US/10291253A
 ; CURRENT FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: PR8706
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: PR8802
 ; PRIOR FILING DATE: 2001-11-12
 ; PRIOR APPLICATION NUMBER: US60/341404
 ; PRIOR FILING DATE: 2001-12-14
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Meloidogyne incognita
 US-10-291-253A-16

Query Match 65.5% Score 38; DB 12; Length 348;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRPPFE 9
 DB 210 MMAGQPPFE 218

Search completed: November 14, 2003, 14:42:09
 Job time : 29 secs

GenCore version 5.1.6
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US-09 protein - protein search, using sw model
Run on: November 14, 2003, 14:34:18 / Search time 21 seconds
without alignments.
50,374 Million cell updates/sec

Title: US-09 736-076-19
Perfect score: 58
Sequence: 1 MLGRRPPFETS 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96169682 residues

Total number of hits satisfying chosen parameters: 183308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_261*
1: pir1*
2: pir2*
3: pir3*
4: pir4*

Note: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	EB	ID	Description
1	55	94.8	682	2	A44493	serum-inducible kinase
2	49	84.5	603	2	S34130	serine/threonine kinase
3	49	84.5	603	2	A47545	protein kinase (EC
4	48	84.5	603	2	A54596	protein kinase
5	46	79.3	465	2	P55394	protein kinase (EC
6	46	79.3	925	2	A55344	protein kinase (EC
7	45	87.6	521	2	A48611	protein kinase (EC
8	44	76.7	576	2	A22117	protein kinase (EC
9	43	74.1	389	2	A52242	protein kinase (EC
10	43	74.1	407	2	A52247	protein kinase (EC
11	41	70.7	631	2	A52286	probable serine/thr
12	39	67.2	153	2	E71526	hypothetical prote
13	39	67.2	403	2	U05974	autophagosome-rela
14	39	67.2	547	2	S44841	K06H7.1 protein
15	39	67.2	556	2	U02084	nuclear factor kap
16	39	67.2	639	2	A12545	protein kinase C (
17	39	67.2	648	2	T43337	calcium-like kinase
18	38	65.5	256	2	A81354	glutamine-binding
19	38	65.5	256	2	T02421	iron(III) ABC tran
20	38	65.5	305	2	T43221	serine/threonine-s
21	33	65.5	329	2	B87790	protein B027.4 [i
22	33	65.5	547	2	T22856	hypothetical prote
23	33	65.5	634	1	S32392	protein kinase C (
24	36	65.5	656	2	U06811	hypothetical prote
25	38	65.5	683	2	T38234	serine/threonine-s
26	38	65.5	705	2	A48144	protein kinase CDC
27	38	65.5	707	1	A51530	protein kinase C (
28	38	65.5	736	1	K18B76	protein kinase C (
29	38	65.5	737	1	S28942	protein kinase C (

30	38	65.5	737	1	K1RTCE	protein kinase C (
31	38	65.5	737	1	K1MSCE	protein kinase C (
32	38	65.5	766	2	S69657	hypothetical prote
33	37	63.8	220	1	B42725	nitrate hydratase
34	37	63.8	345	2	U04665	protein kinase (EC
35	37	63.8	379	2	T23688	hypothetical prote
36	37	63.8	380	2	S70964	pkn5 protein - Myx
37	37	63.8	615	2	T29223	hypothetical prote
38	37	63.8	672	1	K1HJCA	protein kinase C (
39	37	63.8	672	1	K1RTCC	protein kinase C (
40	37	63.8	672	1	K1MSCA	protein kinase C (
41	37	63.8	672	1	K1RBC	protein kinase C (
42	37	63.8	672	1	K1BOC	protein kinase C (
43	37	63.8	676	2	A37237	protein kinase C (
44	37	63.8	682	1	K1BOGC	protein kinase C (
45	37	63.8	697	1	K1RTSC	protein kinase C (

ALIGNMENTS

RESULT 1
A44493
serum-inducible kinase mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Jan-1993 #sequence_revision 18-Nov-1994 #text_change 10-Sep-1997
C:Accession: A44493
R:Simmons, D.L.; Neel, R.G.; Stevens, R.; Evett, G.; Erikson, R.L.
Mol. Cell. Biol. 12, 4164-4169, 1992
A:Title: Identification of an early-growth-response gene encoding a novel putative pr
A:Reference number: A44493; MUID:92375085; PMID:1508211
A:Accession: A44493
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-682 <SIM>
A:Experimental source: F-2 cells
A>Note: sequence extracted from NCBI backbone (NCBI:111721, NCBI:111722)
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hor
C:Keywords: ATP
F:27-331/Domain: protein kinase homology <Kin>

Query Match 94.8% Score 55; DA 2; Length 682;
Best local Similarity 90.9%; Pred. No. 0.036;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPFETS 11
| | | | | | | | | |
DB 270 MLGRRPPFETT 280

RESULT 2
S34130
serine/threonine specific protein kinase PLK (EC 2.7.1.1) - human
N:Alternate names: polo-like protein kinase; protein kinase plk-1
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C:Accession: S34130; J38123; S61543
R:Golsteyn, R.M.; Schultz, S.C.; Bartek, J.; Ziemlecki, A.; Ried, T.; Nigg, E.A.
submitted to the EMBL Data Library, June 1993
A:Description: Cloning and characterization of a novel human protein kinase plk-1 a p
through mitosis.
A:Reference number: S34130
A:Accession: S34130
A:Molecule type: mRNA
A:Residues: 1-603 <GO1>
A:Cross-references: EMBL: X33458; NID: 9312997; PIDN: CAA51837.1; PID: g312993
A:Experimental source: nasopharyngeal carcinoma
R:Holtrich, U.; Wolf, G.; Brauning, A.; Karn, T.; Bohme, B.; Rubsamen-Waigmann, H.,
Proc. Natl. Acad. Sci. U.S.A. 91, 1736-1740, 1994
A:Title: Induction and down-regulation of PLK, a human serine/threonine kinase expres
A:Reference number: A53134; MUID:94173904; PMID:8127874
A:Accession: I38123
A:Status: preliminary; nucleic acid sequence not shown.

A;Molecule type: mRNA
A;Residues: 1-140; P: 142-226; E: 228-603 <RES>
A;Cross-references: EMBL:X75932; NID:g460767; PIDN:CAA03636.1; PID:g460769
A;Experimental source: lung tumor
R;Brauninger, A.; Strehardt, K.; Ruebsaen-Waigmann, H.
Oncogene 11, 193-1800, 1995
A;Title: Identification and functional characterization of the human and murine polo-like
A;Reference number: S61543; MUID:9606904; PMID:747960
A;Accession: S61543
A;Molecule type: DNA
A;Residues: 1-122; T: 124-136 <53A>
A;Cross-references: EMBL:X90725; NID:g106144; PIDN:AA012611; PID:g106144
A;Experimental source: placenta
A;Note: the authors translated the codon AAG for residue 107 as Met
C;Genetics
A;Gene: GDB:PLK
A;Cross-references: GDB:331003
A;Map position: 17pter 17p12
C;Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homol
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;51-305/Domain: protein kinase homology <KIN>
Query Match 84.5%; Score 49; DB 2; Length 603;
Best Local Similarity 72.7%; Pred. No. 0.4;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGRRPPFETS 11
DB 244 LLVGKPPFETS 254
RESULT 4
A47545
Protein kinase (EC 2.7.1.37) Plk - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13 Jun-1995 #sequence_revision 13 Jun-1995 #text_change 24-Sep-1999
C;Accession: A47545
R;Clay, A.J.; McEwen, S.J.; Bertonecello, I.; Wilks, A.M.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4862-4886, 1993
A;Title: Identification and cloning of a protein kinase encoding mouse gene, Plk, relate
A;Reference number: A47545; MUID:91201660; PMID:809944
A;Accession: A47545
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-463 <CLA>
A;Cross-references: GDB:06144; NID:g30945; PIDN:AA01944.1; PID:g309452
C;Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homol
C;Keywords: ATP; phosphotransferase
F;51-305/Domain: protein kinase homology <KIN>
Query Match 84.5%; Score 49; DB 2; Length 603;
Best Local Similarity 72.7%; Pred. No. 0.4;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGRRPPFETS 11
DB 244 LLVGKPPFETS 254
RESULT 4
A54536
Protein kinase mouse
C;Species: Mus musculus (house mouse)
C;Date: 22 Jul-1996 #sequence_revision 02 Jul-1996 #text_change 24-Sep-1999
C;Accession: A54536
R;Baker, R.D.; Jelinek, W.R.
Mol. Cell. Biol. 13, 7793-7801, 1993
A;Title: Cell cycle and terminal differentiation-dependent regulation of the mouse mRN
A;Reference number: A54536; MUID:94067140; PMID:794791
A;Accession: A54536
A;Status: preliminary; translated from GDB:MP10087
A;Molecule type: mRNA
A;Residues: 1-603 <RES>

A;Cross-references: GDB:L19558; NID:g403473; PIDN:AAAL6071.1; PID:g403474
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
F;51-305/Domain: protein kinase homology <KIN>
Query Match 84.5%; Score 49; DB 2; Length 603;
Best Local Similarity 72.7%; Pred. No. 0.4;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGRRPPFETS 11
DB 244 LLVGKPPFETS 254
RESULT 5
B55748
Protein kinase (EC 2.7.1.37) Sak-b - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Dec 1997
C;Accession: B55748
R;Fode, C.; Motro, B.; Yousefi, S.; Heffernan, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
A;Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosoph
A;Reference number: A55748; MUID:94294387; PMID:8022793
A;Accession: B55748
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-465 <PCD>
A;Cross-references: GDB:L29480
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C;Keywords: ATP; phosphotransferase
F;10-265/Domain: protein kinase homology <KIN>
F;18-26/Region: protein kinase ATP-binding motif
Query Match 79.3%; Score 46; DB 2; Length 465;
Best Local Similarity 70.3%; Pred. No. 1.1;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGRRPPFET 10
DB 204 LLIGRRPPFD 213
RESULT 6
A55748
Protein kinase (EC 2.7.1.37) Sak-a - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24 Sep 1999
C;Accession: A55748
R;Fode, C.; Motro, B.; Yousefi, S.; Heffernan, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
A;Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosoph
A;Reference number: A55748; MUID:94294387; PMID:8022793
A;Accession: A55748
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-925 <PCD>
A;Cross-references: GDB:L29479; NID:g487869; PIDN:AA037648.1; PID:g487870
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C;Keywords: ATP; phosphotransferase
F;10-265/Domain: protein kinase homology <KIN>
F;18-26/Region: protein kinase ATP-binding motif
Query Match 79.3%; Score 46; DB 2; Length 925;
Best Local Similarity 70.3%; Pred. No. 2.3;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGRRPPFET 10
DB 204 LLIGRRPPFD 213
RESULT 7
D88640

protein F55A8.2 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 10 May-2001 #sequence_revision 10-May-2001 #text_change 17 May-2002
 C:Accession: D88640
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
 A:Reference number: A75000; MUID:99369613; PMID:9931916
 A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 282, 2012-2018, 1998
 A:Accession: D88640
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-521 <STO>
 A:Cross-references: GB:chr_IV; PION:AAC17086.1; PION:G110149; GSPUS:GN00022; CESP:F55A8.2
 A:Genes: F55A8.2
 A:Map position: 4
 C:Superfamily: cGMP dependent protein kinase; cAMP receptor protein cyclic nucleotide-binding domain
 Query Match 77.6%; Score 45; DB 2; Length 521;
 Best Local Similarity 63.6%; Pred. No. 119;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLIGRPPPET 11
 DB 401 LVIGRPPPET 411
 RESULT 8
 S22127
 C:Species: Drosophila melanogaster
 C>Date: 20 Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999
 C:Accession: S22127
 R:Sunkei, C.E.
 Submitted to the EMBL Data Library, November 1991
 A:Reference number: S22127
 A:Accession: S22127
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-576 <STO>
 A:Cross-references: EMBL:X63361; NID:X63365; PION:CAA44363.1; PION:Q8356
 C:Keywords: ATP; phosphotransferase
 F:131-277/Domain: protein kinase homology <KIN>
 Query Match 75.9%; Score 46; DB 2; Length 576;
 Best Local Similarity 70.0%; Pred. No. 119;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLIGRPPPET 10
 DB 216 LVIGRPPPET 225
 RESULT 9
 S22242
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 18 Jun-1999
 C:Accession: S22242
 R:Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
 Submitted to the EMBL Data Library, October 1992
 A:Description: Eg2, selected by differential screening encodes a new Xenopus protein kinase
 A:Reference number: S22242
 A:Accession: S22242
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-389 <ROG>

A:Cross-references: EMBL:Z17206; NID:G609279; PIDN:CAA78914.1; PID:G609280
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase
 F:119-371/Domain: protein kinase homology <KIN>
 F:127-135/Region: protein kinase ATP-binding motif
 Query Match 74.1%; Score 43; DB 2; Length 389;
 Best Local Similarity 72.8%; Pred. No. 133;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LVGRPPPET 10
 DB 311 LVGRPPPET 319
 RESULT 10
 S22243
 p46Eg265 protein - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1999
 C:Accession: S22243; S34642; I51695
 R:Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
 Submitted to the EMBL Data Library, October 1992
 A:Description: Eg2, selected by differential screening encodes a new Xenopus protein kinase
 A:Reference number: S22242
 A:Accession: S22243
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-407 <ROG>
 A:Cross-references: EMBL:Z17207; NID:G609281; PIDN:CAA78915.1; PID:G609282
 R:Bouvet, P.; Omilli, F.; Arlot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Basset, T.;
 Submitted to the EMBL Data Library, June 1993
 A:Description: Targetted deadenylation of specific mRNAs in Xenopus embryos by a mechanical method
 A:Reference number: S34642
 A:Accession: S34642
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 328-407 <ROG>
 A:Cross-references: EMBL:Z24453; NID:G394756; PIDN:CAA80826.1; PID:G394757
 R:Bouvet, P.; Omilli, F.; Arlot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Basset, T.;
 Mol. Cell. Biol. 14, 1893-1900, 1994
 A:Title: The deadenylation conferred by the 3' untranslated region of a developmental protein
 A:Reference number: I51695; MUID:94158861; PMID:8114721
 A:Accession: I51695
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 328-407 <ROG>
 A:Cross-references: EMBL:Z24453; NID:G394756; PIDN:CAA80826.1; PID:G394757
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
 C:Keywords: ATP; phosphotransferase; protein kinase
 F:138-190/Domain: protein kinase homology <KIN>
 F:146-154/Region: protein kinase ATP-binding motif
 Query Match 74.1%; Score 43; DB 2; Length 407;
 Best Local Similarity 72.8%; Pred. No. 134;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LVGRPPPET 10
 DB 330 LVGRPPPET 339
 RESULT 11
 A57286
 Probable serine/threonine protein kinase (EC 2.7.1.-) fnk - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 10-Sep-1997
 C:Accession: A57286
 R:Donohue, P.C.; Alberts, G.F.; Guo, Y.; Winkles, J.A.
 J. Biol. Chem. 270, 10351-10357, 1995
 A:Title: Identification by targeted differential display of an immediate early gene
 A:Reference number: A57286; MUID:95247749; PMID:7730342
 A:Accession: A57286

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-631 <DN>
A;Cross-references: GB:U22434
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Keywords: ATP; phosphotransferase
E;1-631/Domain: protein kinase homology <KIN>

  Query Match      70.7%  Score 41;  DB 2;  Length 631;
  Best Local Similarity 63.6%  Pred. No. 13;
  Matches 7;  Conservative 2;  Mismatches 2;  Indels 0;  Gaps 0;

QY      1 MLGRPPFFET 11
DB      254 LMGSPFFETA 264

RESULT 12
E;1526
Hypothetical protein CT338 - Chlamydia trachomatis serotype D, strain LW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Accession: E71526
R;Stephens, R.S.; Kaiman, S.; Lammel, C.C.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trad
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: E71526
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-153 <APN>
A;Cross-references: GB:AECC01307; GB:AECC01273; MUID:9426757; PIDN:AA069933.1; PID:G332875
A;Experimental source: serotype D, strain LW-3/Cx
C;Genetics:
A;Gene: CT338

  Query Match      67.2%  Score 19;  DB 2;  Length 153;
  Best Local Similarity 87.5%  Pred. No. 6.8;
  Matches 7;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      3 LGRPFFET 10
DB      11 LGAPFFET 18

RESULT 13
JC5974
Aurora-related kinase 1 (EC 2.7.11.1) - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1999 #sequence_revision 14-Feb-1999 #text_change 01-Jan-2000
C;Accession: JC5974
R;Shindo, M.; Nakano, H.; Kuroyanagi, H.; Matsuda, T.; Matsuda, M.; Gilbert, D.C.; Jenk
Biochem Biophys Res Commun 244, 285-290, 1998
A;Title: cDNA cloning, expression, subcellular localization, and chromosomal assignment
A;Reference number: JC5974; MUID:9818343; PMID:9514911
A;Accession: JC5974
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-403 <SH>
A;Cross-references: GB:AF008551
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Keywords: phosphotransferase
E;1-403/Domain: protein kinase homology <KIN>

  Query Match      67.2%  Score 39;  DB 2;  Length 403;
  Best Local Similarity 60.0%  Pred. No. 19;
  Matches 6;  Conservative 3;  Mismatches 1;  Indels 0;  Gaps 0;

QY      2 LGRPPFFETS 11
DB      323 LVGRPPFEAN 332

RESULT 14
S44841
K06H7.1 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C;Accession: S44841
R;Favell, A.D.
Submitted to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid K06H7.
A;Reference number: S44841
A;Accession: S44841
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-547 <FAV>
A;Cross-references: EMBL:U15314; MUID:9289690; PIDN:AAA28084.1; PID:G289691
C;Genetics:
A;Introns: 25/3; 36/3; 80/3; 149/3; 186/2; 229/3; 311/3
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hor
C;Keywords: ATP; serine/threonine-specific protein kinase
E;265-518/Domain: protein kinase homology <KIN>

  Query Match      67.2%  Score 39;  DB 2;  Length 547;
  Best Local Similarity 60.0%  Pred. No. 26;
  Matches 6;  Conservative 3;  Mismatches 1;  Indels 0;  Gaps 0;

QY      1 MLGRPPFFET 10
DB      457 LLFGQPPFES 466

RESULT 15
JC2004
nuclear factor-kappa B p65 chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: JC2004
R;Ikeda, T.; Honjo, K.; Hirota, Y.; Onodera, T.
Gene 133, 237-242, 1993
A;Title: Isolation of the chicken NF-kappaB p65 subunit-encoding cDNA and characteriz
A;Reference number: JC2004; MUID:94040817; PMID:7916720
A;Accession: JC2004
A;Molecule type: mRNA
A;Residues: 1-558 <IKS>
A;Cross-references: GB:D13721; MUID:9455463; PIDN:BAA02874.1; PID:G460974
C;Comment: This protein contains the Rel homology domain in its amino-terminal 286 a
C;Superfamily: rel transforming protein; rel homology
C;Keywords: DNA binding; phosphoprotein
E;25-310/Domain: rel homology <REL>
E;306-309/Region: nuclear location signal
E;281/Binding site: phosphate (Ser) (covalent) #status predicted

  Query Match      67.2%  Score 39;  DB 2;  Length 558;
  Best Local Similarity 77.5%  Pred. No. 26;
  Matches 7;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;

QY      2 LLGRPPFFET 10
DB      428 LLGQPPFET 436

RESULT 16
A32545
protein kinase C (EC 2.7.11.1) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1999
C;Accession: A32545
R;Rosenthal, A.; Rhee, L.; Yadegari, R.; Faro, R.; Ullrich, A.; Goeddel, D.V.
EMBO J. 6, 433-441, 1987
A;Title: Structure and nucleotide sequence of a Drosophila melanogaster protein kina
A;Reference number: A32545; MUID:87218499; PMID:3107983
A;Accession: A32545
A;Status: preliminary
A;Molecule type: mRNA
```



```
RESULT 25
T38254
C:serine/threonine-specific protein kinase p101 (EC 2.7.11.1) - fission yeast (Schizosaccha
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21 Jul-2000
C:Accession: T38254; T45128
R:Brown, K.; Churcher, C.M.; Barrell, B.G.; Randalstead, M.A.; Wood, V.
Submitted to the EMBL Data Library, August 1995
A:Reference number: Z21781
A:Accession: T38254
A:Status: preliminary; translated from SP/EMBL/DDH1
A:Molecule type: DNA
A:Residues: 1-683 <BPQ>
A:Cross-references: EMBL:Z93559; PIDN:CAH11167.1; GSPDB:YMR00149; SPDB:SPAC23C11.16
A:Experimental source: strain 972h; cosmid C23C11
R:Ohkura, H.; Hagan, J.M.; Glover, D.M.
Genes Dev. 9, 1059-1073, 1995
A:Title: The conserved Schizosaccharomyces pombe kinase p101 is required to form a bipolar
A:Reference number: Z22921; MUID:95262899; PMID:7744248
A:Accession: T45128
A:Status: preliminary; translated from GR/EMBL/DDH3
A:Molecule type: DNA
A:Residues: 1-683 <CHK>
A:Cross-references: EMBL:X85758; NID:9897640; PIDN:CAAB9766.1; PID:9887641
A:Experimental source: strain 972 derivative
C:Genetics:
A:Gene: p101; SPAC23C11.16
A:Map position: 1
A:Function:
A:Description: required to form a bipolar spindle and early in the regulatory cascade th
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: phosphotransferase; protein kinase

Query Match 65.5%; Score 38; DB 2; Length 683;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLUGRPPE 9
DB 239 LLICKPPFQ 241

RESULT 26
A48144
Protein kinase CDC5 (EC 2.7.11.1) - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein kinase PKX2; protein YMA270.1v; protein YMR001c
C:Species: Saccharomyces cerevisiae
C:Date: 30 Jun 1995 #sequence_revision 11-Jun-1995 #text_change 24 Sep-1999
C:Accession: A48144; S53030; S27445
R:Kitada, K.; Johnson, A.; Johnson, L.B.; Saito, A.
Mol. Cell. Biol. 13, 4445-4457, 1993
A:Title: A multicopy suppressor gene of the dominant negative G 1 cell cycle muta
A:Reference number: A48144; MUID:93306420; PMID:822144
A:Accession: A48144
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-705 <KIT>
A:Cross-references: EMBL:M84220; NID:gl72186; PIDN:AAA1000.1; PID:gl72187
R:Devlin, K.; Churcher, C.M.
Submitted to the EMBL Data Library, March 1995
A:Reference number: S53028
A:Accession: S53030
A:Molecule type: DNA
A:Residues: 1-705 <DEV>
A:Cross-references: EMBL:Z49613; NID:9728645; PIDN:CAAB9766.1; PID:9728648; MIPS:YMR001c
A:Experimental source: strain AB972
C:Genetics:
A:Gene: SGD:CDC5; PKX2
A:Cross-references: SGD:S0004603; MIPS:YMR0.1c
A:Map position: 13R
C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolo
C:Keywords: ATP; cell cycle control; phosphotransferase; protein kinase
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology,

Query Match 65.5%; Score 38; DB 1; Length 705;
Best Local Similarity 56.7%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLUGRPPE 9
DB 570 NYAGQPPPE 576

RESULT 28
KIRBCE
Protein kinase C (EC 2.7.11.1) epsilon - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
C:Accession: A29880
R:Ohno, S.; Akita, Y.; Konno, Y.; Imajoh, S.; Suzuki, K.
Cell 53, 731-741, 1988
A:Title: A novel phorbol ester receptor/protein kinase, nPKC, distantly related to th
A:Reference number: A29880; MUID:88223367; PMID:3370672
A:Accession: A29880
A:Molecule type: mRNA
A:Residues: 1-736 <OHN>
A:Cross-references: GB:M20014
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
A:Note: activity is calcium-independent, phospholipid-dependent, and activated by dia
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology;
C:Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotra
F:157-162/Region: pseudophosphorylation motif
F:171-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F:249-298/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F:376-638/Domain: protein kinase homology <Kin>
F:384-392/Region: protein kinase ATP-binding motif
F:171-204/220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:184,187,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:249,279,282,298/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:262,265,287,290/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:407,426,502,504/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 65.5%; Score 38; DB 1; Length 707;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLUGRPPE 9
DB 570 NYAGQPPPE 576

RESULT 28
KIRBCE
Protein kinase C (EC 2.7.11.1) epsilon - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
C:Accession: A29880
R:Ohno, S.; Akita, Y.; Konno, Y.; Imajoh, S.; Suzuki, K.
Cell 53, 731-741, 1988
A:Title: A novel phorbol ester receptor/protein kinase, nPKC, distantly related to th
A:Reference number: A29880; MUID:88223367; PMID:3370672
A:Accession: A29880
A:Molecule type: mRNA
A:Residues: 1-736 <OHN>
A:Cross-references: GB:M20014
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
A:Note: activity is calcium-independent, phospholipid-dependent, and activated by dia
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology,
C:Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotra
```



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F:437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
F:703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match          65.5%; Score 38; DB 1; Length 737;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 600 VMAGQPPPE 608

RESULT 32
S69657
Hypothetical: protein YDR490c - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 22-Aug-1996 #sequence_revision 16-Sep-1996 #text_change 18-Apr-2002
C:Accession: S69657
B:Dietrich, F.S.
Submitted to the EMBL Data Library, August 1995
A:Description: The sequence of S. cerevisiae cosmid 5410, 8035, 8165, and 9787.
A:Reference number: S69554
A:Accession: S69657
A:Molecule type: DNA
A:Residues: 1-766 <DLE>
A:Cross-references: EMBL:U33050; NID:G227726; PIDN:AB649171; PID:G927745; MIPS:YDR490c
C:Genetics:
A:Gene: SGD:PKH;
A:Cross references: SGD:SCC02898
A:Map position: 4R
C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolog
C:Keywords: ATP
F:121-191/Domain: protein kinase homology <KIN>
F:131-139/Region: protein kinase ATP-binding motif

Query Match          65.5%; Score 38; DB 2; Length 766;
Best Local Similarity 54.5%; Pred. No. 56;
Matches 6; Conservative 3; Mismatches 2; Indels 2; Gaps 0;

QY 1 MLLGRPPPE 11
DB 330 MLAGKPPPKAA 340

RESULT 33
B42725
nitrile hydratase (EC 4.2.1.84) beta chain - Pseudomonas chlororaphis (strain B23)
C:Species: Pseudomonas chlororaphis
C:Date: 10-Sep-1999 #sequence_revision 16-Sep-1999 #text_change 16-Jun-2000
C:Accession: B42725
R:Nishiyama, M.; Horinouchi, S.; Kobayashi, M.; Nagatawa, T.; Yamada, H.; Beppu, T.;
J. Bacteriol. 173, 2465-2472, 1991
A:Title: Cloning and characterization of genes responsible for metabolism of nitrile com
A:Reference number: A42725; MCI:91191202; PMID:2014568
A:Accession: B42725
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-220 <NIS>
A:Cross-references: GB:D90216; NID:G216850; PIDN:BA440461; PID:G216853
C:Superfamily: nitrile hydratase beta chain
C:Keywords: carbon-oxygen lyase; hydro lyase

Query Match          63.8%; Score 37; DB 1; Length 220;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LGRPPPE 9
DB 118 ITRPPPE 125

RESULT 34
JC4665

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protein kinase (EC 2.7.1.37) - mouse
N:Alternate names: serine/threonine protein kinase; STK-1 protein
C:Species: Mus musculus (house mouse)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 17-Mar-1999
C:Accession: JC4665
R:Niwa, H.; Abe, K.; Kunisada, T.; Yamamura, K.
Gene 169, 197-201, 1996
A:Title: Cell-cycle-dependent expression of the STK-1 gene encoding a novel murine pu
A:Reference number: JC4665; MUID:96194801; PMID:8647446
A:Accession: JC4665
A:Molecule type: mRNA
A:Residues: 1-345 <NIW>
A:Cross-references: CDBJ:D21099
A:Experimental source: embryonic stem cell
A:Note: The authors translated the codon GCT for residue 328 as Thr
C:Comment: This enzyme regulates a wide array of cellular responses to changing enviro
C:Genetics:
A:Gene: stk-1
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; protein kinase
F:80-332/Domain: protein kinase homology <KIN>
F:88-96/Region: protein kinase ATP-binding motif
F:111/Binding site: ATP (Lys) #status predicted
F:205/Active site: Asp #status predicted

Query Match          63.8%; Score 37; DB 2; Length 345;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 10
DB 271 LMVGNPPPE 280

RESULT 35
T23688
Hypothetical protein M03C11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T23688
R:McMurray, A.
Submitted to the EMBL Data Library, April 1995
A:Reference number: Z:9793
A:Accession: T23688
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-379 <WIL>
A:Cross-references: EMBL:Z49128; PIDN:CAA88953.1; GSPDB:GN00021; CESP:M03C11.1
A:Experimental source: clone M03C11
C:Genetics:
A:Gene: CESP:M03C11.1
A:Map position: 3
A:Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match          63.8%; Score 37; DB 2; Length 379;
Best Local Similarity 72.7%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 11
DB 223 MLRGRTPEFS 233

RESULT 36
S70964
pKns protein - Myxococcus xanthus
N:Alternate names: serine protein kinase homolog
C:Species: Myxococcus xanthus
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
C:Accession: S70964
R:Zhang, W.; Inouye, M.; Inouye, S.
Mol. Microbiol. 20, 435-447, 1996

```


A:Title: Reciprocal regulation of the differentiation of *Myxococcus xanthus* by pkn5 and
A:Reference number: S70964; MUID:96310380; PMID:8733241
A:Accession: S70964
A>Status: preliminary; nucleic acid sequence not shown, translation not shown
A:Molecule type: DNA
A:Residues: 1380 <ZHA>
A:Cross references: EMBL:U40656; NID:g1113924; PID:AA840049.1; PID:g1113925
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C:Genetics:
A:Gene: pkn5

Query Match 63.8%; Score 37; DB 2; Length 180;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 314 MLGRRPPE 322

RESULT 37
T29223
Hypothetical protein F55G1.8 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31 Jan-2000
C:Accession: T29223
R:Murphy, J., Le, T.T.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of *C. elegans* cosmid F55G1
A:Reference number: Z20591
A:Accession: T29223
A>Status: preliminary; translated from GB/FMSL/DNA1
A:Molecule type: DNA
A:Residues: 1615 <MUR>
A:Cross references: EMBL:U58750; PID:AA830647.1; GSPC:BN00020; GESP:F55G1.8
A:Experimental source: strain Bristol N2; clone F55G1
C:Genetics:
A:Gene: GESP:F55G1.8
A:Map position: 4
A:Insertion: 103/3; 201/1; 238/3; 172/3; 413/3; 525/3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homoi

Query Match 63.8%; Score 37; DB 2; Length 615;
Best Local Similarity 60.8%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLGRRPPE 10
DB 825 MLGRRPPE 234

RESULT 38
KIHUCA
Protein kinase C (EC 2.7.11.-) alpha domain
C:Species: *Homo sapiens* (man)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: S09496
R:Finkezel, G., Marre, D., Hug, H
Nucleic Acids Res. 18, 2183, 1990
A:Title: Sequence of human protein kinase C alpha
A:Reference number: S09496; MUID:90245646; PMID:2133640
A:Accession: S09496
A:Molecule type: mRNA
A:Residues: 1-672 <FIN>
A:Cross references: EMBL:X52479; NID:g15492; PID:CAA718.1; PID:g335483
C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-sp
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters,
C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C:Genetics:
A:Gene: GSE:PRKCA
A:Cross references: GDB:128015; OMIM:176960
A:Map position: 17q22-17q23.2

C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k
C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin
F:19-29/Region: phospholipid binding #status experimental
F:22-27/Region: pseudophosphorylation motif
F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
F:152-264/Domain: protein kinase C C2 region homology <K2>
F:337-597/Domain: protein kinase homology <K1N>
F:345-353/Region: protein kinase ATP-binding motif
F:37-67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:50,53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:102,132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:368/Active site: Lys #status predicted
F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

Query Match 63.8%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 531 MLGRRPPE 539

RESULT 39
KIRTC
Protein kinase C (EC 2.7.11.-) alpha - rat
N:Alternate names: protein kinase C type III
C:Species: *Rattus norvegicus* (Norway rat)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: S02248; S02620
R:Ono, Y., Fujii, T., Igarashi, K., Kikkawa, U., Ogita, K., Nishizuka, Y.
Nucleic Acids Res. 16, 5199-5200, 1988
A:Title: Nucleotide sequences of cDNAs for alpha and gamma subspecies of rat brain pr
A:Reference number: S02129; MUID:89262515; PMID:3387228
A:Accession: S02248
A:Molecule type: mRNA
A:Residues: 1-672 <ONO>
A:Cross references: EMBL:X07286; NID:g56913; PID:CAA30266.1; PID:g56914
C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonin-
f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol est
C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein
C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin
F:19-29/Region: phospholipid binding #status experimental
F:22-27/Region: pseudophosphorylation motif
F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
F:152-264/Domain: protein kinase C C2 region homology <K2>
F:337-597/Domain: protein kinase homology <K1N>
F:345-353/Region: protein kinase ATP-binding motif
F:368/Active site: Lys #status predicted
F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status

Query Match 63.8%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 531 MLGRRPPE 539

RESULT 40
KIMSCA
Protein kinase C (EC 2.7.11.-) alpha - mouse
C:Species: *Mus musculus* (house mouse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: S07104; GSC078
R:Megidish, T., Mazurek, N.
Nature 342, 807-811, 1989

A:Title: A mutant protein kinase C that can transform fibroblasts.
A:Reference number: S07104; MUID:9098092; PMID:2601739
A:Accession: S07104
A:Molecule type: mRNA
A:Residues: 1-672 <XEG>
A:Cross-references: GB:X52685; GB:X51603; NID:Q4938; PDB:CA26908.1; PDB:Q49939
A:Experimental source: strain Balb/c
R:Researcher: S. J. Dietrich, A. J. Marks, F.
Gene 74, 465-471, 1988
A:Title: Molecular cloning of mouse protein kinase C-180 cDNA from Swiss 3T3 fibroblasts
A:Reference number: J50078; MUID:8923273; PMID:2463626
A:Accession: J50078
A:Molecule type: mRNA
A:Residues: 1-146; D: 148-217; N: 219-275; AA: 277-314; 366; N: 468-471; N: 473-511
A:Cross references: GB:M25811
A:Note: the authors translated the codon AAC for residue 141 as Lys; the sequence shown
C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific kinase. This protein is a receptor for tumor-promoting phorbol esters.
C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may be important for the zinc-stabilized regions bind diacylglycerol and phorbol esters.
C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
C:Superfamily: protein kinase C (alpha); protein kinase C C2 region homology; protein kinase C; key words: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding
F:19-29/Region: pseudophosphorylation motif
F:22-27/Region: pseudophosphorylation motif
F:37-96/Domain: protein kinase C zinc-binding repeat homology <K21>
F:102-141/Domain: protein kinase C zinc-binding repeat homology <K22>
F:152-164/Domain: protein kinase C C2 region homology <K2>
F:337-397/Domain: protein kinase homology <K1N>
F:345-351/Region: protein kinase ATP-binding motif
F:37-67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:50-53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:102-112,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:115,118,140,141/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:265/Active site: Lys #status predicted
F:63,64/Binding site: phosphate (Thi) (covalent) (by autophosphorylation) #status predicted

Query Match 63.8%; Score 37; DB 1; Length 612;
Best local Similarity 66.7%; Pred. No 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY : MLIGRPFFE 9
ID : MLACQEPED 539

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QM protein - protein search, using sw model

Run On: November 14, 2003, 14:34:37 ; Search time 11 Seconds
(without alignments)
47,027 Million cell updates/sec

Title: US-09-736-076-19
Perfect score: 88
Sequence: 1 MLLGRPPPTS 11

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searchset: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 3%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	55	94.8	682	1 SNK_MOUSE	P53351 mus musculu
2	55	94.8	682	1 SNK_RAT	Q91122 rattus norv
3	45	94.8	685	1 SNK_HUMAN	Q91122 homo sapien
4	49	84.5	603	1 PLK1_HUMAN	P51480 homo sapien
5	49	84.5	603	1 PLK1_MOUSE	Q57832 mus musculu
6	48	84.5	603	1 PLK1_RAT	Q62673 rattus norv
7	45	77.6	282	1 STK6_MOUSE	Q58445 mus musculu
8	44	75.9	576	1 PCLO_MOUSE	P53104 drosophila
9	43	74.1	402	1 STK6_XENLA	Q14820 xenopus lae
10	43	74.1	402	1 STK6_XENLA	Q14820 xenopus lae
11	41	73.7	631	1 SNK_RAT	Q91122 rattus norv
12	41	73.7	631	1 SNK_MOUSE	Q91122 mus musculu
13	41	73.7	646	1 SNK_HUMAN	Q91122 homo sapien
14	40	69.0	156	1 STK6_MOUSE	Q58445 mus musculu
15	40	69.0	344	1 STK6_HUMAN	Q58445 mus musculu
16	39	67.2	403	1 STK6_MOUSE	Q58445 mus musculu
17	39	67.2	558	1 TF65_CHICK	P98152 gallus gall
18	39	67.2	649	1 PLK1_MOUSE	Q57832 mus musculu
19	39	67.2	679	1 KPC1_MOUSE	P51480 drosophila
20	39	67.2	690	1 PKNB_MOUSE	Q91122 mus musculu
21	38	65.5	309	1 STK6_HUMAN	Q58445 mus musculu
22	38	65.5	632	1 PLK2_MOUSE	Q91122 mus musculu
23	38	65.5	634	1 KPC3_MOUSE	P51480 drosophila
24	38	65.5	660	1 PKN1_MOUSE	Q91122 mus musculu
25	38	65.5	683	1 PCLO_MOUSE	Q57832 mus musculu
26	38	65.5	705	1 CDC5_MOUSE	P51480 drosophila
27	38	65.5	707	1 KPC2_MOUSE	P51480 drosophila
28	38	65.5	736	1 KPC2_MOUSE	P51480 drosophila
29	38	65.5	737	1 KPC2_MOUSE	P51480 drosophila
30	38	65.5	737	1 KPC2_MOUSE	P51480 drosophila
31	38	65.5	737	1 KPC2_MOUSE	P51480 drosophila
32	38	65.5	743	1 KPC2_MOUSE	P51480 drosophila
33	38	65.5	1699	1 PCLO_MOUSE	P51480 drosophila

34	37	63.8	220	1 NHAB_PSECL	P27763 pseudomonas
35	37	63.8	343	1 STK6_RAT	O55099 rattus norv
36	37	63.8	345	1 STK6_MOUSE	O70126 mus musculu
37	37	63.8	380	1 PKN5_MOUSE	P54737 myxococcus
38	37	63.8	615	1 PLK3_MOUSE	Q20845 caenorhabdi
39	37	63.8	649	1 KPC1_MOUSE	Q16974 aplysia cal
40	37	63.8	658	1 KPC1_MOUSE	Q25378 lytechinus
41	37	63.8	672	1 KPC1_MOUSE	P04409 bos taurus
42	37	63.8	672	1 KPC1_MOUSE	P17252 homo sapien
43	37	63.8	672	1 KPC1_MOUSE	P20444 mus musculu
44	37	63.8	672	1 KPC1_MOUSE	P10102 oryctolagus
45	37	63.8	672	1 KPC1_MOUSE	P05696 rattus norv

ALIGNMENTS

RESULT 1

ID SNK_MOUSE STANDARD; PRT; 682 AA.

AC P53351;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Serine/threonine protein kinase SNK (EC 2.7.1.-) (Serum inducible

DE kinase).

GN SNK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus

OX NCBI_TaxID=10090;

RN 11

RP SEQUENCE FROM N.A.

RX MEDLINE=92375085; PubMed=15082117

RA Simmons D.L., Neel B.G., Stevens R., Evett G., Erikson R.D.,

RT "Identification of an early-growth-response gene encoding a novel

putative protein kinase."

RL Mol. Cell. Biol. 12:4164-4169(1992).

CC 1- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELLS

CC TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS,

CC WOUND HEALING OR NEOPLASIA.

CC 1- TISSUE SPECIFICITY: BRAIN, LUNG AND HEART.

CC 1- INDUCTION: BY SERUM AND PHORBOL ESTER.

CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CDC5/PCLO SUBFAMILY.

CC 1- SIMILARITY: Contains 2 PCLO box domains.

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or send an email to license@sib-sib.ch).

CC -----

CC EMBL: M96163; -; NOT_ANNOTATED_CDS.

DR PIR: A44493; A44493.

DR MGI: MGI:1099790; Snk.

DR InterPro: IPR000959; PCLO box.

DR InterPro: IPR000719; Prot_kinase.

DR InterPro: IPR002290; Ser_thr_kinase.

DR Pfam: PF00069; pkinase.

DR Pfam: PF00659; PCLO box; 2.

DR ProDom: PD000001; Prot_kinase; 1.

DR SMART: SMC0220; S_TKC; 1.

DR PROSITE: PS50078; PCLO_BOX; 2.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

KW Transferase; Serine/threonine protein kinase; ATP-binding; Repeat

FT DOMAIN 54 59 POLY-HIS.

FT DOMAIN 79 81 PROTEIN_KINASE.

FT NP_BIND 85 93 ATP (BY SIMILARITY).

FT BINDING 108 108 ATP (BY SIMILARITY)
FT ACT SITE 202 202 BY SIMILARITY
FT DOMAIN 507 570 PCLO BOX 1
FT DOMAIN 603 674 PCLO BOX 2
SQ SEQUENCE 682 AA; 778:11 MW; 596DEABF07208A9D CRC64;

Query Match 94.8%; Score 95; DB 1; Length 682;
Best local Similarity 90.9%; Pred. No. 0.011;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGRPPFFETS 11
DB 270 MLLGRPPFFET 280

RESULT 3
SNK_RAT
ID SNK_RAT STANDARD; PRT; 682 AA;
AC Q9R012;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.1) (Serum inducible kinase)
DE Kinase
GN SNK
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Soturognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID:10116;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=9445245; PubMed=10523292;
RA Kauselmann G., Weiler M., Wulff P., Cessberger S., Kontietzko U., Seifried G., Straubli U., Beretta R., Strehardt K., Kuhl D.;
PT "The polo-like protein kinases Pak and Snk associate with a Cal(2+)-and interaction binding protein and are regulated dynamically with synaptic plasticity."
RT EMBO J. 18:5528-5539(1999).
CC FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA (BY SIMILARITY)
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/PCLO SUBFAMILY.
CC SIMILARITY: Contains 2 PCLO box domains.
CC
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CC
CC EMBO: AF136581; AAF08366.1;
LR InterPro: IPR002959; PCLO_box.
LR InterPro: IPR002719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DE Pfam: PF00069; kinase; 1.
DE Pfam: PF00659; PCLO_box; 2.
DR PUF001: PF000001; Prot_kinase; 1.
DR SMART: SMC0220; S_TKC; 1.
DR PROSITE: PS50078; PCLO_BOX; 2.
DR PROSITE: PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP binding; Repeat.
FT DOMAIN 54 59 PCLO-Box.
FT DOMAIN 79 331 PROTEIN KINASE.
FT NF-BING 85 93 ATP (BY SIMILARITY)
FT BINDING 108 108 ATP (BY SIMILARITY)
FT ACT SITE 202 202 BY SIMILARITY
FT DOMAIN 507 570 PCLO BOX 1
FT DOMAIN 603 674 PCLO BOX 2

SQ SEQUENCE 682 AA; 779:19 MW; 58C50DEBDE83D5F3 CRC64;

Query Match 94.8%; Score 55; DB 1; Length 682;
Best local Similarity 90.9%; Pred. No. 0.011;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGRPPFFETS 11
DB 270 MLLGRPPFFET 280

RESULT 3
SNK_HUMAN
ID SNK_HUMAN STANDARD; PRT; 685 AA;
AC Q9NYY3; C60679; Q96CV7; Q9UE61;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.1) (Serum inducible kinase)
DE Kinase
GN SNK
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Guyang B., Dai W.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN 2;
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Anderson K.M., Nerurkar S.S., Hansbury M.J., Fornwald J., Scott G., Bouzyk M., Mui P., Imbruglia C.S., Carlson K., Marshall L.A., Roshak A.K.;
RT "Identification and characterization of human serum-inducible kinase (SNK), a novel member of the polo-kinase family of cell cycle regulators: potential implication for regulation of vascular smooth muscle proliferation."
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN 3;
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg K.L., Feingold S.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang C., Hsieh F., Diatchenko L., Marzetta K., Ferrer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donato M.F., Casavant T.L., Scheetz T.E., Brownstein M., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Dequelen N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.C., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchran J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN 4;
RP SEQUENCE OF 110-408 FROM N.A.
RA Fidler C., Boulwood J., Wang Jabs E., Wainscoat J.S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/PCLO SUBFAMILY.

```
CC 1 SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF059617; AAC14573.1;
CC EMBL: AF223574; AAF62697.1;
CC EMBL: U85755; AAC00575.1;
CC EMBL: BC013879; AAH13879.1;
CC XREF: 607023;
CC INTERPRO: IPR000959; POLO_box.
CC INTERPRO: IPR000719; Prot_kinase.
CC INTERPRO: IPR002290; Ser_thr_kinase.
CC Pfam: PF00659; pkinase.1.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS50078; POLO_BOX; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOF; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP binding; Repeat.
KW DOMAIN 57 64 POLY-RS.
FT DOMAIN 82 334 PROTEIN_KINASE.
FT NP_BIND 89 96 ATP (BY SIMILARITY).
FT BINDING 111 111 ATP (BY SIMILARITY).
FT ACT_SITE 205 205 HY SIMILARITY.
FT DOMAIN 510 573 POLO_BOX_1.
FT DOMAIN 606 677 POLO_BOX_2.
FT CONFLICT 28 28 A -> G (IN REF. 1).
FT SEQUENCE 695 AA; 78236 MW; 6429565FD8105333 CR '64;
SQ
Query March 94.8%; Score 55; DB 1; Length 695;
Best local similarity 90.9%; Pred. No 51017
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLISRPFFET 11
DB 27: MLISRPFFET 283
RESULT 4
FIRL HUMAN STANDARD; PROT. 695 AA.
AC P53350,
DT 01-OCT-1996 (Ref. 34, Created)
DT 01-OCT-1996 (Ref. 34, Last sequence update)
DT 15-SEP-2003 (Ref. 42, Last annotation update)
DE Serine/threonine protein kinase PLK (Ref. 27,11).
DE threonine protein kinase 13) (STPK1).
GN PLK OR PLKI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catartini; Hominidae; Homo.
CX NCBI: TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94289293; PubMed=8018553;
RA Hamaraka R., Maloid S., Smith M.R., O'Donnell C.O., Longo D.L.,
RA Ferris D.K.;
RT "Cloning and characterization of human and murine homologues of the
RT Drosophila polo serine-threonine kinase";
RL Cell Growth Differ. 5:249-257(1994);
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94067140; PubMed=7902533;
RA Lake R.C., Jelinek W.R.;
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RT "Cell cycle- and terminal differentiation-associated regulation of
RT the mouse mRNA encoding a conserved mitotic protein kinase.";
RL Mol. Cell. Biol. 13:7793-7801(1993);
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95051109; PubMed=7962193;
RA Golsteyn R.M., Schultz S.C., Bartek J., Ziemiecki A., Ried T.,
RA Nigg E.A.;
RT "Cell cycle analysis and chromosomal localization of human Plk1, a
RT putative homologue of the mitotic kinases Drosophila polo and
RT Saccharomyces cerevisiae Cdc5.";
RL Cell Sci. 107:1509-1517(1994);
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94173934; PubMed=8127874;
RA Holtrich U., Wolf G., Braeuninger A., Karn T., Boehme B.,
RA Ruebsamen-Waigmann H., Strebhardt K.;
RT "Induction and down-regulation of PLK, a human serine/threonine
RT kinase expressed in proliferating cells and tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:1736-1740(1994);
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Satchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002);
CC 1- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE.
CC 1- SUBCELLULAR LOCATION: Nuclear.
CC 1- TISSUE SPECIFICITY: PLACENTA AND COLON.
CC 1- DEVELOPMENTAL STAGE: ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
CC DURING S PHASE.
CC 1- INDUCTION: BY GROWTH-STIMULATING AGENTS.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC 1- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U01038; AAA56634.1;
CC EMBL: L19559; AAA36659.1;
CC EMBL: X73458; CAA51837.1;
CC EMBL: X75932; CAA53536.1;
CC EMBL: BC002369; AAH02369.1;
CC EMBL: BC003002; AAH03002.1;
CC EMBL: BC014846; AAH14846.1;
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DR	PIR: S34130; S34130.	CC	MEDLINE=94289293; PubMed=8018557;
DR	Genew: HONC19077; PLK.	RA	Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.L.,
DR	GR: P52350; 1.	RA	Ferris D.K.;
DR	MIM: 602028; 1.	RT	"Cloning and characterization of human and murine homologues of the
DR	GO: GO:0004674; Euprotein serine/threonine kinase activity; TAS.	RT	Drosophila polo serine-threonine kinase.";
DR	GO: GO:0007067; Mitosis; TAS.	RL	Cell Growth Differ. 5:249-257(1994).
DR	GO: GO:0008348; Pioncogenesis; TAS.	RN	(3).
DR	GO: GO:0000074; Piregulation of cell cycle; TAS.	RP	SEQUENCE FROM N.A.
DR	InterPro: IPR000959; PCLO_BOX.	RC	TISSUE=Testis;
DR	InterPro: IPR000719; Prot_kinase.	RX	MEDLINE=94067140; PubMed=7902533;
DR	InterPro: IPR002290; Ser_thr_kinase.	RA	Lake R.J., Jelinek W.R.;
DR	Pfam: PF00669; pkinase; 1.	RT	"Cell cycle- and terminal differentiation-associated regulation of
DR	Pfam: PF00659; PCLO_BOX; 2.	RT	the mouse mRNA encoding a conserved mitotic protein kinase.";
DR	ProDom: PD000001; Prot_kinase; 1.	RL	Mol. Cell. Biol. 13:7793-7801(1993).
DR	SMART: SM00220; S_TKC; 1.	CC	1- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
DR	PROSITE: PS00079; PCLO_BOX; 2.	CC	DURING G1 OR S PHASE.
DR	PROSITE: PS00157; PROTEIN_KINASE_ATP; 1.	CC	1- SUBCELLULAR LOCATION: Nuclear.
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.	CC	1- TISSUE SPECIFICITY: NEWBORN AND ADULT SPLEEN, FETAL AND NEWBORN
DR	PROSITE: PS00109; PROTEIN_KINASE_ST; 1.	CC	KIDNEY, LIVER, BRAIN, THYMUS AND ADULT BONE MARROW, THYMUS,
KW	Transferase; Serine/threonine-protein kinase; ATP binding; Repeat;	CC	OVARY AND TESTES.
NL	Nuclear protein.	CC	1- DEVELOPMENTAL STAGE: IN THE THYMUS, LEVELS INCREASED DURING FETAL
FT	DOMAIN 53 305	CC	DEVELOPMENT, WERE HIGHEST IN NEWBORN ANIMALS AND DECREASED IN THE
FT	NP_BIND 59 67	CC	ADULT. IN THE TESTES, THE PLK LEVELS WERE HIGHER IN THE ADULT THAN
FT	BINDING 82 82	CC	IN PREPUBESCENT MICE WHILE IN THE OVARY, THE LEVELS WERE HIGHER IN
FT	ACT_SITE 176 176	CC	THE PREPUBESCENT MICE. ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
FT	DOMAIN 419 460	CC	PHASES. DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
FT	DOMAIN 515 584	CC	AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
FT	CONFLICT 2 2	CC	DURING S PHASE.
FT	CONFLICT 11 11	CC	1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
FT	CONFLICT 58 58	CC	CDC5/PCLO SUBFAMILY.
FT	CONFLICT 60 60	CC	1- SIMILARITY: Contains 2 PCLO box domains.
FT	CONFLICT 73 73	CC	-----
FT	CONFLICT 141 141	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
FT	CONFLICT 229 229	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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FT	CONFLICT 501 501	CC	modified and this statement is not removed. Usage by and for commercial
FT	CONFLICT 601 601	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
SC	SEQUENCE 601 AA; 68254 NW; 17808FL3C1CRH206 CP 64;	CC	or send an email to license@sib-sib.ch).
DR	EMBL: LC6144; AAA39948.1; 1.	CC	-----
DR	EMBL: J01063; AAAS6635.1; 1.	DR	EMBL: LC6144; AAA39948.1; 1.
DR	EMBL: L19558; AAAL6071.1; 1.	DR	EMBL: J01063; AAAS6635.1; 1.
DR	PIR: A47545; A47545.	DR	EMBL: L19558; AAAL6071.1; 1.
DR	PIR: A54596; A54596.	DR	PIR: A47545; A47545.
DR	MGI: 97621; Plk.	DR	PIR: A54596; A54596.
DR	InterPro: IPR000959; PCLO_BOX.	DR	MGI: 97621; Plk.
DR	InterPro: IPR000719; Prot_kinase.	DR	InterPro: IPR000959; PCLO_BOX.
DR	InterPro: IPR002290; Ser_thr_kinase.	DR	InterPro: IPR000719; Prot_kinase.
DR	Pfam: PF00669; pkinase; 1.	DR	InterPro: IPR002290; Ser_thr_kinase.
DR	Pfam: PF00659; PCLO_BOX; 2.	DR	Pfam: PF00669; pkinase; 1.
DR	ProDom: PD000001; Prot_kinase; 1.	DR	Pfam: PF00659; PCLO_BOX; 2.
DR	SMART: SM00220; S_TKC; 1.	DR	ProDom: PD000001; Prot_kinase; 1.
DR	PROSITE: PS00079; PCLO_BOX; 2.	DR	SMART: SM00220; S_TKC; 1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.	DR	PROSITE: PS00079; PCLO_BOX; 2.
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.	DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE: PS00109; PROTEIN_KINASE_ST; 1.	DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;	DR	PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
NL	Nuclear protein.	KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
FT	DOMAIN 53 305	FT	Nuclear protein.
FT	NP_BIND 59 67	FT	DOMAIN 53 305
FT	BINDING 82 82	FT	NP_BIND 59 67
FT	ACT_SITE 176 176	FT	BINDING 82 82
FT	DOMAIN 419 460	FT	ACT_SITE 176 176
FT	DOMAIN 515 584	FT	DOMAIN 417 480
FT	CONFLICT 2 2	FT	DOMAIN 515 584
FT	CONFLICT 11 11	FT	CONFLICT 4 4
FT	CONFLICT 58 58	FT	CONFLICT 15 15
FT	CONFLICT 60 60	FT	CONFLICT 23 23
FT	CONFLICT 73 73	FT	CONFLICT 27 27
FT	CONFLICT 141 141	FT	CONFLICT 29 29
FT	CONFLICT 229 229	FT	CONFLICT 41 41
FT	CONFLICT 301 301	FT	CONFLICT 54 54
FT	CONFLICT 495 495	FT	CONFLICT 495 495
FT	CONFLICT 501 501	FT	CONFLICT 495 495
FT	CONFLICT 601 601	FT	CONFLICT 495 495
SC	SEQUENCE 601 AA; 68254 NW; 17808FL3C1CRH206 CP 64;	FT	CONFLICT 495 495
DR	EMBL: LC6144; AAA39948.1; 1.	DR	EMBL: LC6144; AAA39948.1; 1.
DR	EMBL: J01063; AAAS6635.1; 1.	DR	EMBL: J01063; AAAS6635.1; 1.
DR	EMBL: L19558; AAAL6071.1; 1.	DR	EMBL: L19558; AAAL6071.1; 1.
DR	PIR: A47545; A47545.	DR	PIR: A47545; A47545.
DR	PIR: A54596; A54596.	DR	PIR: A54596; A54596.
DR	MGI: 97621; Plk.	DR	MGI: 97621; Plk.
DR	InterPro: IPR000959; PCLO_BOX.	DR	InterPro: IPR000959; PCLO_BOX.
DR	InterPro: IPR000719; Prot_kinase.	DR	InterPro: IPR000719; Prot_kinase.
DR	InterPro: IPR002290; Ser_thr_kinase.	DR	InterPro: IPR002290; Ser_thr_kinase.
DR	Pfam: PF00669; pkinase; 1.	DR	InterPro: IPR002290; Ser_thr_kinase.
DR	Pfam: PF00659; PCLO_BOX; 2.	DR	Pfam: PF00669; pkinase; 1.
DR	ProDom: PD000001; Prot_kinase; 1.	DR	Pfam: PF00659; PCLO_BOX; 2.
DR	SMART: SM00220; S_TKC; 1.	DR	ProDom: PD000001; Prot_kinase; 1.
DR	PROSITE: PS00079; PCLO_BOX; 2.	DR	SMART: SM00220; S_TKC; 1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.	DR	PROSITE: PS00079; PCLO_BOX; 2.
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.	DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE: PS00109; PROTEIN_KINASE_ST; 1.	DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;	DR	PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
NL	Nuclear protein.	KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
FT	DOMAIN 53 305	FT	Nuclear protein.
FT	NP_BIND 59 67	FT	DOMAIN 53 305
FT	BINDING 82 82	FT	NP_BIND 59 67
FT	ACT_SITE 176 176	FT	BINDING 82 82
FT	DOMAIN 419 460	FT	ACT_SITE 176 176
FT	DOMAIN 515 584	FT	DOMAIN 417 480
FT	CONFLICT 2 2	FT	DOMAIN 515 584
FT	CONFLICT 11 11	FT	CONFLICT 4 4
FT	CONFLICT 58 58	FT	CONFLICT 15 15
FT	CONFLICT 60 60	FT	CONFLICT 23 23
FT	CONFLICT 73 73	FT	CONFLICT 27 27
FT	CONFLICT 141 141	FT	CONFLICT 29 29
FT	CONFLICT 229 229	FT	CONFLICT 41 41
FT	CONFLICT 301 301	FT	CONFLICT 54 54
FT	CONFLICT 495 495	FT	CONFLICT 495 495
FT	CONFLICT 501 501	FT	CONFLICT 495 495
FT	CONFLICT 601 601	FT	CONFLICT 495 495
SC	SEQUENCE 601 AA; 68254 NW; 17808FL3C1CRH206 CP 64;	FT	CONFLICT 495 495
DR	EMBL: LC6144; AAA39948.1; 1.	DR	EMBL: LC6144; AAA39948.1; 1.
DR	EMBL: J01063; AAAS6635.1; 1.	DR	EMBL: J01063; AAAS6635.1; 1.
DR	EMBL: L19558; AAAL6071.1; 1.	DR	EMBL: L19558; AAAL6071.1; 1.
DR	PIR: A47545; A47545.	DR	PIR: A47545; A47545.
DR	PIR: A54596; A54596.	DR	PIR: A54596; A54596.
DR	MGI: 97621; Plk.	DR	MGI: 97621; Plk.
DR	InterPro: IPR000959; PCLO_BOX.	DR	InterPro: IPR000959; PCLO_BOX.
DR	InterPro: IPR000719; Prot_kinase.	DR	InterPro: IPR000719; Prot_kinase.
DR	InterPro: IPR002290; Ser_thr_kinase.	DR	InterPro: IPR002290; Ser_thr_kinase.
DR	Pfam: PF00669; pkinase; 1.	DR	InterPro: IPR002290; Ser_thr_kinase.
DR	Pfam: PF00659; PCLO_BOX; 2.	DR	Pfam: PF00669; pkinase; 1.
DR	ProDom: PD000001; Prot_kinase; 1.	DR	Pfam: PF00659; PCLO_BOX; 2.
DR	SMART: SM00220; S_TKC; 1.	DR	ProDom: PD000001; Prot_kinase; 1.
DR	PROSITE: PS00079; PCLO_BOX; 2.	DR	SMART: SM00220; S_TKC; 1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.	DR	PROSITE: PS00079; PCLO_BOX; 2.
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.	DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE: PS00109; PROTEIN_KINASE_ST; 1.	DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;	DR	PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
NL	Nuclear protein.	KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
FT	DOMAIN 53 305	FT	Nuclear protein.
FT	NP_BIND 59 67	FT	DOMAIN 53 305
FT	BINDING 82 82	FT	NP_BIND 59 67
FT	ACT_SITE 176 176	FT	BINDING 82 82
FT	DOMAIN 419 460	FT	ACT_SITE 176 176
FT	DOMAIN 515 584	FT	DOMAIN 417 480
FT	CONFLICT 2 2	FT	DOMAIN 515 584
FT	CONFLICT 11 11	FT	CONFLICT 4 4
FT	CONFLICT 58 58	FT	CONFLICT 15 15
FT	CONFLICT 60 60	FT	CONFLICT 23 23
FT	CONFLICT 73 73	FT	CONFLICT 27 27
FT	CONFLICT 141 141	FT	CONFLICT 29 29
FT	CONFLICT 229 229	FT	CONFLICT 41 41
FT	CONFLICT 301 301	FT	CONFLICT 54 54
FT	CONFLICT 495 495	FT	CONFLICT 495 495
FT	CONFLICT 501 501	FT	CONFLICT 495 495
FT	CONFLICT 601 601	FT	CONFLICT 495 495
SC	SEQUENCE 601 AA; 68254 NW; 17808FL3C1CRH206 CP 64;	FT	CONFLICT 495 495
DR	EMBL: LC6144; AAA39948.1; 1.	DR	EMBL: LC6144; AAA39948.1; 1.
DR	EMBL: J01063; AAAS6635.1; 1.	DR	EMBL: J01063; AAAS6635.1; 1.
DR	EMBL: L19558; AAAL6071.1; 1.	DR	EMBL: L19558; AAAL6071.1; 1.
DR	PIR: A47545; A47545.	DR	PIR: A47545; A47545.
DR	PIR: A54596; A54596.	DR	PIR: A54596; A54596.
DR	MGI: 97621; Plk.	DR	MGI: 97621; Plk.
DR	InterPro: IPR000959; PCLO_BOX.	DR	InterPro: IPR000959; PCLO_BOX.
DR	InterPro: IPR000719; Prot_kinase.	DR	InterPro: IPR000719; Prot_kinase.
DR	InterPro: IPR002290; Ser_thr_kinase.	DR	InterPro: IPR002290; Ser_thr_kinase.
DR	Pfam: PF00669; pkinase; 1.	DR	InterPro: IPR002290; Ser_thr_kinase.
DR	Pfam: PF00659; PCLO_BOX; 2.	DR	Pfam: PF00669; pkinase; 1.
DR	ProDom: PD000001; Prot_kinase; 1.	DR	Pfam: PF00659; PCLO_BOX; 2.
DR	SMART: SM00220; S_TKC; 1.	DR	ProDom: PD000001; Prot_kinase; 1.
DR	PROSITE: PS00079; PCLO_BOX; 2.	DR	SMART: SM00220; S_TKC; 1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.	DR	PROSITE: PS00079; PCLO_BOX; 2.
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.	DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE: PS00109; PROTEIN_KINASE_ST; 1.	DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;	DR	PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
NL	Nuclear protein.	KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
FT	DOMAIN 53 305	FT	Nuclear protein.
FT	NP_BIND 59 67	FT	DOMAIN 53 305
FT	BINDING 82 82	FT	NP_BIND 59 67
FT	ACT_SITE 176 176	FT	BINDING 82 82
FT	DOMAIN 419 460	FT	ACT_SITE 176 176
FT	DOMAIN 515 584	FT	DOMAIN 417 480
FT	CONFLICT 2 2	FT	DOMAIN 515 584
FT	CONFLICT 11 11	FT	CONFLICT 4 4
FT	CONFLICT 58 58	FT	CONFLICT 15 15
FT	CONFLICT 60 60	FT	CONFLICT 23 23
FT	CONFLICT 73 73	FT	CONFLICT 27 27
FT	CONFLICT 141 141	FT	CONFLICT 29 29
FT	CONFLICT 229 229	FT	CONFLICT 41 41
FT	CONFLICT 301 301	FT	CONFLICT 54 54
FT	CONFLICT 495 495	FT	CONFLICT 495 495
FT	CONFLICT 501 501	FT	CONFLICT 495 495
FT	CONFLICT 601 601	FT	CONFLICT 495 495
SC	SEQUENCE 601 AA; 68254 NW; 17808FL3C1CRH206 CP 64;	FT	CONFLICT 495 495
DR	EMBL: LC6144; AAA39948.1; 1.	DR	EMBL: LC6144; AAA39948.1; 1.
DR	EMBL: J01063; AAAS6635.1; 1.	DR	EMBL: J01063; AAAS6635.1; 1.
DR	EMBL: L19558; AAAL6071.1; 1.	DR	EMBL: L19558; AAAL6071.1; 1.
DR	PIR: A47545; A47545.	DR	PIR: A47545; A47545.
DR	PIR: A54596; A54596.	DR	PIR: A54596; A54596.
DR	MGI: 97621; Plk.	DR	MGI: 97621; Plk.
DR	InterPro: IPR000959; PCLO_BOX.	DR	InterPro: IPR000959; PCLO_BOX.
DR	InterPro: IPR000719; Prot_kinase.	DR	InterPro: IPR000719; Prot_kinase.
DR	InterPro: IPR002290; Ser_thr_kinase.	DR	InterPro: IPR002290; Ser_thr_kinase.
DR	Pfam: PF00669; pkinase; 1.	DR	InterPro: IPR002290; Ser_thr_kinase.
DR	Pfam: PF00659; PCLO_BOX; 2.	DR	Pfam: PF00669; pkinase; 1.
DR	ProDom: PD000001; Prot_kinase; 1.	DR	Pfam: PF00659; PCLO_BOX; 2.
DR	SMART: SM00220; S_TKC; 1.	DR	ProDom: PD000001; Prot_kinase; 1.
DR	PROSITE: PS00079; PCLO_BOX; 2.	DR	SMART: SM00220; S_TKC; 1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.	DR	PROSITE: PS00079; PCLO_BOX; 2.
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.	DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE: PS00109; PROTEIN_KINASE_ST; 1.	DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;	DR	PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
NL	Nuclear protein.	KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
FT	DOMAIN 53 305	FT	Nuclear protein.
FT	NP_BIND 59 67	FT	DOMAIN 53 305
FT	BINDING 82 82	FT	NP_BIND 59 67
FT	ACT_SITE 176 176	FT	BINDING 82 82
FT	DOMAIN 419 460	FT	ACT_SITE 176 176
FT	DOMAIN 515 584	FT	DOMAIN 417 480
FT	CONFLICT 2 2	FT	DOMAIN 515 584
FT	CONFLICT 11 11	FT	CONFLICT 4 4
FT	CONFLICT 58 58	FT	CONFLICT 15 15
FT	CONFLICT 60 60	FT	CONFLICT 23 23
FT	CONFLICT 73 73	FT	CONFLICT 27 27
FT	CONFLICT 141 141	FT	CONFLICT 29 29
FT	CONFLICT 229 229	FT	CONFLICT 41 41
FT	CONFLICT 301 301	FT	CONFLICT 54 54
FT	CONFLICT 495 495	FT	CONFLICT 495 495
FT	CONFLICT 501 501	FT	CONFLICT 495 495
FT	CONFLICT 601 601	FT	CONFLICT 495 495
SC	SEQUENCE 601 AA; 68254 NW; 17808FL3C1CRH206 CP 64;	FT	CONFLICT 495 495
DR			

SE SOURCE: 602 AA; 68300 MW; 1B980646366EALC CRC64;

Query Match	84.5%	Score 43	DB 1	Length 603
Best local Similarity	72.7%	Pred. NO	0.13	
Matches	8	Mismatches	0	Indels
Conservative	3	Gaps	0	

Qy : YLGRFFETS 11

24 AUGUSTS 254

[illegible]

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PLK1:RAT
ID:PLK1:RAT      STANDARD;      PRI: 603 AA.
AC: 942433
DT: 16-OCT-2001 (Ref: 40, Created)
DT: 16-OCT-2001 (Ref: 40, Last sequence update)
DT: 16-OCT-2001 (Ref: 40, Last annotation update)
DE: Serine/threonine-protein kinase PLK (EC 2.7.1.1) (PLK-K1)
GN: PLK1
OS: Rattus norvegicus (Rat).
OC: Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC: Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
CX: NCB:TaxID=10116;
RW: (1)
RP: SEQUENCE FROM N.A.

```

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to licenses@sib-sib.ch).

DR	EXBL: D16189; AAA18885.1; ..				
DR	InterPro: IPR000959; POLO_box				
DR	InterPro: IPR00719; Prot_Kinase				
DR	InterPro: IPR002907; Ser_Thr_kinase				
DR	Pfam: PF00069; Kinase; 1				
DR	Pfam: PF00659; POLO_box; 2				
DR	ProDom: PD000011; Prot_kinase; 1				
DR	SMART: SM00223; S_TK1				
DR	PROSITE: PS00079; POLO_BOX; 2				
DR	PROSITE: PS00109; PROTEIN_KINASE_ATP; 1				
DR	PROSITE: PS00011; PROTEIN_KINASE_DOM; 1				
DR	PROSITE: PS00109; PROTEIN_KINASE_ST				
KW	Transferase; Serine/threonine protein kinase; Anticodon Repeat				
KW	Nuclear protein				
FT	DOMAIN	53	305		PROTEIN_KINASE
FT	NP_BIND	59	67		ATP (BY SIMILARITY)
FT	BINDING	82	82		ATP (BY SIMILARITY)
FT	ACT_SITE	176	176		BY SIMILARITY
FT	DOMAIN	417	480		POLO_BOX_1
FT	DOMAIN	515	584		POLO_BOX_2
SO	SEQUENCE	603 AA	68313 NW	197AF6P8PRT55002	CE0144

Query Match: 84.5%; Score 49; CB 1; Length 60;
Best Local Similarity 72.7%; Pred. No. 0.13;
Matches: 3; Conservative 3; Mismatches 3; Gaps 0

SYNOPSIS OF PROCEEDINGS IN

100

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RESULT 7
STKD_MCUSE
ID STKD_MCUSE STANDARD; PRG; 282 AA.
AC 088445; Q9JLC2;
DT 28-FEB-2003 (Rel. 41, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP 2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 13 (EC 2.7.1.37) (Aurora/Ipl1/Eg2
DE protein 1) (Aurora C).
GN STK13 OR AIE1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=99025616; PubMed=9809744;
RA Tseng T.C., Chen S.H., Hsu Y.P., Tang T.K.;
RT "Protein kinase profile of sperm and eggs: cloning and
RT characterization of two novel testis-specific protein kinases (AIE1
RT AIE2) related to yeast and fly chromosome segregation regulators."
RL DNA Cell Biol. 17:823-833(1998).

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CC use by non profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).

EMBL:	AF054620:	AA025954.1	
EMBL:	AF195272:	AAF25938.1	
HSSP:	Q63450:	AC6	
MGD:	MGI132119:	Stk13	
InterPro:	IPR000719:	Prot_kinase	
InterPro:	IPR002290:	Ser_thr_kinase	
InterPro:	IPR001245:	Tyr_kinase	
Pfam:	PFC0069:	pkinese	
PRINTS:	PR00109:	TYRKINASE	
ProDom:	PD000001:	Prot_kinase; 1	
SMART:	SM00220:	S_TKc; 1	
PROSITE:	PS00107:	PROTEIN_KINASE_ATP;	
PROSITE:	PS00108:	PROTEIN_KINASE_ST;	
PROSITE:	PS00111:	PROTEIN_KINASE_DOMA	
Cell cycle:	Transferrase;	Serine/thre	
DOMAIN	16	266	PROTEIN
NP BIND	22	30	ATP (BY
BINDING	45	45	ATP (BY
ACT SITE	139	139	BY SIMIL
CONSERVED	74	74	PROTEIN


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RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RX MEDLINE=38122855; PubMed=9454730;
RA Boghi C., Giet R., Uzbekov R., Marin N., Chartrain L., Le Guellec R.,
RA Couturier A., Doree M., Philippe M., Prigent C.,
RT "The Xenopus protein kinase pEg2 associates with the centrosome in a
RT cell cycle-dependent manner, binds to the spindle microtubules and is
RT involved in bipolar mitotic spindle assembly.";
RD J. Cell Sci. 111:557-572(1998).
CC 1- FUNCTION: Associates with the centrosome in a cell-cycle dependent
CC manner and invades the microtubules at the poles of the spindle
CC during mitosis suggesting that it may be involved in the correct
CC formation of bipolar mitotic spindles.
CC 1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC 1- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
CC especially from prophase through anaphase. Partially colocalised
CC with gamma tubulin in the centrosome, from S to M phase.
CC 1- TISSUE SPECIFICITY: Highly expressed in ovary and testis.
CC 1- PTM: Phosphorylated.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch.
CC
DR EMBL: Z17207; CAA78915.1;
DR F15: S52243; S52243.
DR HSSP: P24941; IAQ1.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Cell cycle; Transferase; Serine/threonine protein kinase; ATP binding;
KW Phosphorylation.
FT DOMAIN 140 390 PROTEIN KINASE.
FT NP BIND 146 154 ATP (BY SIMILARITY).
FT BINDING 169 169 ATP (BY SIMILARITY).
FT ACT SITE 263 263 BY SIMILARITY.
SQ SEQUENCE 408 AA; 46372 MW; 7E5E9A76E117707E7E6A
Query Match 74.1%; Score 43; DB 1; Length 408;
Best Local Similarity 77.8%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 0; Gaps 0;

QY 2 LSGRPPFET 10
|:|:|
Db 330 LVGKPPFET 338

RESULT 10
ST6L XENLA
ID ST6L XENLA STANDARD; PRT; 405 AA.
AC Q91819;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine protein kinase Eg2-like (EC 2.7.1.37) (p46X1Eg22).
CS Xenopus laevis (African clawed frog).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
CC Xenopodinae; Xenopus.
CX NCBI TaxID=8155;
RN 11

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RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RA Roghi C., Le Guellec R., Paris J., Couturier A., Philippe M.,
RT "Eg2, selected by differential screening encodes a new Xenopus protein
RT kinase family.";
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
CC 1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC 1- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
CC especially from prophase through anaphase. Partially colocalised
CC with gamma tubulin in the centrosome, from S to M phase (By
CC similarity).
CC 1- PTM: Phosphorylated (By similarity).
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch.
CC
DR EMBL: Z17205; CAA78914.1; ALT_INIT.
DR HSSP: P24941; IAQ1.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Cell cycle; Transferase; Serine/threonine protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 140 390 PROTEIN KINASE.
FT NP BIND 146 154 ATP (BY SIMILARITY).
FT BINDING 169 169 ATP (BY SIMILARITY).
FT ACT SITE 263 263 BY SIMILARITY.
SQ SEQUENCE 408 AA; 46461 MW; 97F6A69C7357AEE8 CRC64;
Query Match 74.1%; Score 43; DB 1; Length 408;
Best Local Similarity 77.8%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSGRPPFET 10
|:|:|
Db 330 LVGKPPFET 338

RESULT 11
CNK_RAT
ID CNK_RAT STANDARD; PRT; 615 AA.
AC Q9R011;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytokine-inducible serine/threonine-protein kinase (EC 2.7.1.37) (FGF-
DE inducible kinase) (Fragment).
GN CNK OR FNK.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI TaxID=10116;
RN 11
SEQUENCE FROM N.A.
RX MEDLINE=99452760; PubMed=10523297;
RA Kauselmann G., Weiler M., Wulff P., Jessberger S., Konietzko U.,
RA Scafid J., Stauber J., Bereiter-Hahn J., Streibhardt K., Kuhl D.,
RT "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and
RT integrin-binding protein and are regulated dynamically with synaptic
RT plasticity.";

```

EMBL J. 18:5528-5533(1999).

CC FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN REGULATING M

CC PHASE FUNCTIONS DURING THE CELL CYCLE. MAY ALSO BE PART OF THE

CC SIGNALING NETWORK CONTROLLING CELLULAR ADHESION. IN VITRO, IS ABLE

CC TO PHOSPHORYLATE CDC25C AND CASEIN (BY SIMILARITY).

CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC SUBUNIT: BINDS TO THE CALCIUM/INTEGRIN-BINDING PROTEIN (CIB). THIS

CC INTERACTION PROBABLY OCCURS VIA THE POLO-BOX DOMAIN.

CC SUBCELLULAR LOCATION: WHEN INDUCED, IT TRANSLOCATES INTO THE

CC CYTOSOL OF ACTIVATED NEURONS.

CC TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN POST MITOTIC

CC NEURONS.

CC INDUCTION: BY THE INTENSE ACTIVITY ASSOCIATED WITH SEIZURES.

CC PTM: PHOSPHORYLATED AS CELLS ENTER MITOSIS AND DEPHOSPHORYLATED AS

CC CELLS EXIT MITOSIS (BY SIMILARITY).

CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CDC5/PCLO SUBFAMILY.

CC SIMILARITY: Contains 2 PCLO box domains.

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EMBL; AF136584; AAF08367.1; -

DR InterPro; IPR0000959; PCLO_box.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR Pfam; PF00669; Pkinase; 1.

DR Pfam; PF00659; PCLO_box; 2.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SMC0220; S_TKC; 1.

DR PROSITE; PS00078; PCLO_BOX; 2.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Transferase; Serine/threonine-protein kinase; ATP binding; Repeat;

KW Phosphorylation.

FT NON TER 1 1

FT DOMAIN 31 283 PROTEIN KINASE.

FT NE BIND 37 45 ATP (BY SIMILARITY).

FT BINDING 60 60 ATP (BY SIMILARITY).

FT ACT SITE 154 154 BY SIMILARITY.

FT DOMAIN 440 503 PCLO_BOX_1.

FT DOMAIN 537 607 PCLO_BOX_2.

FT NON TER 619 619

SC SEQUENCE 619 AA; 6860 MW; 68600.000 Da; 1.01 kDa.

Query Match 70.7% Score 415.00 E-100 Local Ids

Best local Similarity 63.6% Pred. No. 4

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0

QY 1 MLLGRPPFFETS 11

DB 222 LLCSPFPETA 232

RESULT 12

CNK_MOUSE

ID CNK_MOUSE STANDARD; PRT: 631 AA

AC Q6C822; Q6C822; Q9R009;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytokine-inducible serine/threonine-protein kinase (EC 2.7.1.37) (FGF-

DE inducible kinase).

GN CNK OR FNK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN=N1H Swiss;

RX MEDLINE=95247749; PubMed=7730342;

RA Donohue P.C., Alberts G.F., Guc Y., Winkles J.A.;

RT "Identification by targeted differential display of an immediate early

RT gene encoding a putative serine/threonine kinase.";

RL J. Biol. Chem. 270:10351-10357(1995).

RN [2]

RP SEQUENCE OF 333-437 FROM N.A. (ISOFORM 2).

RC STRAIN=N1H Swiss;

RA Kauselmann G., Weiler M., Kuhl D.;

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP FUNCTION, AND PHOSPHORYLATION.

RX MEDLINE=98343954; PubMed=9677325;

RA Chase D., Feng Y., Hanshaw P., Winkles J.A., Longo D.L., Ferris D.K.;

RT "Expression and phosphorylation of fibroblast-growth-factor-inducible

RT kinase (Fnk) during cell-cycle progression.";

RL Biochem. J. 333:655-660(1998).

CC FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN REGULATING M

CC PHASE FUNCTIONS DURING THE CELL CYCLE. MAY ALSO BE PART OF THE

CC SIGNALING NETWORK CONTROLLING CELLULAR ADHESION. IN VITRO, IS ABLE

CC TO PHOSPHORYLATE CDC25C AND CASEIN (BY SIMILARITY).

CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC SUBUNIT: BINDS TO THE CALCIUM/INTEGRIN-BINDING PROTEIN (CIB). THIS

CC INTERACTION PROBABLY OCCURS VIA THE POLO-BOX DOMAIN (BY

CC SIMILARITY).

CC SUBCELLULAR LOCATION: Membrane-associated (By similarity).

CC ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q60806-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q60806-2; Sequence=VSP_004927;

CC TISSUE SPECIFICITY: EXPRESSED IN SKIN.

CC PTM: PHOSPHORYLATED AS CELLS ENTER MITOSIS AND DEPHOSPHORYLATED AS

CC CELLS EXIT MITOSIS.

CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CDC5/PCLO SUBFAMILY.

CC SIMILARITY: Contains 2 PCLO box domains.

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EMBL; U21392; AAC52191.1; -

DR EMBL; U22434; AAC52192.1; -

DR EMBL; AF136586; AAF08369.1; -

DR PIR; A57286; A57286.

DR MGD; MGI:109604; Cnk.

DR InterPro; IPR0000959; PCLO_box.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR Pfam; PF00669; Pkinase; 1.

DR Pfam; PF00659; PCLO_box; 2.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SMC0220; S_TKC; 1.

DR PROSITE; PS00078; PCLO_BOX; 2.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;

KW Phosphorylation; Alternative splicing.

FT DOMAIN 63 315 PROTEIN KINASE.

FT NE BIND 69 77 ATP (BY SIMILARITY).

FT BINDING 92 92 ATP (BY SIMILARITY).

FT ACT_SITE 156 186 BY SIMILARITY.

FT DOMAIN 455 518 POLO BOX 1;
FT DOMAIN 552 622 POLO BOX 2;
FT VAPSRIC 373 373 L -> LVSGGLMRTSTGHPPVRR (in isoform 2);
FT CONFLICT 386 386 /FTID=VSP_004927;
SQ SEQUENCE 631 AA; 70012 MW; 20853341870DS1D2 CRK14;
Query Match 70.7%; Score 41; DB 1; Length 631;
Best Local Similarity 63.6%; Pred. No. 4.6;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLLGRPPFFETS 11
DB 253 LLCGSPPFFETA 264
RESULT 14
CNK_HUMAN
ID CNK_HUMAN STANDARD; PRT; 646 AA
AC Q9R4P4; Q15767;
ET 16-OCT-2001 (Rel. 40, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Cytokine-inducible serine/threonine protein kinase (EC 2.7.1.37) (FGF-inducible kinase) (proliferation-related kinase).
DE Inducible kinase.
GN CNK OR FNK OR PRK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=20493044; PubMed=11039900;
RA Holtzman U., Wolf G., Yuan J., Beresiter-Hahn J., Kuhn T., Weiler M., Kauselmann G., Rehli M., Andreesen R., Kaufmann M., Kuhl U., Stetshardt K.;
RA "Adhesion induced expression of the serine/threonine kinase Fnk in human macrophages";
RA Oncogene 19:4832-4839(2000).
RN [2]
RP SEQUENCE OF 28-646 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96125093; PubMed=9702627;
RA Li B., Gouyang B., Pan H., Reissmann P.T., Sharon D.C., Aracci R., Lu L., Dai W.;
RA "Prk, a cytokine-inducible human protein serine/threonine kinase whose expression appears to be down-regulated in lung carcinomas";
RA J. Biol. Chem. 271:19492-19498(1996).
RN [3]
RP CHARACTERIZATION;
RX MEDLINE=98019242; PubMed=9353331;
RA Gouyang B., Pan H., Lu L., Li J., Stetshardt K., Sharon D.C., Dai W.;
RA "Human Prk is a conserved protein serine/threonine kinase involved in regulating V phase functions";
RA J. Biol. Chem. 272:28646-28651(1997).
RN [4]
RP CHARACTERIZATION;
RX MEDLINE=20027391; PubMed=10557092;
RA Gouyang B., Li W., Pan H., Meadows J., Hoffmann I., Dai W.;
RA "The physical association and phosphorylation of C125C protein phosphatase by Prk";
RA Oncogene 18:6029-6036(1999).
RL -1- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN REGULATING M PHASE FUNCTIONS DURING THE CELL CYCLE. MAY ALSO BE PART OF THE SIGNALING NETWORK CONTROLLING CELLULAR ADHESION. IN VITRO, IS ABLE TO PHOSPHORYLATE CDC25C AND CASEIN.
CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphorylated protein.
CC -1- SUBUNIT: BINDS TO THE CALCIUM/INTERIN-BINDING PROTEIN (CIB). THIS INTERACTION PROBABLY OCCURS VIA THE POLO-BOX DOMAIN.
CC -1- SUBCELLULAR LOCATION: Membrane-associated.
CC -1- TISSUE SPECIFICITY: TRANSCRIPTS ARE HIGHLY DETECTED IN PLACENTA, LUNG, FOLLOWED BY SKELETAL MUSCLE, HEART, PANCREAS, OVARIES AND

CC KIDNEY AND WEAKLY DETECTED IN LIVER AND BRAIN. MAY HAVE A SHORT HALF-LIFE. IN CELLS OF HEMATOPOIETIC ORIGIN, STRONGLY AND EXCLUSIVELY DETECTED IN TERMINALLY DIFFERENTIATED MACROPHAGES. TRANSCRIPTS EXPRESSION APPEARS TO BE DOWN-REGULATED IN PRIMARY LUNG TUMOR.
CC -1- INDUCTION: CYTOKINE AND CELLULAR ADHESION TRIGGER FNK INDUCTION.
CC -1- PTM: PHOSPHORYLATED AS CELLS ENTER MITOSIS AND DEPHOSPHORYLATED AS CELLS EXIT MITOSIS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC5/POLO SUBFAMILY.
CC -1- SIMILARITY: Contains 2 POLO box domains.
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CC EMBL; AC293866; CAC13659.1;
CC EMBL; U56998; AAC50637.1; ALT_INIT;
CC Genew; HGNC:2154; CNK.
CC GK; Q9H4B4;
CC MIM; 602913;
CC GO; GO:0004674; P:protein serine/threonine kinase activity; TAS.
CC GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
CC GO; GO:0000374; P:regulation of cell cycle; TAS.
CC InterPro; IPR000959; POLO_box.
CC InterPro; IPR00719; Prot_kinase.
CC InterPro; IPR02290; Ser_thr_kinase.
CC Pfam; PF0069; pkinase; 1.
CC Pfam; PF0659; POLO_box; 2.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM0C220; S_TKc; 1.
CC PROSITE; PS00078; POLO_BOX; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat; Phosphorylation.
KW DOMAIN 62 314 PROTEIN KINASE.
FT NP_BIND 68 76 ATP (BY SIMILARITY).
FT BINDING 91 91 ATP (BY SIMILARITY).
FT ACT_SITE 185 185 BY SIMILARITY.
FT DOMAIN 470 537 POLO_BOX_1.
FT DOMAIN 567 637 POLO_BOX_2.
FT CONFLICT 99 99 V -> A (IN REF. 2).
FT CONFLICT 353 353 V -> G (IN REF. 2).
FT CONFLICT 419 419 H -> D (IN REF. 2).
FT CONFLICT 464 470 FSEWVGF -> VSKWVDY (IN REF. 2).
FT CONFLICT 522 522 R -> P (IN REF. 2).
SQ SEQUENCE 646 AA; 71789 MW; C20147C0CFC8A3B4 CRC64;
Query Match 70.7%; Score 41; DB 1; Length 646;
Best Local Similarity 63.6%; Pred. No. 4.6;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLLGRPPFFETS 11
DB 253 LLCGSPPFFETA 263
RESULT 14
STKC_PIG
ID STKC_PIG STANDARD; PRT; 156 AA.
AC Q9N3X0;
DT 28-FEB-2003 (Rel. 41, Created);
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora-B) (Fragment).
GN STK12.


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OS Sus scrofa (Pig).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
OX NCBI_TaxID:9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=small intestine;
RX MEDLINE=2222238; PubMed=12270407;
RA Brian F., Hosseini S.M., Lorf T., Luens S., Ringe B.
RT "Differential gene expression during intestinal ischemia/reperfusion
injury";
RL Transplant. Proc. 34:2302-2302(2002).
CC [1]
CC FUNCTION: Maybe directly involved in regulating the cleavage of
polar spindle microtubules and is a key regulator for the onset of
cytokinesis during mitosis (By similarity).
CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC SUBCELLULAR LOCATION: Localized to the midzone of central spindle
in late anaphase and concentrated into the midbody in telophase
and cytokinesis. Colocalized with gamma tubulin in the mid-body
(By similarity).
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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or send an email to licenses@ebi.ac.uk).
CC
DR EMBL: AF244364; AAF61735.1;
DR InterPro: IPR002052; Nucleotidyl transferase;
DR InterPro: IPR002719; Protein kinase;
DR InterPro: IPR022907; Ser/thr_pkinase;
DR InterPro: IPR012451; Tyr_pkinase;
DR Pfam: PF00369; pkinase; 1;
DR PRINTS: PR0104; TYRKINASE;
DR PRODOM: PD00001; Prot_kinase; 1;
DR PROSITE: PS00011; PROTEIN_KINASE_LCK_1;
DR PROSITE: PS0108; PROTEIN_KINASE_ST_1;
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
FT NON_TER 1 156
FT DOMAIN <1 >156 PROTEIN_KINASE
FT ACT_SITE 51 51 BY SIMILARITY
FT NON_TER 156 156
SQ SEQUENCE 156 AA; 17867 MW; 12.4 kDa; 4.80% GC;
Query Match 69.03; Score 11.05; E-value 1.0e-04
Best Local Similarity 54.93; Prob. 0.000166
Matches 6; Conservative 4; Mismatches 1; Gaps 0;
QY 1 MILLERPFPEFS 11
DQ 11 MILLERPFPEFS 127
RESULT 11
STRC HUMAN
ID STRC_HUMAN STANDARD; PRO; 344 AA
AC Q96J54; Q14630; Q6C446; Q95083; Q96J57; Q9UQ46;
DT 29-FEB-2003 (Rel. 41, Created)
DT 29-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 12 (EC 2.7.1.37). Aurora- and Ipl1-
DE like midbody-associated protein 1 (Aim1) (Aurora/BIC1-related kinase
DE 2). Aurora-related kinase 2 (ARK2) (Aurora B).
GN STK12 OR AIM1 OR ARK2 OR AIK2.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catartiodactyla; Hominiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=98183439; PubMed=9514916;
RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
RA Gilbert D.S., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
RT "cDNA cloning, expression, subcellular localization, and chromosomal
assignment of mammalian aurora homologues, aurora-related kinase (ARK)
1 and 2";
RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98225855; PubMed=9809983;
RA Tatsuka M., Katayama H., Ota T., Tanaka T., Odashima S., Suzuki F.,
RA Terada Y.;
RT "Multinuclearity and increased ploidy caused by overexpression of the
aurora- and Ipl1 like midbody-associated protein mitotic kinase in
human cancer cells";
RL Cancer Res. 58:4811-4816(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver, and Spleen;
RX MEDLINE=99077743; PubMed=9858806;
RA Kimura M., Matsuda Y., Yoshioka T., Sumi N., Okano Y.;
RT "Identification and characterization of STK12/Aik2: a human gene
related to aurora of Drosophila and yeast Ipl1";
RL Cytogenet. Cell Genet. 82:147-152(1998).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21364697; PubMed=11471245;
RA Prigent C., Gill R., Trower M., Sanseau P.;
RT "In silico cloning of a new protein kinase, Aik2, related to
Drosophila aurora using the new tool: EST Blast";
RL In Silico Biol. 1:123-128(1999).
RN [5]
RP SEQUENCE FROM N.A.
RA Zhang Q., Yu L., Bi A.;
RT "Cloning of a novel human gene homologous to mouse STK-1";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, Lymph, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong S.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellanc N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.C., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP REVIEW.
RX MEDLINE=21355577; PubMed=11413462;
RA Nigg E.A.;
RT "Mitotic kinases as regulators of cell division and its checkpoints";
RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
CC [1]
CC FUNCTION: May be directly involved in regulating the cleavage of
polar spindle microtubules and is a key regulator for the onset of
cytokinesis during mitosis.
CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC SUBCELLULAR LOCATION: Localized to the midzone of central spindle
in late anaphase and concentrated into the midbody in telophase
```

and cytokinesis. Colocalized with gamma tubulin in the mid-body.
TISSUE SPECIFICITY: High level expression seen in the thymus. It
is also expressed in the spleen, lung, testis, colon, placenta and
fetal liver. Expressed during S and G2/M phase and expression is
upregulated in cancer cells during M phase.
DISEASE: Disruptive regulation of expression is a possible
mechanism of the perturbation of chromosome integrity in cancer
cells through its dominant-negative effect on cytokinesis.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
AURORA SUBFAMILY.

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or send an email to licenses@ebi-sis.ch.

EMBL: AF008552; AAC12709.1;
EMBL: AB011450; BAA32136.1;
EMBL: AB011446; BAA82709.1;
EMBL: AF004022; AAB65786.1;
EMBL: AF015254; AAC98891.1;
EMBL: BC000442; AAH00442.1;
EMBL: BC009751; AAH09751.1;
EMBL: BC013303; AAH13303.1;
EMBL: Q61450; I406.
Genbank: HGNC:11330; STK12.
RefSeq: Q96G04;
MIM: 604920.
InterPro: IPR02052; N6_Mtase.
InterPro: IPR02219; Prot_kinase.
InterPro: IPR02290; Ser_thr_kinase.
InterPro: IPR01245; Tyr_kinase.
Pfam: PF00269; pkinase; 1.
ProDom: PD000001; Prot_kinase; 1.
SMART: SM00220; S_TKc; 1.
SMART: SM00219; TyrKc; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
PROSITE: PS00108; PROTEIN_KINASE_ST_1.
PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
KW: Cell cycle; transferase; Serine/threonine protein kinase; ATP binding.
FT DOMAIN 77 327 PROTEIN KINASE.
FT BINDING 83 91 ATP (BY SIMILARITY).
FT BINDING 106 106 ATP (BY SIMILARITY).
FT ACT_SITE 200 200 BY SIMILARITY.
FT CONFLICT 14 15 RQ -> R IN REF. 1.
FT CONFLICT 70 70 E -> R IN REF. 4 AND 5.
FT CONFLICT 162 162 E -> Y IN REF. 4 AND 5.
FT CONFLICT 167 169 QKS -> R IN REF. 3.
FT CONFLICT 179 179 T -> T YR IN REF. 4.
FT CONFLICT 180 180 I -> V IN REF. 3.
FT CONFLICT 226 226 P -> T IN REF. 3.
FT CONFLICT 249 250 MH -> D IN REF. 3.
FT CONFLICT 271 271 MISSING IN REF. 3.
FT CONFLICT 298 298 T -> M IN REF. 6; AAH09751; AAH13303.
SQ SEQUENCE 344 AA; 39280 MW; 8125E3E5A1F5170 CF 64;

Query Match 69.8%; Score 40; E: 1e-10; Length 114;
Best local similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 4; Mismatches 1; Gaps 0;

QY 1 MLUGRPFFETS 11
266 LLVGNPFFESA 276

RESULT 16
STK5 HUMAN STANDARD; PRT; 403 AA.
AC Q14965; Q60445; Q75873; Q9BQD6; Q9G0R4;
PT 28 FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine kinase 6 (EC 2.7.1.37) (Serine/threonine kinase 15)
DE (Aurora/IPL1-related kinase 1) (Aurora-related kinase 1) (HARK1)
DE (Aurora-A) (Breast-tumor-amplified kinase)
GN STK6 OR STK15 OR AIK OR ARK1 OR AURA OR BTA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=97298083; Pubmed=9153231;
RA Kimura M., Kotani S., Hattori T., Sumi N., Yoshioka T., Todokoro K.,
Chano Y.
RT "Cell cycle-dependent expression and spindle pole localization of a
novel human protein kinase, Aik, related to Aurora of Drosophila and
yeast Ipl1."
RL J. Biol. Chem. 272:13766-13771(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98183439; Pubmed=9514916;
RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.
RT "cDNA cloning, expression, subcellular localization, and chromosomal
assignment of mammalian aurora homologues, aurora-related kinase (ARK)
1 and 2."
RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=98442657; Pubmed=9771714;
RA Zhou H., Kuang J., Zhong L., Kuo W.-L., Gray J.W., Sahin A.,
Brinkley B.R., Sen S.
RT "Tumour amplified kinase STK15/BTAk induces centrosome amplification,
aneuploidy and transformation."
RL Nat. Genet. 20:189-193(1998).
RN [4]
RP SEQUENCE FROM N.A.
RA Wang L., Thibodeau S.N.
RT "Mutational analysis of the STK15 gene in human tumors."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; Pubmed=11780052;
RA Delidakis P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Beasley C.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Chapman C.C., Clapp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coulson A., Coville G.J., Deadman P., Dhani P.D., Dunn M.,
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.D., Martin S.L., McConnachie L.J., McIlroy K., McMurray A.A.,
Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
Skuce C.D., Smith M.J., Soderlund C., Steward C.A., Sulston J.E.,
Swann R.M., Sycamore N., Taylor R., Tee L., Thomas J.W., Thorpe A.,
Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Wilmink L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.
RT "The DNA sequence and comparative analysis of human chromosome 20."
RL Nature 414:865-97(2001).

RA SEQUENCE FROM N.A.
PC TISSUE=Cervix, Colon, Kidney, and Muscle;
PX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,
RA Klapper R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.C.,
RA Altschul S.F., Zeeberg E., Buettow K.H., Schaefer C.H., Agar R.K.,
RA Hopkins R.F., Jordan H., Moore T., Nak S., Wang J., Heath E.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin J.M., Hong E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scherz T.E.,
RA Brownstein M., Usdin T.E., Toshiyuki S., Gattner P., Prange C.,
RA Pata S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
RA Busk S.A., McEwan P.J., McKernan R.J., Malek D.A., Guetart P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Soderstrom E.C., Liu X., Hicks E.A.,
RA Fahy J., Hulton E., Ketteran M., Vautier A., Rodriguez J., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G.,
RA Hakesley R.W., Touchman J.W., Green E.D., Jackson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.V.,
RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Skolnik D.S.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marla Y.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences".
RI From: Nucleic Acids Sci. U.S.A. 99:14499-14903:2002;
RN [7]
RP CELL-CYCLE REGULATION.
RX MEDLINE=21306577; PubMed=11413462;
RA Tanaka M., Jeda A., Kanamori H., Ideguchi H., Yano J., Kitajima S.,
RA Ishigatsubo Y.,
RT "Cell cycle dependent regulation of human aurora A transcription is
RT mediated by periodic repression of B47F1".
RG J. Biol. Chem. 277:10719-10726(2002).
RN [8]
RP REVIEW.
RX MEDLINE=21306577; PubMed=11413462;
RA Nigg E.A.,
RT "Mitotic kinases as regulators of cell division at its checkpoints".
RI Nat. Rev. Mol. Cell Biol. 2:212-223(2001).
CC 1 FUNCTION: May play a role in cell cycle regulation during anaphase
CC and/or telophase, in relation to the function of the
CC centrosome/spindle pole region during chromosome segregation.
CC May be involved in microtubule formation and/or stabilization.
CC May play a key role during tumor development and progression.
CC CATALYTIC ACTIVITY: ATP + a protein + H₂O -> a phosphorylated
CC SUBCELLULAR LOCATION: Localized on centrosomes in interphase cells
CC and at each spindle pole in mitosis.
CC TISSUE SPECIFICITY: Highly expressed in testis and kidney in
CC skeletal muscle, thymus and spleen. Also highly expressed in
CC colon, ovary, prostate, brain, endometrium, heart, and placenta.
CC Cancer cell lines. Expressed in a variety of human tumor cell lines in
CC G1/S, accumulates during G₂M, and localizes on spindle poles in
CC PMV phosphorylated.
CC DISEASE: Defects in STK6 are most likely to be associated with centrosome
CC alterations including aneuploidy.
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CA CAUTION: Ref.1 sequence differs from that shown due to frameshifts
CC in positions 105, 125, 129, 235 and 241.
CC CAUTION: Although authors have considered STK6 and STK15 as two
CC different proteins, it is clear that they are the same protein.
CC
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CC entities requires a license agreement. (See <http://www.ebi.ac.uk/submit/submit.html>
CC or send an email to license@ebi.ac.uk.)
CC
CC EXP. 084212; BAA23592.1; AAF29547
CC EXP. 084212; AAC12708.1;
CC EXP. 084212; AAC23448.1;
CC EXP. 084212; AAC63902.1;

DR EMBL; AF195947; AAF29508.1;
DR EMBL; AF195942; AAF29508.1; JOINED.
DR EMBL; AF195943; AAF29508.1; JOINED.
DR EMBL; AF195944; AAF29508.1; JOINED.
DR EMBL; AF195945; AAF29508.1; JOINED.
DR EMBL; AF195946; AAF29508.1; JOINED.
DR EMBL; AL121914; CAC12717.1;
DR EMBL; BC001280; AAF01280.1;
DR EMBL; BC002493; AAF02493.1;
DR EMBL; BC006423; AAF06423.1;
DR EMBL; BC027464; AAF27464.1;
DR GK; O14965;
DR MIM; 602687;
DR YIM; 603072;
DR HSSP; P24941; LECH.
DR Genew; HGNC:11409; STK6.
DR Genew; HGNC:11393; STK15.
DR GO; GO:0005634; Cytosol; TAS.
DR GO; GO:0005819; Cytosol; TAS.
DR GO; GO:0007367; Proliferation; TAS.
DR GO; GO:0006468; Proliferation; TAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; STK; 1.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW phosphorylation.
FT DOMAIN 133 383 PROTEIN KINASE.
FT NP_BIND 139 147 ATP (BY SIMILARITY).
FT BINDING 162 162 ATP (BY SIMILARITY).
FT ACT_SITE 256 256 BY SIMILARITY.
FT CONFLICT 31 31 F > I (IN REF. 3).
FT CONFLICT 57 57 V -> I (IN REF. 2).
SQ SEQUENCE 403 AA; 45829 MW; 125F3594834CD157 CRC64;

Query Match 67.2% Score 39; DB 1; Length 403;
Best Local Similarity 60.0% Pred. No. 6.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LGGPPPPETS 1;
DB 323 LVGPPPPPPPP 332

RESULT 17
TF65 CHICK STANDARD; PKT; 558 AA.
AC P98152;
DT 01-OCT-1996 (Ref. 34, Created).
DT 01-OCT-1996 (Ref. 34, Last sequence update).
DT 28-FEB-2003 (Ref. 41, Last annotation update).
DE Transcription factor p65 (Nuclear factor NF-kappa-B p65 subunit).
GN RELA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=94040817; PubMed=7916720;
RA Ikeda T., Honjo K., Hirota Y., Onodera T.,
RT "Isolation of the chicken NF-kappa B p65 subunit-encoding cDNA and
RT characterization of its products".
RL Gene 193:120-124(1993).
CC 1 FUNCTION: p65 IS A SUBUNIT OF THE NUCLEAR FACTOR KAPPA-B, A SECOND

CC MESSENGER, WHICH ACTIVATES THE TRANSCRIPTION OF A NUMBER OF GENES
CC IN MULTIPLE TISSUES. THE INHIBITORY EFFECT OF I-KAPPA-B UPON
CC NF-KAPPA-B IN THE CYTOPLASM IS EXERTED PRIMARILY THROUGH THE
CC INTERACTION WITH P65. P65 SHOWS A WEAK DNA-BINDING SITE WHICH
CC COULD CONTRIBUTE DIRECTLY TO DNA BINDING IN THE NF-KAPPA-B
CC COMPLEX.
CC SUBUNIT: ACTIVE NF-KAPPA-B IS A HETERODIMER OF AN ABOUT 50 kDa
CC DNA-BINDING SUBUNIT AND THE WEAK DNA-BINDING SUBUNIT P65. TWO
CC HETERODIMERS MIGHT FORM A LABILE TETRAMER.
CC SUBCELLULAR LOCATION: NUCLEAR, BUT ALSO FOUND IN THE CYTOPLASM
CC IN AN INACTIVE FORM COMPLEXED TO AN INHIBITOR (I-KAPPA-B).
CC TISSUE SPECIFICITY: SPLEEN; LOWER LEVEL IN BRAIN.
CC SIMILARITY: BELONGS TO THE REL/DORSAL FAMILY.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: D13721; BAA02874.1; --
CC PIR: JC2004; JC2004.
CC HSSP: OC4207; I1KN.
CC InterPro: IPR002909; IPT TIG.
CC InterPro: IPR003451; NF_Rel_dor_fam.
CC Pfam: PF00554; RHD; 1.
CC Pfam: PF01833; TIG; 1.
CC PRINTS: PR00057; NKBTMNSCPFC.
CC SMART: SM00429; IPT; 1.
CC PROSITE: PS01204; REL_1; 1.
CC PROSITE: PS00254; REL_2; 1.
KW DNA binding; Transcription regulation; Activator; Nuclear protein;
KW Phosphorylation.
FT DOMAIN 25 311 REL LIKE (RHD).
FT DOMAIN 305 309 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 281 291 PHOSPHORYLATION (BY PKA) (POTENTIAL).
SC SEQUENCE 558 AA; 60371 MW; 0528D159A4D4V836 CR764;
Query Match 67.2%; Score 39; DB 1; Length 558;
Best Local Similarity 77.8%; Pred. No. 9.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CY 2 ILGRRPPPFET 10
|||
428 ILGDRPPPFET 436
RESULT 18
PLK1 CAENL STANDARD: PRT 449 AA
AC P34331; C6162; C76763;
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence updated)
DT 28-FEB-2003 (Rel. 41, Last annotation updated)
DE Serine/threonine-protein kinase plk1 (EC 2.7.11.1) (polio-like
DE kinase-1).
DF Kinase-1.
GN PLK-1 OR PLK1 OR C14B9.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI TaxID=6239;
RN 1;
RP SEQUENCE FROM N.A. (ISOFORM B).
RX NEXLINE=99304501; PubMed=10376213;
RA Qiyang B., Wang Y., Dai W.;
RT "Caenorhabditis elegans contains structural homologs of human p34 and
RT Plk1".
RL DNA Seq. 10:109-113(1999).
RN 1;
RP SEQUENCE FROM N.A. (ISOFORM A), FUNCTION, AND SUBCELLULAR LOCATION.
RX STRAIN-Bristol N2;

RX MEDLINE=20190108; PubMed=10660671;
RA Chase D., Serafinas C., Ashcroft N., Kosinski M., Longo D.,
RA Ferris D.K., Golden A.;
RT "The polo-like kinase PLK-1 is required for nuclear envelope breakdown
RT and the completion of meiosis in Caenorhabditis elegans.";
RL Genesis 26:26-41(2000).
RN 13;
RP SEQUENCE FROM N.A.
RX STRAIN-Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton C., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstein L., Wilkinson-Sproat J.,
RA Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C
RT elegans.";
RL Nature 368:32-38(1994).
RN 14;
RP REVISIONS, AND ALTERNATIVE SPLICING.
RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: Required for oocyte nuclear envelope breakdown before
CC entry of oocyte into spermatheca. In mitotic cells, plays a role
CC in spindle organization and centrosome maturation. In meiotic
CC cells, required for spindle dynamics and probably for spindle
CC attachment to the chromosomes. Zygotic role in the development of
CC the germline and nerve cord.
CC !- SUBCELLULAR LOCATION: In mitosis, remains associated with
CC centrosomes entering prophase through to anaphase. During
CC metaphase, found at the chromosomes of the metaphase plate. In
CC meiosis, detected at centrosomes after pronuclear meeting in post-
CC meiotic 1-cell embryos. Associated with chromatin during
CC chromosome segregation of anaphase and in the region between the
CC dividing chromosomes. Cytoplasmic in mature, unfertilized oocytes.
CC ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=b;
CC IsoId=P34331-1; Sequence-Displayed;
CC Name=a;
CC IsoId=P34331-2; Sequence=VSP 034928;
CC !- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC !- SIMILARITY: Contains 2 POLO box domains.
CC
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CC
CC EMBL: AF057165; AAC14129.1; --
CC EMBL: AF080581; AAC34661.1; --
CC EMBL: L15188; AAA27947.2; --
CC EMBL: L15188; AAM22025.1; --
CC PIR: T43337; T43337.
CC HSSP: Q61450; 1A06.
CC WormPep: C14B9.4a; CE26649.
CC WormPep: C14B9.4b; CE30602.
CC GO: 0005634; C:nucleus; IEP.
CC GO: 0005524; F:ATP binding activity; ISS.
CC GO: 0004674; F:protein serine/threonine kinase activity; ISS.
CC GO: 0007417; P:central nervous system development; IMP.
CC GO: 0007098; P:centrosome cycle; IMP.
CC GO: 0007077; P:mitotic nuclear envelope breakdown; IMP.

CP GO: 30:0003052; P: mitotic spindle assembly; IMP.
CP GO: 30:0006468; P: protein amino acid phosphorylation; ISS.
CP InterPro: IPR000959; POLO_box.
CP InterPro: IPR000719; Prot_kinase.
CP InterPro: IPR002290; Ser_Thr_kinase.
CP InterPro: IPR001245; Tyr_kinase.
CP Pfam: PF00659; POLO_box; 2.
CP Pfam: PF00659; Prot_kinase; 1.
CP SMART: SM0019; TyrKc; 1.
CP PROSITE: PS00278; POLO_BOX; 2.
CP PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CP PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CP PROSITE: PS00117; PROTEIN_KINASE_DOM; 1.
KW ATP binding; Serine/threonine protein kinase; Transmembrane Repeat;
KW Nuclear protein; Alternative splicing.
FT DOMAIN 38 290 PROTEIN_KINASE.
FT NP_BIND 45 52 ATP (BY SIMILARITY).
FT BINDING 67 67 ATP (BY SIMILARITY).
FT ACT_SITE 162 162 BY SIMILARITY.
FT DOMAIN 420 485 POLO_BOX_1.
FT DOMAIN 520 589 POLO_BOX_2.
FT VARSPC 63 89 VENERIN [S] MTEVQ (in isoform a).
FT /FTID=VSP_004928.
SQ SEQUENCE 649 AA; 73633 MW; 54D969F74C07A41B CDS; 647647

Query Match 67.2% Score 197 DB 11 Length 643
Best local Similarity 60.0% Pred. No. 11
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY : MLDGRPPPET 10
CQ : 229 LLSQQPPFES 238

RESULT 19
XREF DRONE
ID KP01 DRONE STANDARD; PRT. 679 AA
AC F05130; Q9V7V6; Q9V7V7;
DT 13-AUG-1987 (Rel. 05, Created);
DT 26-FEB-2004 (Rel. 41, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Protein kinase C, brain isozyme (E02711) (PKC) (DIFFUSIBLE);
GN PKCβ3E OR PKC; CR CG6622;
OS Drosophila melanogaster (Fruit fly);
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Euryptera;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydriidae; Drosophilidae; Drosophila;
CX MCB; TaxID 7223;
RN :
RT SEQUENCE FROM N.A. (ISOFORM A);
STRAIN: Canton S. and Oregon-R;
RX MEDLINE=87218499; PubMed=3107993;
RA Rosenthal A., Klee L., Yadegar R., Iino R., Claret A., Goeddel D.V.;
RT "Structure and nucleotide sequence of a Drosophila melanogaster
protein kinase C gene."
RI EMBL J. 6:433-441 (1987).
RV [2]
RP SEQUENCE FROM N.A.
RC STRAIN: Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams V.D., Cealniker S.E., Holt R.A., Evans C.A., Mayne C.D.,
RA Arakatis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George P.A., Lewis S.E., Richards S., Ashburner M., Fenderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Branton R.C., Rogers Y.-H.C., Blatt R.G., Chapple V., Pfeiffer B.D.,
RA Wan K.H., Coyle C., Baxter E.G., Heat G., Nelson R.P., Miklos G.D.G.,
RA Abiri C.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
RA Sallaw R.M., Basu A., Baxendale J., Bayraktaroglu M., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman R.P., Bhandari B., Bolshakov S.,
RA Bozkova D., Botchan M.R., Bouck C., Brokstein P., Brattler P.,
RA Butts K.C., Busam C.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chetty S.M., Cawley S., Dahlke C., Haverport L.B., Davies P.,
RA de Pablos B., Selcher A., Song Z., Mays A.E., New T., Ikenz S.N.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov D.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.C., Wei M.-H., Ibegwam C.,
RA Kalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Jiang Y., Lin X.,
RA Liu X., Mattei H., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkuiov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy Y., Murphy R., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195 (2000).
RN [3].
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN: Berkeley; TISSUE=Ovary;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Kronmiller B., Li P.W., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA Cealniker S.E.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=PO5130.1; Sequence=Displayed;
CC Name=Short;
CC IsoId=PO5130.2; Sequence=VSP_004743;
CC Note=No experimental confirmation available;
CC TISSUE SPECIFICITY: HEAD NEURAL TISSUE.
CC -!- MISCELLANEOUS: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-
CC DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF OREGON-R.
CC -!- SIMILARITY: Contains 2 zinc dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. PKC
CC SUBFAMILY.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: X05076; CAA28736.1;
DR EMBL: X05279; CAA28890.2;
DR EMBL: X05280; CAA28890.2; JOINED.
DR EMBL: X05261; CAA28890.2; JOINED.
DR EMBL: X05282; CAA28890.2; JOINED.
DR EMBL: X05283; CAA28890.2; JOINED.
DR EMBL: AEC038C5; AAF57932.1;
DR EMBL: AEC038C5; AAF57933.1;
DR EMBL: AY050003; AAM1131.1;
DR HSSP: P05697; 1:BN.


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DR FlyBase: FBgn0003091; PKCS3E.
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IDA.
DR GO: GO:0004687; P:protein amino acid phosphorylation; IDA.
DR InterPro: IPR000008; C2.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00130; DAG_PE-bind; 1.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00028; DAGPEDOMAIN.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00129; C2; 1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00495; C2_DOMAIN_1; 1.
DR PROSITE: PS00004; C2_DOMAIN_2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00106; PROTEIN_KINASE_ST; 1.
KW Calcium binding; Repeat; ATP-binding; Transferase.
KW Serine/threonine-protein kinase; Multigene family; Zinc.
KW Phospho-ester binding; Alternative splicing.
FT DOMAIN 46 104 PHOSPHO-ESTER AND DAG BINDING 1.
FT DOMAIN 120 169 PHOSPHO-ESTER AND DAG BINDING 2.
FT DOMAIN 191 278 C2 DOMAIN.
FT DOMAIN 350 608 PROTEIN KINASE.
FT NP_BIND 355 364 ATP (BY SIMILARITY).
FT BINDING 379 379 ATP (BY SIMILARITY).
FT BINDING 474 474 BY SIMILARITY.
FT ACT_SITE 474 474 CGYGGYAWNG > WG (in isoform short).
FT VARIANTS 67 77 /FTID=VSP 004743.
FT VARIANTS 437 437 M->L.
FT VARIANTS 605 608 F > S (in REF. 10).
FT CONFLICT 634 648 DVSNEKQPTSEKTO > MDTTSSSHQKQK (in REF. 11).
FT CONFLICT 649 679 MISSING IN REF. 11.
FT CONFLICT 670 679 3RD AND 4TH RESIDUE OF C2.
SQ SEQUENCE 670 AA; 77695 MW; 30564518180000 Da; 0.

Query Match 67.2%; Score 39; DR 1; Length 690;
Best local similarity 66.7%; Pred No 12;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPF 9
IIII
DB 542 MLLVQPPFD 550

Query Match 67.2%; Score 39; DR 1; Length 690;
Best local similarity 66.5%; Pred No 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPF 9
IIII
DB 217 MLLGRPPPF 224

RESULT 21
STKD_HUMAN
ID STKD_HUMAN STANDARD: PRT; 309 AA.
AC Q9UCB9; Q60681; Q75442; Q9UPK5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 13 (EC 2.7.1.37) (Aurora/Ipl1/Eg2
DE protein 2) (Aurora/Ipl1-related kinase 3) (Aurora-C).
GN STK13 OR AIE2 OR AIK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOPFORM 1).
RC TISSUE=Testis;
RX MEDLINE=99025616; PubMed=9809744;
RA Tseng T.-C., Chen S.-H., Esu Y.-P.P., Tang T.-K.;

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RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pess: G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: Contains 4 PASTA domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AEC14680; AAN24413.1; --
DR InterPro: IPR005543; PASTA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF03793; PASTA; 2.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00740; PASTA; 4.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase.
KW ATP binding; Repeat; Complete proteome.
FT DOMAIN 14 28- PROTEIN KINASE.
FT DOMAIN 399 467 PASTA 1.
FT DOMAIN 468 536 PASTA 2.
FT DOMAIN 539 601 PASTA 3.
FT DOMAIN 602 666 PASTA 4.
FT DOMAIN 667 689 GLY-RICH.
FT NP_BIND 20 28 ATP (BY SIMILARITY).
FT BINDING 43 43 ATP (BY SIMILARITY).
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 690 AA; 72243 MW; 6A419E8CED5D92D CRC64;

Query Match 67.2%; Score 39; DR 1; Length 690;
Best local similarity 67.5%; Pred No 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPF 9
IIII
DB 217 MLLGRPPPF 224

RESULT 21
STKD_HUMAN
ID STKD_HUMAN STANDARD: PRT; 309 AA.
AC Q9UCB9; Q60681; Q75442; Q9UPK5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 13 (EC 2.7.1.37) (Aurora/Ipl1/Eg2
DE protein 2) (Aurora/Ipl1-related kinase 3) (Aurora-C).
GN STK13 OR AIE2 OR AIK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOPFORM 1).
RC TISSUE=Testis;
RX MEDLINE=99025616; PubMed=9809744;
RA Tseng T.-C., Chen S.-H., Esu Y.-P.P., Tang T.-K.;

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DR GC: GC02007049; P: cell cycle; NAS.
DR GC: GC02006468; P: protein amino acid phosphorylation; ISS.
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00659; POLO_box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00379; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
KW ATP binding; Serine/threonine-protein kinase; Transferase; Repeat;
KW Nuclear protein.
FT DOMAIN 36 287 PROTEIN_KINASE.
FT NP_BIND 43 50 ATP (BY SIMILARITY).
FT BINDING 65 65 ATP (BY SIMILARITY).
FT ACT_SITE 159 159 BY SIMILARITY.
FT DOMAIN 412 476 POLO_BOX_1.
FT DOMAIN 511 580 POLO_BOX_2.
SQ SEQUENCE 632 AA; 72071 MW; 1B2EBB54C15A5B29 CRC64;

Query Match 65.5%; Score 18; EB 1; Length 612;
Best local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPIPET 10
DB 236 LFGHPFES 235

RESULT 21
KPC3_DOMONE
ID KPC3_DOMONE STANDARD; PRT: 634 AA.
AC P16078; Q9VAC6;
DT 01 APR 1998 (Rel. 14, Created;
DT 01 APR 1998 (Rel. 14, Last sequence update;
DT 16 OCT 2001 (Rel. 40, Last annotation update;
FE Protein kinase C (EC 2.7.11) (PDB: 1BPK0985;
GN PKC08E OR PKC3 OR CG1954;
OS Drosophila melanogaster (Fruit fly);
OC Eukaryota; Metazoa; Arthropoda; Insecta; Diptera;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscophila;
OC Ephydroidea; Ephydroidea; Muscophila;
OX NCBI_TaxID:7227;
KW 111
RF SEQUENCE FROM N.A.
RX MEDLINE:8924932; PubMed:272775;
RA Schaeffer E., Smith D., Marden D., et al. 1989. Isolation and characterization of 15 cDNA clones for protein kinase C genes, including one specifically expressed in fat body and cells.
RT "Isolation and characterization of 15 cDNA clones for protein kinase C genes, including one specifically expressed in fat body and cells".
RN Cell 57:403-412 (1989).
RP SEQUENCE FROM N.A.
RC STRAIN: Berkeley;
PX MEDLINE:20196006; PubMed:10731132;
RA Adams M.D., Colanker S.E., Holt R.A., Evans C.A., Kenwayne J.D.,
RA Ananides P.G., Scherer S.E., Li F.W., Hoskins R.A., Galie R.B.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,
RA Sutton G.S., Wortman J.R., Yandell M.D., Zhang Z., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazer V., Chang M., Hoiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Holt R., Nelson M., Nickles G.L.G.,
RA Abli J.F., Aghayani A., An H.-J., Andrews P., Baxendale C.,
RA Ballew R.M., Bass A., Baxendale C., Bayraktaroglu B., Baxendale C.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya S., Bickel S.,
RA Borkova O., Botchan M.R., Bouck C., Brinkstein P., Brinkstein P.,
RA Burtis K.C., Busam D.A., Butler H., Calton E., Carter A., Chandra I.,
RA Cherry C.M., Cawley S., Dahlke C., Davoport L.P., Davies P.,
RA de Fabios B., Delcher A., Deng Z., Miya A.D., Shaw J., Sheng S.M.,
RA Deisen K., Deup L.E., Downes M., Dusan Rocha S., Ecker B., Dunn B.,
RA Durbin K.J., Evangelista C.C., Fritsch E., Fritsch E., Fritschmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorelli J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez C.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Calali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Verkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiados I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195 (2000).
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- MISCELLANEOUS: THIS IS A CALCIUM-ACTIVATED.
CC PHOSPHOLIPID-DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- SIMILARITY: CONTAINS 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL: J04848; AAA28816.1;
DR EMBL: AE003768; AAP6646.1; AAT_INIT.
DR PIR: B32392; B32392.
DR HSSP: P28867; IPTO.
DR FlyBase: FBgn0001093; PKC98E.
DR InterPro: IPR002219; DAG_PE_bind.
DR InterPro: IPR000961; pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00130; DAG_PE_BIND; 1.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00433; pkinase_C1.
DR PRINTS: PR00008; DAGPECDOMAIN.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Multigene family; Zinc;
KW Phorbol-ester binding.
FT DOMAIN 72 121 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 147 196 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 303 360 PROTEIN_KINASE.
FT NP_BIND 309 312 ATP (BY SIMILARITY).
FT BINDING 332 332 ATP (BY SIMILARITY).
FT ACT_SITE 427 427 BY SIMILARITY.
SQ SEQUENCE 634 AA; 71156 MW; 3AE3A3D6B7A276BA CRC64;

Query Match: 65.5%; Score 18; DB 1; Length 614;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 DB 495 MVAQCPPE 503

RESULT 24
 PKN1 COREP STANDARD; PRT: 683 AA;
 AC QHFL15;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Probable serine/threonine protein kinase (EC 2.7.1.37)
 GN CE0033;
 OS Corynebacterium efficiens;
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Corynebacterineae; Corynebacteriaceae; Corynebacterium;
 CX NCBI_TaxID=152794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
 RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
 RA Ikeda K., Suzuki Y., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
 RA Usuda Y., Sugimoto S.;
 RT "The entire genomic sequence of Corynebacterium efficiens YS-314";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DSJ databases.

CC 1 CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC 1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC 1 SIMILARITY: Contains 3 PASTA domains.
 CC
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 CC or send an email to licenses@sb.sib.ch.

CC
 CC EMBL: AF005214; BAC16843.1;
 CC InterPro: IPR005543; PASTA;
 CC InterPro: IPR00719; Prot_kinase
 CC InterPro: IPR002290; Ser_thr_kinase
 CC InterPro: IPR01245; Tyr_kinase
 CC Pfam: PF01933; PASTA; 3
 CC Pfam: PF00601; Kinase; 1
 CC ProDom: PD000017; Prot_kinase; 1
 CC SMART: SM00340; PASTA; 3;
 CC SMART: SM00220; STK; 1;
 CC SMART: SM0019; TyKc; 1;
 CC PROSITE: PS00187; PROTEIN_KINASE_ATP; 1;
 CC PROSITE: PS0011; PROTEIN_KINASE_DOM; 1;
 CC PROSITE: PS00109; PROTEIN_KINASE_ST; 1;
 CC KW Hypothetical protein; Transferase; Serine/threonine protein kinase;
 KW ATP-binding; Repeat; Complete proteome
 FT DOMAIN 9 278 PROTEIN KINASE
 FT DOMAIN 377 443 PASTA 1;
 FT DOMAIN 444 512 PASTA 1;
 FT DOMAIN 513 577 PASTA 1;
 FT NP BIND 15 23 ATP (BY SIMILARITY)
 FT BINDING 38 38 ATP (BY SIMILARITY)
 FT ACT SITE 136 136 BY SIMILARITY
 SC SEQUENCE 660 AA; 69646 MW; D35U797EB0254491 (CDD4)

Query Match: 65.5%; Score 18; DB 1; Length 607;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9

DB 207 LVTGRPPPE 215

RESULT 25
 PJO1 SCHPO STANDARD; PRT: 683 AA;
 ID PJO1 SCHPO
 AC P50528;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Serine/threonine-protein kinase pJO1 (EC 2.7.1.37)
 GN PJO1 OR SPAC23C11.6;
 OS Schizosaccharomyces pombe (Fission yeast);
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes;
 CX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=95262899; PubMed=7744248;
 RA Ohkura H., Hagan I.M., Glover D.M.;

RT "The conserved Schizosaccharomyces pombe kinase pJO1, required to
 RT form a bipolar spindle, the actin ring, and septum, can drive septum
 RT formation in G1 and G2 cells.";
 RL Genes Dev. 9:1059-1073(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor P., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hurt S., Jagels K.,
 RA James K., Jones D., Jones M., Leather S., Huckle E.J., Hurt S., Jagels K.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skilton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward C., Vekicart G., Aert R., Robben J., Grymonprez B.,
 RA Weijens I., Vanstreels E., Pieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Moesti D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardou C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito G.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Bartell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:871-882(2002).

CC 1- FUNCTION: REQUIRED TO FORM A BIPOLAR SPINDLE, THE ACTIN RING AND
 CC SEPTUM. FUNCTIONS UPSTREAM OF THE WHOLE SEPTUM FORMATION PATHWAY,
 CC INCLUDING ACTIN RING FORMATION (REGULATED BY LATE SEPTATION GENES)
 CC AND SEPTAL MATERIAL DEPOSITION (REGULATED BY EARLY SEPTATION
 CC GENES). BEHAVES AS A "SEPTUM-PROMOTING FACTOR", AND COULD ALSO BE
 CC INVOLVED IN INDUCING OTHER LATE EVENTS OF CELL DIVISION.
 CC 1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLO SUBFAMILY.
 CC 1- SIMILARITY: Contains 2 POLO box domains.

CC
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CC
 CC EMBL: AF005214; BAC16843.1;
 CC InterPro: IPR005543; PASTA;
 CC InterPro: IPR00719; Prot_kinase
 CC InterPro: IPR002290; Ser_thr_kinase
 CC InterPro: IPR01245; Tyr_kinase
 CC Pfam: PF01933; PASTA; 3
 CC Pfam: PF00601; Kinase; 1
 CC ProDom: PD000017; Prot_kinase; 1
 CC SMART: SM00340; PASTA; 3;
 CC SMART: SM00220; STK; 1;
 CC SMART: SM0019; TyKc; 1;
 CC PROSITE: PS00187; PROTEIN_KINASE_ATP; 1;
 CC PROSITE: PS0011; PROTEIN_KINASE_DOM; 1;
 CC PROSITE: PS00109; PROTEIN_KINASE_ST; 1;
 CC KW Hypothetical protein; Transferase; Serine/threonine protein kinase;
 KW ATP-binding; Repeat; Complete proteome
 FT DOMAIN 9 278 PROTEIN KINASE
 FT DOMAIN 377 443 PASTA 1;
 FT DOMAIN 444 512 PASTA 1;
 FT DOMAIN 513 577 PASTA 1;
 FT NP BIND 15 23 ATP (BY SIMILARITY)
 FT BINDING 38 38 ATP (BY SIMILARITY)
 FT ACT SITE 136 136 BY SIMILARITY
 SC SEQUENCE 660 AA; 69646 MW; D35U797EB0254491 (CDD4)

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EMBL: X85758; CAA59766.1; -
 EMBL: Z98569; CAB1167.1; -
 PIR: T38254; T38254.
 HSSP: Q61450; 1A06.
 GeneDB Spombe; SPAC23C11.16; -
 InterPro: IPR000959; POLO_box.
 InterPro: IPR000719; Prot_kinase.
 InterPro: IPR002290; Ser_thr_kinase.
 Pfam: PF00659; PKinase; 1.
 Pfam: PF00659; POLO_box; 2.
 ProDom: PD000001; Prot_kinase; 1.
 SVART: SM00220; S_TKC; 1.
 SVART: SM00220; S_TKC; 2.
 PROSITE: PS00078; POLO_BOX; 2.
 PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
 Transferase; Serine/threonine-protein kinase; ATP binding; Repeat.
 DOMAIN 41 296 PROTEIN_KINASE
 NP_BIND 47 55 ATP (BY SIMILARITY)
 BINDING 69 69 ATP (BY SIMILARITY)
 ACT_SITE 163 163 BY SIMILARITY
 DOMAIN 500 567 POLO_BOX 1
 DOMAIN 604 670 POLO_BOX 2
 SEQUENCE 583 AA; 77301 MW; F1C0CEFF9B913917 CRC64;

Query Match 65.5%; Score 18; DB 1; Length 683;
 Best local similarity 55.6%; Pred. No. 18;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLJGRPPFE 9
 :|:|:|:
 DE 233 LLIGKPPFQ 241

RESULT 26
 CDC5_YEAST
 ID CDC5_YEAST STANDARD; PRT; 705 AA.
 AC P32562;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cell cycle protein kinase CDC5/MSD2 (EC 2.7.11.37).
 OS Cell cycle protein kinase CDC5/MSD2 (EC 2.7.11.37).
 CC CDC5 OR PKX2 OR YSD2 OR YMR001C OR YMR270.03C.
 CC Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4912;
 RN 11
 RE SEQUENCE FROM N.A.
 FC STRAIN=A364A;
 EX MEDLINE 93309479; PubMed=8321244;
 RA Kitada K., Sugino A., Johnston L.H., Johnson A.M.
 RT "A multicopy suppressor gene of the Saccharomyces cerevisiae G1 cell
 cycle mutant gene dbf4 encodes a protein kinase and is identified as
 CDC5."
 RL Mol. Cell. Biol. 13:4445-4457(1993)
 RN 12
 RE SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX PubMed=9169872;
 RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
 RA Connor R., Dedman K., Devlin K., Gentles S., Harlin N., Hunt S.,
 RA Jagers K., Iye G., Moule S., Odell C., Pearson P., Rajadream M.A.,
 RA Rice P., Skelton J., Walsh S., Whitehead S., Bartell P.G.
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
 XIII."
 RL Nature 387:90-93(1997).
 RN 13
 RP PHOSPHORYLATION OF SCCL.
 RX PubMed=11371343;

RA Alexandru G., Uhlmann F., Mechtler K., Poupart M.-A., Nasmyth K.;
 RT "Phosphorylation of the cohesin subunit Scc1 by Polo/Cdc5 kinase
 regulates sister chromatid separation in yeast."
 RL Cell 105:459-472(2001).
 CC -!- FUNCTION: Protein kinase required for the cell cycle.
 CC Phosphorylates SCC1/MCD.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLO SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 POLO box domains.
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EMBL: M84220; AAA02576.1; -
 EMBL: Z49613; CAA88516.1; -
 PIR: A48144; A48144.
 HSSP: Q63450; 1A06.
 SGD: S0004603; CDC5.
 GO: GO:0005634; Cnucleus; IDA.
 GO: GO:0036261; P:DNA dependent DNA replication; IDA.
 GO: GO:0036468; P:protein amino acid phosphorylation; IDA.
 InterPro: IPR000959; POLO_box.
 InterPro: IPR000719; Prot_kinase.
 InterPro: IPR002290; Ser_thr_kinase.
 InterPro: IPR001245; Tyr_kinase.
 Pfam: PF00659; PKinase; 1.
 Pfam: PF00659; POLO_box; 2.
 PRINTS: PR00109; TYRKINASE.
 ProDom: PD000001; Prot_kinase; 1.
 SMART: SM00220; S_TKC; 1.
 PROSITE: PS00078; POLO_BOX; 2.
 PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW Cell cycle; Cell division; Serine/threonine-protein kinase;
 KW Transferase; ATP-binding; Repeat.
 FT DOMAIN 82 337 PROTEIN_KINASE.
 FT NP_BIND 88 96 ATP (BY SIMILARITY).
 FT BINDING 110 110 ATP (BY SIMILARITY).
 FT ACT_SITE 204 204 BY SIMILARITY.
 FT DOMAIN 520 587 POLO_BOX 1.
 FT DOMAIN 619 692 POLO_BOX 2.
 SQ SEQUENCE 705 AA; 81030 MW; 85A25F1BBEAA3DC CRC64;

Query Match 65.5%; Score 38; DB 1; Length 705;
 Best local similarity 55.6%; Pred. No. 19;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLJGRPPFE 9
 :|:|:|:
 DB 274 LLIGKPPFQ 282

RESULT 27
 KPC2_CAEEL
 ID KPC2_CAEEL STANDARD; PRT; 707 AA.
 AC P34885;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1995 (Rel. 38, Last annotation update)
 DE Protein kinase C like 2 (EC 2.7.11.-) (PKC2B).
 GN KIN-13 OR PKC1B.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelecoidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN 11


```
RP SEQUENCE FROM N.A.
RC STRAIN: Bristol N2;
RX MEDLINE=94179345; PubMed=8132661;
RA Land M., Islas-Trejo A., Freedman J.H., Rubin C.S.;
RT "Structure and expression of a novel, neuronal protein kinase C
RT (PKC1B) from Caenorhabditis elegans. PKC1B is expressed selectively
RT in neurons that receive, transmit, and process environmental
RT signals";
RL J. Biol. Chem. 269:9234-9244(1994)
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS.
CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH MEMBRANES AND THE
CC CYTOSKELETON.
CC -!- TISSUE SPECIFICITY: EXPRESSED SELECTIVELY IN NEURONS THAT RECEIVE,
CC TRANSMIT AND PROCESS ENVIRONMENTAL SIGNALS
CC -!- SIMILARITY: Contains 2 zinc dependent phorbol ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC
CC -----
CC EMBL; U00181; AAA18259.1;
CC EMBL; U00965; AAA17996.1;
CC PIR; A33530; A33530.
CC HSSP; P28867; IPTQ.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000961; Pkinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00168; C2; 1.
CC Pfam; PF00130; DAG_PE-bind; 2.
CC Pfam; PF00069; Pkinase; 1.
CC Pfam; PF00433; Pkinase_C; 1.
CC PRINTS; PR00008; DAGPEDOMAIN.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00109; C1; 2.
CC SMART; SM00239; C2; 1.
CC SMART; SM0133; S_TK_X; 1.
CC SMART; SM0128; S_TKC; 1.
CC PROSITE; PS00004; C2_DOMAIN_2; 1.
CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
CC PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP binding; Zinc;
KW Phorbol-ester binding; Repeat; Membrane; Cytoskeleton.
FT DOMAIN 1 98 C2 DOMAIN.
FT DOMAIN 171 221 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 249 298 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 378 638 PROTEIN KINASE.
FT NP BIND 384 392 ATP (BY SIMILARITY).
FT BINDING 407 407 ATP (BY SIMILARITY).
FT ACT SITE 502 502 BY SIMILARITY.
SQ SEQUENCE 707 AA; 80122 MW; 3CCFA2C8A7A7B644 CDT64;

Query Match 65.9% Score 19.05 E-17 Length 707
Best Local Similarity 66.7% Pred. No 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
  |||
  500 MLAGQPPFE 578
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```
RESULT 28
KPCE_RABBIT
ID KPCE_RABBIT STANDARD; PRT; 736 AA.
AC P10830;
DT 01-JUL-1989 (Ref. 1); Created;
DT 01-JUL-1989 (Ref. 1); Last sequence update;
DT 15-JUL-1999 (Ref. 38); Last annotation update;
DE Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
GN PKCE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88223367; PubMed=3370672;
RA Chao S., Akita Y., Komro Y., Imajoh S., Suzuki K.;
RT "A novel phorbol ester receptor/protein kinase, nPKC, distantly
RT related to the protein kinase C family.";
RL Cell 53:731-741(1988)
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch)
CC
CC -----
CC EMBL; M20014; AAA31426.1;
CC HSSP; P28867; IPTQ.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000961; Pkinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00168; C2; 1.
CC Pfam; PF00130; DAG_PE-bind; 2.
CC Pfam; PF00069; Pkinase; 1.
CC Pfam; PF00433; Pkinase_C; 1.
CC PRINTS; PR00008; DAGPEDOMAIN.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00109; C1; 2.
CC SMART; SM00239; C2; 1.
CC SMART; SM0133; S_TK_X; 1.
CC SMART; SM0128; S_TKC; 1.
CC PROSITE; PS00004; C2_DOMAIN_2; 1.
CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
CC PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
KW Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 1 99 C2 DOMAIN.
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 407 667 PROTEIN KINASE.
FT NP BIND 413 421 ATP (BY SIMILARITY).
FT BINDING 436 436 ATP (BY SIMILARITY).
FT ACT SITE 531 531 BY SIMILARITY.
```

```
FT MOD_RES 702 702 PROSPHORYLATION (AUTO-) (POTENTIAL)
FT MOD_RES 709 709 PROSPHORYLATION (AUTO-) (POTENTIAL)
SQ SEQUENCE 236 AA: 83515 MW: 26104FEE59E9B5EB CRC64;

Query Match 65.5%; Score 18; DB 1; Length 737;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 599 MLAGQPPFE 607

RESULT 29
KPCE_HUMAN STANDARD; PRT: 737 AA.
AC Q02156; Q9JER8;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.11-) (nPKC-epsilon)
GN PKCE OR PKCE
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
OX NCBI_TaxID:9606;
RN [1]
RE SEQUENCE FROM N.A.
RX MEDLINE 93003319; PubMed=13826051
RA Pasta P., Strickland M.B., Holmes W., Locatis C.R., Ballas L.M.,
RA Burns D.J.;
RT "Sequence and expression of human protein kinase C epsilon."
RD Biochim Biophys Acta 1132:154-160(1993)
EN
FP SEQUENCE OF 1-116 FROM N.A.
RA Watsonson R.;
RL Submitted (JAN 1999) to the EMBL/GenBank/DDB databases.
CC FUNCTION: THIS IS CALCIUM INDEPENDENT, PHOSPHOLIPID DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS.
CC SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAINS.
CC SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC SIMILARITY: BELONGS TO THE SPK/PRK FAMILY OF PROTEIN KINASES.
CC PKC SUPERFAMILY.
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CC EM2L X65293; CAA46388.1;
CC EMBL U51244; AAC09855.1;
CC F01 S28943; S28942;
CC R55P P28867; IPRC;
CC GENP: HGNC:19401; PRKCE;
CC MW: 176975;
CC GO: GO:0005624; Membrane fraction; TAS
CC GO: GO:0004697; G-protein kinase C activity; TAS;
CC GO: GO:0004871; Signal transducer activity; TAS;
CC GO: GO:0006917; Proliferation of apoptosis; TAS
CC GO: GO:0006468; Phosphorylation of protein; TAS
CC InterPro: IPR000008; C2;
CC InterPro: IPR000019; DAG-PE-bind
CC InterPro: IPR000961; PKinase_C;
CC InterPro: IPR000219; Prot_kinase
CC InterPro: IPR000290; Ser_Thr_kinase
CC Pfam: PF00130; DAG-PE-bind; 2;
CC Pfam: PF00069; PKinase; 1;
CC Pfam: PF00433; PKinase_C; 1;
CC PRINTS: PR00008; DAGPEDOMAIN;
CC ProDom: PD000001; Prot_kinase; 1;
CC SMART: SM00109; C1; 2;
CC SMART: SM00239; C2; 1;
CC SMART: SM00133; S_TK_X; 1;
CC SMART: SM00220; S_TK; 1;
CC PROSITE: PS00004; C2_DOMAIN_2; 1;
CC PROSITE: PS00479; DAG-PE_BIND_DOM_1; 2;
CC PROSITE: PS00081; DAG-PE_BIND_DOM_2; 2;
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1;
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1;
KW Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 1 93 C2 DOMAIN
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1;
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2;
FT DOMAIN 408 668 PROTEIN KINASE
FT NP_BIND 414 422 ATP (BY SIMILARITY)
FT BINDING 437 437 ATP (BY SIMILARITY)
FT ACT_SITE 532 532 BY SIMILARITY
FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL)
FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL)
SQ SEQUENCE 737 AA: 83573 MW: 85032D0A091A1F7F CRC64;

Query Match 65.5%; Score 38; DB 1; Length 737;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 600 MLAGQPPFE 608

RESULT 30
KPCE_MOUSE STANDARD; PRT: 737 AA.
AC P16054;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.11-) (nPKC-epsilon)
GN PRKCE OR PKCE OR PKTEA;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus;
OX NCBI_TaxID:10090;
RN [1]
RE SEQUENCE FROM N.A.
RX MEDLINE 89137541; PubMed=29176567
RA Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
RT "Unique substrate specificity and regulatory properties of
RT PKC epsilon: a rationale for diversity."
RL FEBS Lett. 243:351-357(1989)
RN [2]
RE SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE 98127436; PubMed=9467942;
RA Wang Q., Acs P., Goodnight J., Blumberg P.M., Mischak H.,
RA Mushinski J.F.;
RT "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and
RT epsilon chimeras, is responsible for conferring tumorigenicity to
RT NIH3T3 cells, whereas both regulatory and catalytic domains of
RT PKC-epsilon contribute to in vitro transformation."
RL Oncogene 16:53-60(1998)
RN [3]
RE SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Wheeler E.;
RL Submitted (JAN 1999) to the EMBL/GenBank/DDB databases.
```

```
FT MOD_RES 702 702 PROSPHORYLATION (AUTO-) (POTENTIAL)
FT MOD_RES 709 709 PROSPHORYLATION (AUTO-) (POTENTIAL)
SQ SEQUENCE 236 AA: 83515 MW: 26104FEE59E9B5EB CRC64;

Query Match 65.5%; Score 18; DB 1; Length 737;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 599 MLAGQPPFE 607

RESULT 29
KPCE_HUMAN STANDARD; PRT: 737 AA.
AC Q02156; Q9JER8;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.11-) (nPKC-epsilon)
GN PKCE OR PKCE
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
OX NCBI_TaxID:9606;
RN [1]
RE SEQUENCE FROM N.A.
RX MEDLINE 93003319; PubMed=13826051
RA Pasta P., Strickland M.B., Holmes W., Locatis C.R., Ballas L.M.,
RA Burns D.J.;
RT "Sequence and expression of human protein kinase C epsilon."
RD Biochim Biophys Acta 1132:154-160(1993)
EN
FP SEQUENCE OF 1-116 FROM N.A.
RA Watsonson R.;
RL Submitted (JAN 1999) to the EMBL/GenBank/DDB databases.
CC FUNCTION: THIS IS CALCIUM INDEPENDENT, PHOSPHOLIPID DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS.
CC SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAINS.
CC SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC SIMILARITY: BELONGS TO THE SPK/PRK FAMILY OF PROTEIN KINASES.
CC PKC SUPERFAMILY.
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CC
CC EM2L X65293; CAA46388.1;
CC EMBL U51244; AAC09855.1;
CC F01 S28943; S28942;
CC R55P P28867; IPRC;
CC GENP: HGNC:19401; PRKCE;
CC MW: 176975;
CC GO: GO:0005624; Membrane fraction; TAS
CC GO: GO:0004697; G-protein kinase C activity; TAS;
CC GO: GO:0004871; Signal transducer activity; TAS;
CC GO: GO:0006917; Proliferation of apoptosis; TAS
CC GO: GO:0006468; Phosphorylation of protein; TAS
CC InterPro: IPR000008; C2;
CC InterPro: IPR000019; DAG-PE-bind
CC InterPro: IPR000961; PKinase_C;
CC InterPro: IPR000219; Prot_kinase
CC InterPro: IPR000290; Ser_Thr_kinase
CC Pfam: PF00130; DAG-PE-bind; 2;
CC Pfam: PF00069; PKinase; 1;
CC Pfam: PF00433; PKinase_C; 1;
CC PRINTS: PR00008; DAGPEDOMAIN;
CC ProDom: PD000001; Prot_kinase; 1;
CC SMART: SM00109; C1; 2;
CC SMART: SM00239; C2; 1;
CC SMART: SM00133; S_TK_X; 1;
CC SMART: SM00220; S_TK; 1;
CC PROSITE: PS00004; C2_DOMAIN_2; 1;
CC PROSITE: PS00479; DAG-PE_BIND_DOM_1; 2;
CC PROSITE: PS00081; DAG-PE_BIND_DOM_2; 2;
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1;
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1;
KW Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 1 93 C2 DOMAIN
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1;
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2;
FT DOMAIN 408 668 PROTEIN KINASE
FT NP_BIND 414 422 ATP (BY SIMILARITY)
FT BINDING 437 437 ATP (BY SIMILARITY)
FT ACT_SITE 532 532 BY SIMILARITY
FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL)
FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL)
SQ SEQUENCE 737 AA: 83573 MW: 85032D0A091A1F7F CRC64;

Query Match 65.5%; Score 38; DB 1; Length 737;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 600 MLAGQPPFE 608

RESULT 30
KPCE_MOUSE STANDARD; PRT: 737 AA.
AC P16054;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.11-) (nPKC-epsilon)
GN PRKCE OR PKCE OR PKTEA;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus;
OX NCBI_TaxID:10090;
RN [1]
RE SEQUENCE FROM N.A.
RX MEDLINE 89137541; PubMed=29176567
RA Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
RT "Unique substrate specificity and regulatory properties of
RT PKC epsilon: a rationale for diversity."
RL FEBS Lett. 243:351-357(1989)
RN [2]
RE SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE 98127436; PubMed=9467942;
RA Wang Q., Acs P., Goodnight J., Blumberg P.M., Mischak H.,
RA Mushinski J.F.;
RT "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and
RT epsilon chimeras, is responsible for conferring tumorigenicity to
RT NIH3T3 cells, whereas both regulatory and catalytic domains of
RT PKC-epsilon contribute to in vitro transformation."
RL Oncogene 16:53-60(1998)
RN [3]
RE SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Wheeler E.;
RL Submitted (JAN 1999) to the EMBL/GenBank/DDB databases.
```

CC FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS.
CC -1- SIMILARITY: Contains 2 zinc-dependent phorbol ester and DAG
CC binding domains.
CC -1- SIMILARITY: Contains 1 C2 domain
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: AF028009; AAB84189.1; -
CC EMBL: AF925507; AAG53692.1; -
CC PIR: S02270; KIMSCS;
CC HSSP: P28867; IPTQ;
CC MGD: MG127599; PKce.
CC GO: GO:004699; F:calcium independent protein kinase C activity; ICA.
CC InterPro: IPR000008; C2;
CC InterPro: IPR002219; DAG_PE-bind.
CC InterPro: IPR000961; PKinase_C;
CC InterPro: IPR000719; Prot_kinase
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00168; C2; 1;
CC Pfam: PF00130; DAG_PE-bind; 2;
CC Pfam: PF00169; PKinase; 1;
CC Pfam: PF00433; PKinase_C; 1;
CC PRINTS: PR00008; DAGPEDOMAIN;
CC PRODOM: PD000001; Prot_kinase; 1;
CC SMART: SM00109; C1; 2;
CC SMART: SM00239; C2; 1;
CC SMART: SM0133; S_TK_X; 1;
CC SMART: SM0220; S_TKC; 1;
CC PROSITE: PS0004; C2 DOMAIN 2; 1;
CC PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2;
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
CC PROSITE: PS00117; PROTEIN_KINASE_DOM; 1;
CC PROSITE: PS0108; PROTEIN_KINASE_ST; 1;
CC Repeat: ATP-binding; Transferase; Phosphorylation;
CC Serine/threonine protein kinase; Phorbol ester binding; Zinc.
CC DOMAIN 1 99 C2 DOMAIN
CC FT DOMAIN 177 320 PHORBOL ESTER AND DAG BINDING 1
CC FT DOMAIN 243 294 PHORBOL ESTER AND DAG BINDING 2
CC FT DOMAIN 408 668 PROTEIN KINASE
CC FT NP_BIND 414 422 ATP (BY SIMILARITY)
CC FT BINDING 429 437 ATP (BY SIMILARITY)
CC FT ACT_SITE 532 532 BY SIMILARITY
CC FT MOL_RES 703 703 PHOSPHORYLATION AND - CATALYTIC
CC FT MOL_RES 710 710 PHOSPHORYLATION AND - CATALYTIC
CC SQ SEQUENCE 737 AA; 83560 MW; 3AEBB8C10C09B9726064.
CC
CC Query Match 65.58; Score 18; DR 1; Low ID 107;
CC Best local Similarity 66.78; Procl No 20;
CC Matchclass 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CC
CC QY 1 MLLGRPFEE 9
CC 1 1 1 1
CC DB 600 VMAGQPFEE 608
CC
CC RESULT 11
CC KPCB PAT STANDARD; PST 100 AA
CC 10 KPCB PAT
CC AC P09217
CC 10 VAR 1989 (Rel. 10; Created:

DT 01-MAR-1989 (Rel. 10; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.11.-) (nPKC-epsilon).
GN PKCE OR PKCE
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID:10116;
RN 1;
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=88198270; PubMed 2834397;
RA Cho Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Nishizuka Y.;
RT "The structure, expression, and properties of additional members of
RT the protein kinase C family.";
RL FEBS Lett. 226:125-128(1987).
CC -1- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS.
CC -1- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -1- SIMILARITY: Contains 1 C2 domain.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: M18331; AAA41872.1; -
CC PIR: B28163; KIRTCB.
CC PDB: 1GM1; 25-00T-01.
CC InterPro: IPR000008; C2;
CC InterPro: IPR002219; DAG_PE-bind.
CC InterPro: IPR000961; PKinase_C;
CC InterPro: IPR000719; Prot_kinase
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00168; C2; 1;
CC Pfam: PF00130; DAG_PE-bind; 2;
CC Pfam: PF00069; PKinase; 1;
CC Pfam: PF00433; PKinase_C; 1;
CC PRINTS: PR00008; DAGPEDOMAIN;
CC PRODOM: PD000001; Prot_kinase; 1;
CC SMART: SM00109; C1; 2;
CC SMART: SM00239; C2; 1;
CC SMART: SM0133; S_TK_X; 1;
CC SMART: SM0220; S_TKC; 1;
CC PROSITE: PS50004; C2 DOMAIN 2; 1;
CC PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2;
CC PROSITE: PS50091; DAG_PE_BIND_DOM_2; 2;
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1;
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1;
CC Repeat: ATP-binding; Transferase; Phosphorylation;
CC Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
CC 3D-structure. 1 99 C2 DOMAIN
CC FT DOMAIN 170 220 PHORBOL ESTER AND DAG BINDING 1
CC FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2
CC FT DOMAIN 408 468 PROTEIN KINASE

```
FT NO BIND 414 422 ATP (BY SIMILARITY)
FT BINDING 437 437 ATP (BY SIMILARITY)
FT ACT SITE 532 532 BY SIMILARITY
FT MOD RES 703 703 PHOSPHORYLATION (AUTO) (POTENTIAL)
FT MOD RES 710 710 PHOSPHORYLATION (AUTO) (POTENTIAL)
SQ SEQUENCE 737 AA; 83478 MW; 6AD63998FDD2659F CR764;

Query Match 65.5%; Score 38; DB 1; Length 743;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 603 MMAGQPPPE 608

RESULT 32
KPC2 APLCA STANDARD; PRT; 743 AA.
AC Q16975;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calcium-independent protein kinase C (EC 2.7.11.1) (APL 11);
GN PKC2;
OS Aplysia californica (California sea hare);
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyrea; Opisthobranchia; Anaspidea;
OC Aplysiidae; Aplysiidae; Aplysia;
OX NCBI TaxID=6500;
RN 1;
RP SEQUENCE FROM N.A.;
RX MEDLINE=91332620; PubMed=1869917;
RA Kruger K.E., Sossin W.S., Sacktor T.O., Bergold P.D., Ben-Shaen S.,
RA Schwartz J.H.;
PT "Cloning and characterization of Ca2+-independent and Ca2+-
independent PKCs expressed in Aplysia sensory cells."
RL J. Neurosci. 11:2303-2313(1991);
RV 12;
RP CHARACTERIZATION;
RX MEDLINE=93194877; PubMed=8449941;
RA Sossin W.S., Diaz-Arastia R., Schwartz J.H.;
RT "Characterization of two isoforms of protein kinase C in the nervous
system of Aplysia californica."
RA J. Biol. Chem. 268:5762-5768(1993);
RV 14;
KE DOMAIN 2;
RX MEDLINE=92244410; PubMed=6346455;
RA Sossin W.S., Schwartz J.H.;
RT "Ca2+-independent protein kinase C isoform 2 contains an internal domain
similar to the C2 consensus sequence."
RA Trends Biochem. Sci. 18:207-208(1993);
RV 14;
RP CHARACTERIZATION;
RX MEDLINE=93334636; PubMed=9668085;
RA Pepio A.M., Fan X., Sossin W.S.;
RT "The role of C2 domains in Ca2+-activated and Ca2+-independent protein
kinase Cs in Aplysia."
RA J. Biol. Chem. 273:19040-19048(1998);
RV 15;
RP ERRATUM;
RA Pepio A.M., Fan X., Sossin W.S.;
RL J. Biol. Chem. 273:22856-22856(1998);
RV 16;
RP CHARACTERIZATION;
RX MEDLINE=98138438; PubMed=9477951;
RA Pepio A.M., Sossin W.S.;
RT "The C2 domain of the Ca(2+)-independent protein kinase C Apl 11
inhibits phorbol ester binding to the C1 domain in a phosphatidic
acid sensitive manner."
RA Biochemistry 37:1256-1263(1998);
RV 17;
RP FUNCTION; THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
SERINE AND THREONINE-SPECIFIC ENZYME.
```

```
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS (BY
CC SIMILARITY).
CC -!- ENZYME REGULATION: REQUIRES HIGH LEVELS OF PHOSPHATIDYL SERINE TO
CC BE ACTIVATED. THE PRESENCE OF THE C2 DOMAIN LOWERS THE AFFINITY OF
CC PROTEIN KINASE C ACTIVATORS FOR THE C1 DOMAINS AND THIS INHIBITION
CC CAN BE REMOVED BY PHOSPHATIDYL SERINE. PHOSPHATIDIC ACID, HOWEVER,
CC IS MUCH MORE POTENT THAN PHOSPHATIDYL SERINE IN REDUCING C2 DOMAIN-
CC MEDIATED INHIBITION, SUGGESTING THAT PHOSPHATIDIC ACID MAY BE A
CC REQUIRED COFACTOR FOR THE ACTIVATION OF APL 11.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN NERVOUS TISSUES, OVOTESTIS AND
CC GUT.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- PKC SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EXBL; N94884; AAA27771.1;
CC HSSP; P28867; IPTQ.
CC InterPro: IPR000308; C2.
CC InterPro: IPR002219; DAG_PE_bind.
CC InterPro: IPR000961; Pkinase_C.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam; PF00168; C2; 1.
CC Pfam; PF03130; DAG_PE_bind; 2.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00433; pkinase_C; 1.
CC PRINTS; PR00008; DAGPECDOMAIN.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SMC0109; C1; 2.
CC SMART; SMC0239; C2; 1.
CC SMART; SMC0133; S_TK_X; 1.
CC SMART; SMC0220; S_TKX; 1.
CC PROSITE; PS00499; C2_DOMAIN_1; FALSE_NEG.
CC PROSITE; PS00004; C2_DOMAIN_2; 1.
CC PROSITE; PS01479; DAG_PE_BIND_DOM_1; 2.
CC PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Transferase; Serine/threonine-protein kinase;
KW Phorbol-ester binding; Zinc; Repeat.
KW DOMAIN 1 108 C2 DOMAIN
FT DOMAIN 177 226 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 248 297 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 403 663 PROTEIN KINASE.
FT NP_BIND 409 417 ATP (BY SIMILARITY).
FT BINDING 432 432 ATP (BY SIMILARITY).
FT ACT_SITE 527 527 BY SIMILARITY.
SQ SEQUENCE 743 AA; 84413 MW; 4C982C563CA2B659 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 743;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 595 MMAGQPPPE 603

RESULT 33
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DPOL THEG8 STANDARD; PRT: 1699 AA.
AC Q9HH84;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7) (Contains: Endonuclease PI-Tspge81
DE (EC 3.1.1.1) (Tsp-GE8 pol-1 intein); Endonuclease PI-Tspge81
DE (EC 3.1.1.1) (Tsp-GE8 pol-2 intein);
GN POL OR POL-1;
OS Thermococcus sp. (strain GER)
CC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
CC Thermococcus
CX NCBI_TaxID=109593;
RN [1]
RP SEQUENCE FROM N.A.
RA Querrelou J.J.B., Cambon M.A., Lesongeur F., Barbier G.
RT "Thermococcales taxonomy and phylogeny based on the comparative use of
RT 16S rDNA, 16S-23S rDNA intergenic spacer and family B DNA polymerase
RT genes";
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE
CC EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY (BY SIMILARITY).
CC - FUNCTION: PI TSPGE81 AND PI-TSPGE811 ARE ENDONUCLEASES
CC (POTENTIAL).
CC - CATALYTIC ACTIVITY: N deoxyribo-5'-triphosphate + N diphosphate
CC + dNTP(N).
CC 1 PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
CC A POST-TRANSLATIONAL EXCISION OF THE INTERVENING REGION (INTEIN)
CC FOLLOWED BY PEPTIDE LIGATION.
CC - SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE B FAMILY.
CC - SIMILARITY: IN THE INTEIN SECTION, BELONGS TO THE HOMING
CC ENDONUCLEASE FAMILY.
CC
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CC
CC EMBL: AC255333; CAC12850.1;
CC HSSP: P56689; ITGO.
CC InterPro: IPR006172; DNA_pol_B
CC InterPro: IPR006134; DNA_pol_B_dom
CC InterPro: IPR026133; DNA_pol_B_exo
CC InterPro: IPR033586; Hedgehog_hinr
CC InterPro: IPR033587; Hedgehog_hinr
CC InterPro: IPR033541; Intein
CC InterPro: IPR033542; INTEIN
CC InterPro: IPR034042; Intein_endon
CC InterPro: IPR034578; Pol2.
CC Pfam: PF03136; DNA_pol_B; 3.
CC Pfam: PF03104; DNA_pol_B_exo; 1.
CC PRINTS: PR00379; INTEIN.
CC SMART: SM00305; HintC; 2.
CC SMART: SM00306; HintN; 2.
CC SMART: SM00486; POLBC; 1.
CC TIGRFAMs: TIGR01443; intein_Cteit; 1.
CC TIGRFAMs: TIGR01445; intein_Nteit; 1.
CC TIGRFAMs: TIGR00592; pol2; 2.
CC PROSITE: PS00116; DNA POLYMERASE B; FALSE_NEG
CC PROSITE: PS50818; INTEIN_CTER; 2.
CC PROSITE: PS50819; INTEIN_ENDONUCLEASE; 2.
CC PROSITE: PS50817; INTEIN_NTER; 2.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Hydrolase; Nuclease; Exonuclease; Multifunctional enzyme;
KW Protein splicing; Autocatalytic cleavage; Endonuclease; Intein homing.
FT CHAIN 1 491 DNA POLYMERASE, 1ST PART.
FT CHAIN 492 1026 ENDONUCLEASE PI TSPGE81
FT CHAIN 1027 1075 DNA POLYMERASE, 2ND PART.
FT CHAIN 1076 1464 ENDONUCLEASE PI-TSPGE811

FT CHAIN 1465 1699 DNA POLYMERASE, 3RD PART.
SQ SEQUENCE 1699 AA; 197323 MW; F389B4351F0B12D3 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 1699;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLIGRPPEETS 11
DB 629 ILGLPPEETS 639

RESULT 34
NHAB PSECL STANDARD; PRT: 220 AA.
AC P27763;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrile hydratase subunit beta (EC 4.2.1.84) (Nitrilase) (NHase).
GN NTHB.
OS Pseudomonas chlororaphis (Pseudomonas aureofaciens)
CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC Pseudomonadaceae; Pseudomonas.
CX NCBI_TaxID=333;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-23 AND 158-170.
RC STRAIN=B23;
RX MEDLINE=91193202; PubMed=2013568;
RA Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
RA Beppu T.;
RT "Cloning and characterization of genes responsible for metabolism of
RT nitrile compounds from Pseudomonas chlororaphis B23";
RL J. Bacteriol. 173:2465-2472(1991).
CC - FUNCTION: NHASE CATALYZES THE HYDRATION OF VARIOUS NITRILE
CC COMPOUNDS TO THE CORRESPONDING AMIDES. INDUSTRIAL PRODUCTION OF
CC ACRYLAMIDE IS NOW BEING DEVELOPED USING SOME OF THESE ENZYMES.
CC - CATALYTIC ACTIVITY: An aliphatic amide + a nitrile + H(2)O.
CC - SUBUNIT: Heterodimer of an alpha and a beta chain.
CC - SIMILARITY: BELONGS TO THE NITRILE HYDRATASE SUBUNIT BETA FAMILY.
CC
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CC
CC EMBL: D90216; BAA4446.1;
CC PIR: B42725; B42725.
CC HSSP: P13449; 2AHJ.
CC InterPro: IPR003168; NHase_beta.
CC Pfam: PF02211; NHase_beta; 1.
CC Lyase.
SQ SEQUENCE 220 AA; 24545 MW; 191AE1C5F14D4864 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 220;
Best Local Similarity 75.0%; Pred. No. 8.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLGRPPFE 9
DB 118 ITGRPPFE 125

RESULT 35
STKC RAT STANDARD; PRT: 343 AA.
AC Q55C99;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 43, Last annotation update)

DE Serine/threonine protein kinase 12 (EC 2.7.11.37) (Aurora and Ip11-
like midbody-associated protein 1) (AIM-1) (Aurora-B).
GN STK12 OR AIM1.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98119810; PubMed=945092;
RA Terada Y., Tatsuka M., Suzuki F., Yasuda Y., Fujita S., Inoue M.,
RT "AIM-1, a mammalian midbody-associated protein required for
cytokinesis.";
RL EXRC J. 17:667-676(1998).
CC -- FUNCTION: Maybe directly involved in regulating the cleavage of
CC polar spindle microtubules and is a key regulator for the onset of
CC cytokinesis during mitosis (By similarity).
CC -- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
CC in late anaphase and concentrated into the midbody in telophase
CC and cytokinesis. Colocalized with gamma tubulin in the mid-body
CC (By similarity).
CC -- TISSUE SPECIFICITY: High level expression seen in the testis. It
CC is also expressed in the spleen, lung and heart. Expressed in the
CC 32/M phase of the cell cycle.
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC RMSD: D89731; BAA23794.1;
DR HSNP: Q63450; IAC6.
DR InterPro: IPR002052; N6_Mtase.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR012457; Tyr_kinase.
DR Pfam: PF00069; pkinase.1.
DR PROSITE: PS00001; Prot_kinase.1.
DR SMART: SM00220; S_TKC.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST_1.
DR PROSITE: PS00117; PROTEIN_KINASE_TYR_1.
KW Cell cycle; Transferase; Serine/threonine protein kinase; ATP binding.
FT DOVAIN 80 330 PROTEIN KINASE.
FT NE BIND 86 94 ATP (BY SIMILARITY).
FT BINDING 109 109 ATP (BY SIMILARITY).
FT ACT SITE 203 203 BY SIMILARITY.
SQ SEQUENCE 143 AA; 39234 MW; 22B740D20E287598 CF; 164;
Query Match 63.8%; Score 17; DB 1; Length 340
Best local similarity 50.0%; Pred. No. 14;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGRPPPFET 10
DB 269 LMVGNPPFES 278
RESULT 36
STKC_VGUSF
ID STKC_MOUSE STANDARD; PRT; 345 AA.
AC Q70126; Q61882;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 12 (EC 2.7.11.37) (Aurora-related

DE kinase 2) (Serine/threonine protein kinase 5) (STK-1) (Aurora-B).
GN STK12 OR STK5 OR ARK2 OR STK1.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=96194801; PubMed=9647446;
RA Niwa H., Abe K., Kunisada T., Yamamura K.,
RT "Cell-cycle-dependent expression of the STK-1 gene encoding a novel
RT murine putative protein kinase";
RL Gene 169:197-201(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=98183439; PubMed=9514916;
RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.,
RT "cDNA cloning, expression, subcellular localization, and chromosomal
RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
RT 1 and 2.";
RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuier G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares V.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliahy S.J.,
RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -- FUNCTION: May be directly involved in regulating the cleavage of
CC polar spindle microtubules and is a key regulator for the onset of
CC cytokinesis during mitosis (By similarity).
CC -- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
CC in late anaphase and concentrated into the midbody in telophase
CC and cytokinesis. Colocalized with gamma tubulin in the mid-body
CC (By similarity).
CC -- TISSUE SPECIFICITY: Expressed in testis, intestine and spleen. All
CC of them are tissues that contain a large number of proliferating
CC cells. Expressed during S phase, in a cell-cycle-
CC dependent fashion.
CC -- DEVELOPMENTAL STAGE: Strongly expressed in 8.5 and 12.5 dpc.
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC
CC EMBL: D21099; BAA04658.1;

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DR EMBL: U69107; AAC12683.1; -
DR EMBL: BC003263; AAC03261.1; -
DR HSSP: Q63450; 1A06.
DR MGD: MG1107168; Stk12.
DR InterPro: IPR002052; N6_Mtase.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00117; PROTEIN_KINASE_DOM; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 82 332 PROTEIN_KINASE.
FT NP_BIND 88 96 ATP (BY SIMILARITY).
FT BINDING 111 111 ATP (BY SIMILARITY).
FT ACT_SITE 205 205 BY SIMILARITY.
FT CONFLICT 44 44 R > W (IN REF. 10).
SQ SEQUENCE 345 AA; 39324 MW; C11D9B6BDEAD0A0 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 490;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 10
   ||| |||
DK 291 LNVGNPPPS 280

RESULT 10
PLK3_YXXXA STANDARD; PRT; 380 AA.
ID PK05_YXXXA
AC P94137;
DT 01-OCT-1996 (Rel. 34, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DI 16-FEB-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase pkn5 EC 2.7.11.37.
DE PKN5.
GN PKN5.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Delta proteobacteria; Myxococciales;
OC Cystobacteriaceae; Myxococcaceae; Myxococcus
OX NCBI_TaxID=34.
RN 11.
RP SEQUENCE FROM N.A.
RC STRAIN=9701.
RX MEDLINE=94310101; PubMed 8793241.
RA Zhang W., Inouye M., Inouye S.
RT "Regulation of the differentiation of Myxococcus xanthus
   by Pkn5 and Pkn6, eukaryotic like serine protein kinases."
RE Mol. Microbiol. 20:435-447(1996).
FT 1 FUNCTION: Pkn5 and pkn6 may have reciprocal roles in growth and
   development. Pkn5 may be a kinase that negatively regulates
   development.
CC 1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphorylated
   protein.
CC 1- SUBCELLULAR LOCATION: Cytoplasmic
CC DEVELOPMENTAL STAGE: Expressed constitutively throughout the life
   cycle, with slight increases at an early stage of development.
CC 1- PTM: Autophosphorylated at serine residues.
CC 1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC
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DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00117; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 9 378 PROTEIN_KINASE.
FT NP_BIND 15 23 ATP (BY SIMILARITY).
FT BINDING 38 38 ATP (BY SIMILARITY).
FT ACT_SITE 244 244 BY SIMILARITY.
SQ SEQUENCE 380 AA; 41924 MW; DC3ADFB24420C1F1 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 380;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
   ||| |||
DB 314 LLSGRPPPD 322

RESULT 38
PLK3_CAEEI STANDARD; PRT; 615 AA.
ID PLK3_CAEEI
AC Q20845;
DI 28-FEB-2003 (Rel. 41, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase plk-3 (EC 2.7.11.-) (Polo-like
   kinase 3).
GN PLK-3 OR PLC2 OR F5501.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 11.
RP SEQUENCE FROM N.A.
RX MEDLINE=99304501; PubMed-10376213;
RA Ouyang B., Wang Y., Dai W.;
RT "Caenorhabditis elegans contains structural homologs of human plx and
   plx-1."
RI DNA Seq. 10:109-113(1993);
RN 12.
RP SEQUENCE FROM N.A.
RC STRAIN= Bristol NE1;
RA Murray J., Le T.
RT Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC 1- FUNCTION: May be required for cell division and may have a role
   during G1 or S phase (By similarity).
CC 1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CC5/POLO SUBFAMILY.
CC 1- SIMILARITY: Contains 2 POLO box domains.
CC
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DR EMBL: AF059024; AAC14425.1; -
DR EMBL: U58750; AAR00642.1; -
DR PIR: T29223; T29223.
DR HSSP: Q63450; 1A06.
DR Wor-Pep; F55G1.H; CE07285.
DR GO: GO:0005624; Cytoplasm; ISS.
DR GO: GO:0005624; ATP binding activity; ISS.
DR GO: GO:0004674; Protein serine/threonine kinase activity; ISS.
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DR GO: 000606468; Piprotein amino acid phosphorylation; ISS.
 DR InterPro: IPR000959; PCLO_box.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00659; PCLO_box; 2.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00117; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00078; PCLO_BOX; 2.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase; Repeat;
 KW Nucleic acid protein.
 FT DOMAIN 35 286 PROTEIN_KINASE.
 FT NP_BIND 41 49 ATP_BY_SIMILARITY.
 FT BINDING 64 64 ATP_BY_SIMILARITY.
 FT ACT_SITE 158 158 BY_SIMILARITY.
 FT DOMAIN 402 463 PCLO_BOX_1.
 FT DOMAIN 505 573 PCLO_BOX_2.
 SQ SEQUENCE 615 AA; 70436 MW; D510C727329C4R26 CR664;
 Query Match 63.8%; Score 37; DB 1; Length 615;
 Best Local Similarity 60.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MLGRRPPE 10
 DB 285 MLGRRPPE 234
 RESULT 3;
 KPC1 APLCA STANDARD; PRT; 640 AA.
 AC Q16974;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calcium-dependent protein kinase C (EC 2.7.11.1) (AFL 1)
 GN PKC1.
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
 OC Aplysioidea; Aplysiidae; Aplysia.
 OX NCBI:TaxID=6500;
 RN 1;
 RP SEQUENCES FROM NIA
 RX MEDLINE=91332620; PubMed=1869919;
 RA Kruger K.S., Sossin W.S., Sacktor T.M., Kornhuber H.H., Johansson S.,
 RA Schwartz J.H.;
 RT "Cloning and characterization of Ca2+-dependent and Ca2+-
 RT independent PKCs expressed in Aplysia sensory cells."
 RL J. Neurosci. 11:2303-2313(1991).
 RN 1;
 RP CHARACTERIZATION.
 RX MEDLINE=93194877; PubMed=8449941;
 RA Sossin W.S., Diaz-Arastia R., Schwartz J.H.;
 RT "Characterization of two isoforms of protein kinase C in the nervous
 RT system of Aplysia californica."
 RL J. Biol. Chem. 268:5763-5768(1993).
 RN 1;
 RP CHARACTERIZATION.
 RX MEDLINE=98334636; PubMed=9668035;
 RA Peipo A.M., Fan X., Sossin W.S.;
 RT "The role of C2 domains in Ca2+-activated and Ca2+-independent protein
 RT kinase Cs in Aplysia."
 RL J. Biol. Chem. 273:19040-19048(1998).
 RN 1;
 RP ERRATUM
 RA Peipo A.M., Fan X., Sossin W.S.;
 RL J. Biol. Chem. 273:22856-22856(1998).
 CC FUNCTION: THIS IS CALCIUM-DEPENDENT, PHOSPHOLIPID-DEPENDENT,
 CC SERINE AND THREONINE-SPECIFIC KINASE. ACTIVATION OF PKC BY

CC SEROTONIN RESULTS IN PRESYNAPTIC FACILITATION OF DEPRESSED
 CC SENSORY-TO-MOTOR NEURON SYNAPSES, WHICH IS THOUGHT TO UNDERLIE
 CC BEHAVIORAL DISINHIBITION.
 CC FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
 CC SIMILARITY).
 CC ENZYME REGULATION: ACTIVATED BY PHOSPHATIDYL SERINE.
 CC SUBCELLULAR LOCATION: CYTOSOL; CYTOSOL; TRANSLOCATED TO NEURONAL
 CC MEMBRANES.
 CC SIMILARITY: Contains 2 zinc dependent phorbol-ester and DAG
 CC binding domains.
 CC SIMILARITY: Contains 1 C2 domain.
 CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; M94883; AAA27770.2;
 CC HSSP; P05697; ITBN.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR002219; DAG_PE-bind.
 DR InterPro: IPR000361; Pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00130; DAG_PE-bind; 2.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00433; Pkinase_C; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TKc; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00499; C2_DOMAIN_1; 1.
 DR PROSITE; PS00004; C2_DOMAIN_2; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Transferase; Serine/threonine protein kinase;
 KW Phorbol ester binding; Zinc; Repeat;
 FT DOMAIN 22 71 PHORBOL-ESTER AND DAG BINDING 1;
 FT DOMAIN 86 135 PHORBOL-ESTER AND DAG BINDING 2;
 FT DOMAIN 157 244 C2 DOMAIN.
 FT DOMAIN 320 578 PROTEIN_KINASE.
 FT NP_BIND 326 334 ATP (BY SIMILARITY).
 FT BINDING 349 349 ATP (BY SIMILARITY).
 FT ACT_SITE 444 444 BY SIMILARITY.
 SQ SEQUENCE 649 AA; 74079 MW; A53253399284E330 CR664;
 Query Match 63.8%; Score 37; DB 1; Length 649;
 Best Local Similarity 60.7%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLGRRPPE 9
 DB 512 MLGRRPPE 520
 RESULT 40
 KPC1_LYTP1 STANDARD; PRT; 658 AA.
 ID KPC1_LYTP1
 AC Q25379;

GenCore version 5.1.6
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Query protein protein search, using sw model
Run on: November 14, 2003, 14:34:38 / Search time 35 Seconds
(without alignment)
81.102 Million cell updates/sec

Title: US-09-736 076-19
Perfect score: 58
Sequence: 1 MLLGRPPFETS 11
Scoring table: BLOSUM62
Gapop 10.0 / Gapext 0.5
Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database				SPTRMBL 23:			
				1: sp_archae:			
				2: sp_bacteria:			
				3: sp_fungi:			
				4: sp_human:			
				5: sp_invertebrate:			
				6: sp_mammal:			
				7: sp_mito:			
				8: sp_organelle:			
				9: sp_phage:			
				10: sp_plant:			
				11: sp_rodent:			
				12: sp_virus:			
				13: sp_vertebrate:			
				14: sp_unclassified:			
				15: sp_virus:			
				16: sp_bacteriaph:			
				17: sp_archaeap:			
SUMMARIES				Description			
Result No.	Score	Query Match	Length DB ID				
1	55	94.8	316 6 Q9BDK4	Q9BDK4 sus scrofa			
2	55	94.8	372 4 Q8N7M6	Q8N7M6 homo sapien			
3	55	94.8	666 13 Q9CXS4	Q9CXS4 xenopus lae			
4	55	94.8	682 11 Q8K226	Q8K226 mus musculu			
5	49	84.5	526 6 Q9BDP8	Q9BDP8 sus scrofa			
6	49	84.5	598 13 P70032	P70032 xenopus lae			
7	49	84.5	623 5 Q81U35	Q81U35 asterina pe			
8	48	82.8	769 5 Q97143	Q97143 drosophila			
9	46	79.3	324 11 Q9CVR6	Q9CVR6 mus musculu			
10	46	79.3	925 11 Q8RQ15	Q8RQ15 mus musculu			
11	46	79.3	925 11 Q64702	Q64702 mus musculu			
12	46	79.3	970 4 Q96Q95	Q96Q95 homo sapien			
13	46	79.3	970 4 Q00444	Q00444 homo sapien			
14	46	79.3	970 4 Q81YF0	Q81YF0 homo sapien			
15	45	77.6	568 5 Q8MX06	Q8MX06 caenorhabdi			
16	45	77.6	582 5 Q9GRE7	Q9GRE7 pericentriol			

Pred. No. is the number of results predicted by database to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

17	45	77.6	749	5 Q8MXG7	Q8mxg7 caenorhabdi
18	45	77.6	780	5 Q76360	Q76360 caenorhabdi
19	44	75.9	485	13 Q9CXS2	Q9CXS2 xenopus lae
20	44	75.9	557	13 Q9CXS3	Q9CXS3 xenopus lae
21	44	75.9	767	5 Q15882	Q15882 trypanosoma
22	43	74.1	80	13 Q91891	Q91891 xenopus lae
23	43	74.1	673	5 Q62567	Q62567 suberites d
24	43	74.1	677	5 Q96997	Q96997 geodia cydo
25	42	72.4	456	5 Q8MYF1	Q8myf1 dictyosteli
26	41	70.7	346	13 Q8CXS8	Q8CXS8 brachydanio
27	41	70.7	524	11 Q8K0J7	Q8K0J7 mus musculu
28	41	70.7	646	4 Q96CV1	Q96cv1 homo sapien
29	39	67.2	153	16 Q84342	Q84342 chlamydia t
30	39	67.2	235	5 Q9GP07	Q9gp07 leishmania
31	39	67.2	358	5 Q00872	Q00872 leishmania
32	39	67.2	692	16 Q8G6P9	Q8g6p9 bifidobacte
33	39	67.2	1337	2 Q9KCN7	Q9Kcn7 myxococcus
34	38	65.5	240	11 Q63432	Q63432 rattus norv
35	38	65.5	256	16 Q9PPA6	Q9ppa6 campylobact
36	38	65.5	256	16 Q9WXT3	Q9wxt3 thermotoga
37	38	65.5	257	16 Q8Y2A0	Q8y2a0 ralstonia s
38	38	65.5	305	5 Q01427	Q01427 caenorhabdi
39	38	65.5	332	16 Q9ACZ9	Q9ajz9 streptomyce
40	38	65.5	434	16 Q8EM12	Q8emi2 oceanobacil
41	38	65.5	538	17 Q8Z2C9	Q8zzc9 pyrobaculum
42	38	65.5	554	5 Q95T78	Q95t78 drosophila
43	38	65.5	605	10 Q93ZJ9	Q93zj9 arabidopsis
44	38	65.5	656	10 Q9S770	Q9s770 arabidopsis
45	38	65.5	660	16 Q8FUI5	Q8fui5 corynebacte

ALIGNMENTS

RESULT 1:
Q9BDK4
ID Q9BDK4 PRELIMINARY; PRT; 316 AA.
AC Q9BDK4;
DT Q1-JUN-2001 (TREMBLrel. 17, Created)
DT Q1-JUN-2001 (TREMBLrel. 17, last sequence update)
DT Q1-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Serum-inducible kinase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CX NCBI TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Anger M., Kues W.A., Klima J., Motlik J., Carnwath J.W., Niemann H.;
RT "Porcine serum-inducible kinase";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF348424; AAK27154.1; -;
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00669; pkinase; 1.
DR Pfam; PF03659; POLO_box; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50078; POLO_BOX; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER 1
FT NON_TER 316
SQ SEQUENCE 316 AA; 35330 MW; F63BBE4A2691D62F CRC64;

Query Match 94.8%; Score 55; DB 6; Length 316;
Best Local Similarity 90.9%; Pred. No. 0.029;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGRPPFETS 11
|||
Db 25 MLLGRPPFETS 35


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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Polc-like protein kinase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
CX KCF; TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Anger M., Kuos W.A., Klima J., Mielenz M., Motlik M., Garnswath G.W.,
RA Nurnann H.
RT "Expression of polc-like kinase in cell cycle synchronized porcine
RT fetal fibroblasts".
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF339021; AAK28550.1; -.
DE HSSP; Q63450; 1A06.
DR InterPro; IPR000959; POLC_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLC_box; 2.
DR ProDom; PD000000; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00078; POLC_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00010; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER; 1.
FT NON_TER; 526 526
SQ SEQUENCE 526 AA; 60399 MW; 1AF6A8E509B2CBP2 CRC64;

Query Match 84.5%; Score 49; DB 4; Length 506;
Best Local Similarity 72.7%; Pred. No. 0.66;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGGRPPFETS 11
DB 199 LLVGKPPFETS 209

RESULT 6
PRT32
ID P20042 PRELIMINARY; IPT; 508 AA
AC P20042
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Flx1.
OS Xenopus laevis African clawed frog.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoana, Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96355660; PubMed=8703070;
RA Kumagai A., Dunphy W.G.;
RT "Purification and molecular cloning of Flx1, a cdc2-regulatory kinase
RT from Xenopus egg extracts.";
RL Science 273:1377-1380(1996);
CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U58205; AAC60017.1; -.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR000959; POLC_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLC_box; 2.
DR ProDom; PD000000; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00078; POLC_BOX; 2.
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DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 598 AA; 68211 MW; 2467195911F225E6 CRC64;

Query Match 84.5%; Score 49; DB 13; Length 598;
Best Local Similarity 72.7%; Pred. No. 0.74;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGGRPPFETS 11
DB 235 LLVGKPPFETS 245

RESULT 7
Q8IU35
ID Q8IU35 PRELIMINARY; PRT; 623 AA.
AC Q8IU35;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Polc-like kinase.
GN PLK.
OS Asterina pectinifera (Starfish).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
CX NCBI_TaxID=7594;
RN [1]
RP SEQUENCE FROM N.A.
RA Uchida T.O., Tachibana K., Kishimoto T.;
RT "Starfish Plk.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB084465; BAC22692.1; -.
KW Kinase.
SQ SEQUENCE 623 AA; 70929 MW; CFC01900802D724A CRC64;

Query Match 84.5%; Score 49; DB 5; Length 623;
Best Local Similarity 72.7%; Pred. No. 0.78;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGGRPPFETS 11
DB 220 LLVGKPPFETS 230

RESULT 8
Q97143
ID Q97143 PRELIMINARY; PRT; 769 AA.
AC Q97143;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SAK protein.
GN SAK OR CG7186.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazei R.G., Champe W., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Benson K.Y., Berns P.V., Berman P.P., Bhandari D., Bolshakov S.
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DR InterPro: IPR000959; POLO_box.  
DR InterPro: IPR000719; Prot_kinase.  
DR InterPro: IPR002290; Ser_thr_kinase.  
DR InterPro: IPR001245; Tyr_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR PRODOM: PDC02001; Prot_kinase; 1.  
DR SMART: SM00220; S_TKG; 1.  
DR PROSITE: PS00078; POLO_BOX; 1.  
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.  
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.  
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.  
KW ATP-binding; Kinase; Transferase.  
SQ SEQUENCE 570 AA; 108955 MW; 55215615F8B8E0F C5764.  
  
Query Match: 79.3%; Score 46; DB 4; Length 568;  
Best Local Similarity 70.0%; Pred. No: 4;  
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY : MLGRRPPFET 10  
III I I  
DB 204 LLIGRRPFDT 213  
  
RESULT 14  
Q81YF0 PRELIMINARY; PRT; 970 AA.  
AC Q81YF0  
DT 01-VAR-2003 (TrEMBLrel. 23, Created).  
DT 01-VAR-2003 (TrEMBLrel. 23, Last sequence update).  
DT 01-VAR-2003 (TrEMBLrel. 23, Last annotation update).  
DE Similar to serine/threonine protein kinase.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homin  
CX NCB: TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Straussberg R.;  
RA Submitted (JUL 2002) to the EMBL/GenBank/CCDB databases.  
KW Kinase; Serine/threonine-protein kinase.  
SQ SEQUENCE 970 AA; 108971 MW; 4D66F5FD983211A6 C9CF4.  
  
Query Match: 79.3%; Score 46; DB 4; Length 568;  
Best Local Similarity 70.0%; Pred. No: 4;  
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY : MLGRRPPFET 10  
III I I  
DB 204 LLIGRRPFDT 213  
  
RESULT 15  
Q8MXG6 PRELIMINARY; PRT; 568 AA.  
AC Q8MXG6  
DT 01-VAR-2003 (TrEMBLrel. 22, Created).  
DT 01-VAR-2003 (TrEMBLrel. 22, Last sequence update).  
DT 01-VAR-2003 (TrEMBLrel. 23, Last annotation update).  
DE ECL-4 protein, corresponding sequence F55A8.2d.  
GN F55A8.2 OR ES5.4.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Eubaditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
CX NCB: TaxID:6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA NEDLINE=99069613; PubMed=9851416;  
RA Waterston R.;  
RT Genome sequence of the nematode C. elegans: a platform for
```

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RT Investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Landston Y., Wohldmann P., Duckels G.;  
RT "The sequence of C. elegans cosmid F55A8".  
RL Submitted (JUN 1998) to the EMBL/GenBank/CCDB databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (AUG-2002) to the EMBL/GenBank/CCDB databases.  
DR EMBL: AF067612; AAM980111; -;  
DR WormPep; F55A8.2d; CE31542.  
DR InterPro: IPR002373; CAMP_kin.  
DR InterPro: IPR002374; GMP_kin.  
DR InterPro: IPR000595; CNMP_binding.  
DR InterPro: IPR000961; pkinase C.  
DR InterPro: IPR000719; Prot_kinase.  
DR InterPro: IPR002290; Ser_thr_pkinase.  
DR InterPro: IPR001245; Tyr_pkinase.  
DR Pfam: PF00027; CNMP_binding; 2.  
DR Pfam: PF00069; pkinase; 1.  
DR Pfam: PF00433; pkinase C; 1.  
DR PRINTS: PR00103; CAMPKINASE.  
DR PRINTS: PR00104; GMPKINASE.  
DR PRODOM: PDC02001; Prot_kinase; 1.  
DR SMART: SM00100; CNMP; 1.  
DR SMART: SM00220; S_TKG; 1.  
DR SMART: SM00133; S_TKX; 1.  
DR SMART: SM00219; TYRK; 1.  
DR PROSITE: PS00889; CNMP_BINDING_1; 1.  
DR PROSITE: PS00889; CNMP_BINDING_2; 1.  
DR PROSITE: PS00042; CNMP_BINDING_3; 2.  
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.  
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.  
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.  
KW ATP-binding; Transferase.  
SQ SEQUENCE 568 AA; 65094 MW; 423AB3BD6E52ACF4 C9C64;  
  
Query Match: 77.6%; Score 45; DB 5; Length 568;  
Best Local Similarity 63.6%; Pred. No: 4;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MLGRRPPFET 11  
III I I  
DB 448 LMLGRRPFQAS 458  
  
RESULT 16  
Q9GRB7 PRELIMINARY; PRT; 582 AA.  
AC Q9GRB7  
DT 01-VAR-2001 (TrEMBLrel. 16, Created).  
DT 01-VAR-2001 (TrEMBLrel. 16, Last sequence update).  
DT 01-VAR-2003 (TrEMBLrel. 23, Last annotation update).  
DE Polo-like kinase.  
GN UPJK.  
OS Hemiecentrotus pulcherrimus (Sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinozoa; Euechinozoa; Echinacea; Echinoida; Strongylocentrotidae;  
OC Hemiecentrotus.  
CX NCB: TaxID:7650;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yonemura I., Fujimoto H., Mabuchi I.;  
RT "Cloning of sea urchin plk".  
RL Submitted (MAY-2000) to the EMBL/GenBank/CCDB databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Yonemura I., Fujimoto H., Mabuchi I.;  
RT "Cloning of sea urchin polo-like kinase".
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RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB043997; RAB18588.1; -
 DR InterPro: IPR001395; AldoKet_red.
 DR InterPro: IPR000959; POLO_box.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00639; POLO_box; 2.
 DR ProDom: P000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00063; ALDO-KETO REDUCTASE; 1.
 DR PROSITE: PS00078; POLO_BOX; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine protein kinase; Transferase.
 SQ SEQUENCE 582 AA; 66429 MW; A1774AQCACEDDESD CRC64;

Query Match 77.6%; Score 45; DB 5; Length 582;
 Res: Local Similarity 70.0%; Pred. No. 4.1;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFET 10
 DB 216 LMLGRPPFET 227

RESULT 17
 Q8MXG7
 ID Q8MXG7 PRELIMINARY; PRT; 749 AA.
 AC Q8MXG7
 DT 01-OCT-2003 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE EGL-4 protein (corresponding sequence F55A8.2c).
 GN F55A8.2 OR EGL-4.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 EV MEDLINE=99049613; PubMed=9851916;
 RA Waterston R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans sequencing consortium
 RL Science 242:2012-2018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Langston Y., Wohldmann P., Duckels G.,
 RT "The sequence of C. elegans cosmid F55A8.1";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (AJG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF067612; AAM99010.1; -
 DR WormPep: F55A8.2c; CE31541.
 DR InterPro: IPR002373; cAMP_kin.
 DR InterPro: IPR002374; cGMP_kin.
 DR InterPro: IPR000595; cNMP_binding.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00027; cNMP_binding; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00433; pkinase_C; 1.
 DR PRINTS: PR00103; CAMPKINASE.

DR PRINTS: PR00104; CGMPKINASE.
 DR ProDom: P000001; Prot_kinase; 1.
 DR SMART: SM00100; cNMP; 2.
 DR SMART: SM00220; S_TKC; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR SMART: SM00219; Tyr_KC; 1.
 DR PROSITE: PS00888; cNMP_BINDING_1; 2.
 DR PROSITE: PS00889; cNMP_BINDING_2; 2.
 DR PROSITE: PS00042; cNMP_BINDING_3; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 749 AA; 84497 MW; ADE0H9F5354D93C6 CRC64;

Query Match 77.6%; Score 45; DB 5; Length 749;
 Best Local Similarity 63.6%; Pred. No. 5.3;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFETS 11
 DB 629 LMLGRPPFQAS 639

RESULT 18
 Q76360
 ID Q76360 PRELIMINARY; PRT; 780 AA.
 AC Q76360;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical 86.7 kDa protein F55A8.2 in chromosome IV.
 GN F55A8.2.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Langston Y., Wohldmann P., Duckels G.,
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; MAY BE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF067612; AAD36954.1; -
 DR EMBL: AF067612; AAD36953.1; -
 DR HSSP: P05132; 1APM.
 DR WormPep: F55A8.2a; CE19897.
 DR WormPep: F55A8.2b; CE19898.
 DR InterPro: IPR002374; cGMP_kin.
 DR InterPro: IPR000595; cNMP_binding.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00027; cNMP_binding; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00433; pkinase_C; 1.
 DR PRINTS: PR00104; CGMPKINASE.
 DR ProDom: P000001; Prot_kinase; 1.
 DR SMART: SM00100; cNMP; 2.
 DR SMART: SM00220; S_TKC; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR PROSITE: PS00888; cNMP_BINDING_1; 2.
 DR PROSITE: PS00889; cNMP_BINDING_2; 2.
 DR PROSITE: PS00042; cNMP_BINDING_3; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.

Query Match 75.9% Score 43; DB 5; Length 763;
 Best Local Similarity 63.6%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 11
 EL 244 MLVGRPPPE 244

RESULT 22
 Q91891
 ID Q91891 PRELIMINARY; PRT; 80 AA;
 AC Q91891;
 DT 01-NOV-1996 (TREMBLrel. 01, Created;
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update;
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update;
 DE Hypothetical 9.4 kDa protein (fragment);
 CS Xenopus laevis (African clawed frog);
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 CC Xenopodinae; Xenopus;
 CX NCBI_TaxID=8355;
 RN 1;
 RP SEQUENCE FROM N.A.
 PA Rouvet P., Cellili F., ARLOT-BONNEVAIN Y., Lejaqueux V., Pochi C.,
 Bassez T., OSBORNE H.;
 RT "Coordinately controlled by the 3' untranslated region of a
 RT developmentally controlled mRNA in xenopus embryos is switched to
 RT polyadenylationby deletion of a short sequences element";
 RL Mol. Cell. Biol. 14:1893-1900(1995);
 DR EMBL:224451; CNA8C826.1;
 DR InterPro: IPR000719; Prot kinase;
 CR Pfam: PF00669; pkinase; 1;
 DR ProDom: PD000001; Prot kinase; 1;
 DR PROSITE: PS00107; PROTEIN_KINASE_DOM; 1;
 KW Hydrophobic protein; ATP-binding; Transferase;
 FT NON_TER 1
 SC SEQUENCE 80 AA; 9388 MW; 8DF05DBA14BE14FF CRC64;

Query Match 74.1% Score 43; DB 13; Length 763;
 Best Local Similarity 77.8%; Pred. No. 11;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMLGRPPPE 10
 EL 4 MLVGRPPPE 11

RESULT 20
 Q96997
 ID Q96997 PRELIMINARY; PRT; 677 AA;
 AC Q96997;
 DT 01-AUG-1998 (TREMBLrel. 07, Created;
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update;
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update;
 DE Serine/threonine protein kinase;
 CS Suberites domuncula (Sponge);
 CC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 CC Hydrozoa; Suberitidae; Suberites;
 CX NCBI_TaxID=55567;
 RN 1;
 RP SEQUENCE FROM N.A.
 RA Mueller W.E.G.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases;
 RN 12;
 RP SEQUENCE FROM N.A.
 RX VEDLINE=96394688; PubMed=8798142;
 RA Kruse M., Gamulin V., Cetkovic B., Pichler M., Mueller W.E.G.;
 RA Mueller W.E.G.;
 RT "Molecular evolution of the Metazoa protein kinase C family;
 RT family";
 RL Mol. Biol. Evol. 43:374-383(1996);
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 EMBL: Y13099; CAA73553.1;
 DR HSSP; P28867; IPTQ;
 DR InterPro: IPR000008; C2;
 DR InterPro: IPR001064; Crystallin;
 DR InterPro: IPR002219; DAG_PE-bind;
 DR InterPro: IPR000961; Pkinase_C;
 DR InterPro: IPR000719; Prot kinase;
 DR InterPro: IPR002290; Ser_thr_pkinase;
 DR Pfam: PF00168; C2; 1;
 DR Pfam: PF00130; DAG_PE_bind; 2;
 DR Pfam: PF00069; pkinase; 1;
 DR Pfam: PF00433; pkinase_C; 1;
 DR PRINTS: PR00360; C2DOMAIN;
 DR PRINTS: PR00008; DAGPEDOMAIN;
 DR ProDom: PD000001; Prot kinase; 1;
 DR SMART: SMC0109; C1; 2;
 DR SMART: SMC0239; C2; 1;
 DR SMART: SMC0220; S_TKc; 1;
 DR SMART: SM00133; S_TK_X; 1;
 DR PROSITE: PS00499; C2_DOMAIN_1; 1;
 DR PROSITE: PS00004; C2_DOMAIN_2; 1;
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1;
 DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2;
 DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2;
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1;
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1;
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase;
 SQ SEQUENCE 673 AA; 73344 MW; 96D24E55497C293 CRC64;

Query Match 74.1% Score 43; DB 5; Length 673;
 Best Local Similarity 77.8%; Pred. No. 11;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 EL 535 MLVGRPPPE 543

RESULT 24
 Q96997
 ID Q96997 PRELIMINARY; PRT; 677 AA;
 AC Q96997;
 DT 01-MAY-1999 (TREMBLrel. 10, Created;
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update);
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update);
 DE Protein kinase C;
 GN PKC2;
 CS Geodia cydonium (Sponge);
 CC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 CC Astrophorida; Geodiidae; Geodia;
 CX NCBI_TaxID=6047;
 RN 1;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99147839; PubMed=10023072;
 RA Seack C., Kruse M., Mueller W.E.G., Mueller W.E.G.;
 RT "Promoter and exon intron structure of the protein kinase C gene from
 RT the marine sponge Geodia cydonium: Evolutionary considerations and
 RT promoter activity";
 RL Biochim. Biophys. Acta 1444:241-253(1999);
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC 1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 DR EMBL: Y17882; CAA76911.1;
 DR HSSP; P28867; IPTQ;
 DR InterPro: IPR000008; C2;
 DR InterPro: IPR001064; Crystallin;
 DR InterPro: IPR002219; DAG_PE-bind;
 DR InterPro: IPR000961; Pkinase_C;
 DR InterPro: IPR000719; Prot kinase;
 DR InterPro: IPR002290; Ser_thr_pkinase;
 DR Pfam: PF00168; C2; 1;
 DR Pfam: PF00130; DAG_PE_bind; 2;

DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00433; pkinase_C; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00088; DAGPEDOMAIN.
DR PfamDom: PF000001; Prot_kinase; 1.
DR SMART: SM00039; C1; 2.
DR SMART: SM00039; C2; 1.
DR SMART: SM00020; S_TKc; 1.
DR SMART: SM00033; S_TK_X; 1.
DR PROSITE: PS00499; C2_DOMAIN; 1.
DR PROSITE: PS00004; C2_DOMAIN; 1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM; 1.
DR PROSITE: PS00081; DAG_PE_BIND_DOM; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 477 AA; 76787 MW; 800025081B3DEA13 CRC64;

Query Match: 74.1%; Score 437; DB 51; Length 487;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLIQRRPPE 9
DB 519 MIVGRPFD 547

RESULT 26
Q8XGJ7
ID Q8XGJ7 PRELIMINARY; PR7; 346 AA.
AC Q8XGJ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aurora-like serine/threonine kinase (Fragment).
GN STKA.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7935;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22035902; PubMed=12036978;
RA Gollig G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,
RA Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y., Nissen R M.,
RA Hopkins N.;
RT "Insertional mutagenesis in zebrafish rapidly identifies genes
essential for early vertebrate development."
RL Nat. Genet. 31:135-140(2002).
DR EMBL: AY099518; AAY28206.1; 1.
DR InterPro: IPR002052; N6_Mtase.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR01245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PfamDom: PDC00001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; Tyr_Kc; 1.
DR PROSITE: PS00032; N6_MTASE; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER
SQ SEQUENCE 346 AA; 39977 MW; C8A2CEC221C7C2D9 CRC64;

Query Match: 70.7%; Score 417; DB 13; Length 346;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 2 LIGRPFFET 10
DB 269 LVGNFFET 277

RESULT 27
Q8XGJ7
ID Q8XGJ7 PRELIMINARY; PR7; 504 AA.
AC Q8XGJ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN CNK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUN 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC031160; AAH11901.1;
DR MGI: 109604; Cnk
DR InterPro: IPR000959; Pkinase box

DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00433; pkinase_C; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00088; DAGPEDOMAIN.
DR PfamDom: PF000001; Prot_kinase; 1.
DR SMART: SM00039; C1; 2.
DR SMART: SM00039; C2; 1.
DR SMART: SM00020; S_TKc; 1.
DR SMART: SM00033; S_TK_X; 1.
DR PROSITE: PS00499; C2_DOMAIN; 1.
DR PROSITE: PS00004; C2_DOMAIN; 1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM; 1.
DR PROSITE: PS00081; DAG_PE_BIND_DOM; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 477 AA; 76787 MW; 800025081B3DEA13 CRC64;

Query Match: 74.1%; Score 437; DB 51; Length 487;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLIQRRPPE 9
DB 519 MIVGRPFD 547

RESULT 26
Q8XGJ7
ID Q8XGJ7 PRELIMINARY; PR7; 346 AA.
AC Q8XGJ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aurora-like serine/threonine kinase (Fragment).
GN STKA.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7935;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22035902; PubMed=12036978;
RA Gollig G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,
RA Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y., Nissen R M.,
RA Hopkins N.;
RT "Insertional mutagenesis in zebrafish rapidly identifies genes
essential for early vertebrate development."
RL Nat. Genet. 31:135-140(2002).
DR EMBL: AY099518; AAY28206.1; 1.
DR InterPro: IPR002052; N6_Mtase.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR01245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PfamDom: PDC00001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; Tyr_Kc; 1.
DR PROSITE: PS00032; N6_MTASE; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER
SQ SEQUENCE 346 AA; 39977 MW; C8A2CEC221C7C2D9 CRC64;

Query Match: 70.7%; Score 417; DB 13; Length 346;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 2 LIGRPFFET 10
DB 269 LVGNFFET 277

RESULT 27
Q8XGJ7
ID Q8XGJ7 PRELIMINARY; PR7; 504 AA.
AC Q8XGJ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN CNK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUN 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC031160; AAH11901.1;
DR MGI: 109604; Cnk
DR InterPro: IPR000959; Pkinase box

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DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR01245; Tyr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00659; POLO_box; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00378; POLO_BOX; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATF; 1.
DR PROSITE: PS00117; PROTEIN_KINASE_DCM; 1.
DR PROSITE: PS00118; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Transferase
SQ SEQUENCE 504 AA; 55546 MW; F04BF70R5D2730B9 Q5104.

Query Match 70.7%; Score 41; DB 11; Length 504;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
DB 254 LLOGSPFFETA 264

RESULT 29
Q96CV1 PRELIMINARY; PRT; 646 AA.
AC Q96CV1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
FT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
CS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo
CX NCBI_TaxID=9606;
[!]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE Brain;
RA Strausberg R.;
RL Submitted (SEP 2001) to the EMBL/GenBank/DDBJ databases.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: BC013899; AAH13899.1;
DI InterPro: IPR000959; POLO_box.
DI InterPro: IPR000719; Prot_kinase.
DI InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00659; pkinase; 1.
DR Pfam: PF00659; POLO_box; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00378; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATF; 1.
DR PROSITE: PS00117; PROTEIN_KINASE_DCM; 1.
DR PROSITE: PS00118; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 646 AA; 71628 MW; 3242AC00902865B8 CRC64;

Query Match 70.7%; Score 41; DB 4; Length 646;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLGRPPFFETS 11
DB 253 LLOGSPFFETA 263

535011 29
Q94342 PRELIMINARY; PRT; 153 AA.
AC Q94342;
DT 01-NOV-1998 (TrEMBLrel. 38, Created)
DI 01-NOV-1998 (TrEMBLrel. 38, Last sequence update)

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DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein CT338.
GN CT338.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
CX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/JW-3/Cx;
RX MEDLINE=99000809; PubMed-9784136;
RA Stephens R.S., Kaitan S., Lammel C.J., Fan C., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genore sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis";
RL Science 282:754-759(1998);
DR EMBL: AE001307; AAC67933.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 153 AA; 17828 MW; 5AE9E4E28FF8B17C CRC64;

Query Match 67.2%; Score 39; DB 16; Length 153;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGRPPFFET 10
DB 11 LGAPPFET 18

RESULT 30
Q9GP07 PRELIMINARY; PRT; 235 AA.
AC Q9GP07;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DI 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative mitogen-activated protein kinase (Fragment).
GN MPK1.
OS Leishmania amazonensis.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
CX NCBI_TaxID=5659;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UV79;
RA Wiese M., Goercke I.;
RT "Homologues of LMPK, a mitogen-activated protein kinase from
RT Leishmania mexicana, in different leishmania species.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AJ298021; CAC17612.1;
DR HSSP: P24941; IHCS.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS00351; MAPK; 1.
DR PROSITE: PS00117; PROTEIN_KINASE_DCM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
FT NON_TER 235
SQ SEQUENCE 235 AA; 26791 MW; 7FEDF167C0FB03B7 CRC64;

Query Match 67.2%; Score 39; DB 5; Length 235;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFFET 9
DB 192 MLLGRPFET 200

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RESULT 31
Q63432 PRELIMINARY: PRT: 358 AA.
AC Q63432
DT 01-JUL-1997 (TrEMBLrel. 24, Created)
DT 01-JUL-1997 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE VAP-kinase homologue.
GN VPK.
OS Leishmania mexicana.
OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID:5665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MNYC/92/62/M379;
RX MEDLINE=98232503; PubMed=9564064;
RA Wiese M.;
RT "A pitogen-activated protein (MAP) kinase homologue of Leishmania mexicana is essential for parasite survival in the infected host.";
RL EMBO J. 17:2619-2628(1998);
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: Z95887; CAB09307.1; -.
DR HSSP: Q00534; BIR.
DR InterPro: IPR001527; MAP_kin.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SMC0220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATF; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DCM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine protein kinase; Transferase.
SQ SEQUENCE 358 AA; 41151 MW; 702E43C6057D8D4F CRC64;

Query Match 67.2%; Score 39; DB 5; Length 358;
Best Local Similarity 88.9%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPF 9
Db 412 MLLGRLEFE 220

RESULT 32
Q63432 PRELIMINARY: PRT: 358 AA.
AC Q63432
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Probable serine/threonine-protein kinase PksB
GN PksB OR BLOS89.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
CC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID:216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Scheil M.A., Karmirantzou M., Snel P., Vilanova D., Berger B.,
RA Pessi G., Zwaalen M.-C., Desiere F., Bork P., Bellay M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002);
DR EMBL: AE014680; AAN24413.1; -.
KW Kinase; Complete proteome.
SQ SEQUENCE 690 AA; 72243 MW; 6A10EABCE0D9D20D CRC64;

Query Match 67.2%; Score 39; DB 16; Length 690;

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Best Local Similarity 87.5%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPF 8
Db 217 MLLGRPPF 224

RESULT 33
Q9KJN7 PRELIMINARY: PRT: 1337 AA.
AC Q9KJN7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative serine/threonine protein kinase.
GN PKND2.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
CC Cystobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID:34;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DZ2;
RX MEDLINE=20032045; PubMed=10564511;
RA Cho K., Zusman D.R.;
RT "Sporulation timing in Myxococcus xanthus is controlled by the espAB locus.";
RL Mol. Microbiol. 34:714-725(1999);
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DZ2;
RA Cho K., Zusman D.R.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF163841; AAF87930.1; -.
DR InterPro: IPR007119; Prot_kinase.
DR InterPro: IPR014403; TPR.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00525; TPR; 4.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SMC0028; TPR; 3.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1337 AA; 144738 MW; 60B6E8CA4C92499D CRC64;

Query Match 67.2%; Score 39; DB 2; Length 1337;
Best Local Similarity 87.5%; Pred. No. 1.3e-02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPF 8
Db 242 MLLGRPPF 249

RESULT 34
Q63432 PRELIMINARY: PRT: 240 AA.
AC Q63432
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rat protein kinase C-family related (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID:10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87147193; PubMed=3469647;
RA Housley G.M., O'Brian C.A., Johnson M.D., Kirschmeier P.,
RA Weinstein I.B.;
RT "Isolation of cDNA clones encoding protein kinase C: Evidence for a protein kinase C-related gene family.";

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RJ Proc. Natl. Acad. Sci. U.S.A. 84:1065-1069(1987).
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: M15923; AAA41877.1; -.
DR HSSP: Q63450; 1A06.
DR InterPro: IPR000919; Prot_kinase.
DR Pfam: PF002290; Ser_thr_kinase.
DR ProDom: P000001; Prot_kinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON-TER 1 240
FT NON-TER 240
SQ SEQUENCE 240 AA; 26648 MW; 289910FF257E4F62 CRC64;

Query Match 65.5%; Score 38; DB 16; Length 256;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPFFS 9
DB 204 MMAGQPPPE 212
PRT: 256 AA.

RESULT 35
Q9PPA6 PRELIMINARY; PRT: 256 AA.
AC Q9PPA6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15; Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20; Last annotation update)
DE Glutamine-binding periplasmic protein.
GN GUNB OR GUNB7.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
CC Campylobacteraceae; Campylobacter.
CX NCB: TaxID 197;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=20150912; PubMed=10698204;
RA Parkhill J., Wren B.W., Mungall K., Ketley C.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jorgels K., Kariyasev A.V., Moule S., Pallen M.J., Peck G.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrett B.G.;
RT "The genome sequence of the food-borne pathogen, Campylobacter jejuni,
RT reveals hypervariable sequences".
RL Nature 403:665-668(2000).
DR EMBL: AJ139076; CAB73082.1;
DR HSSP: P10344; 1WDN.
DR InterPro: IPR001311; SBP/glu_receptor.
DR InterPro: IPR001618; SBP_bac_3.
DR Pfam: PF00497; SBP_bac_3; 1.
DR SMART: SM00062; PRPB; 1.
KW Complete proteome.
SQ SEQUENCE 256 AA; 28913 MW; 6CE440DE6AF019CF CRC64;

Query Match 65.5%; Score 38; DB 16; Length 256;
Best Local Similarity 72.7%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLGRRPPFFS 11
DB 25 MELGYPPFFEMS 35
PRT: 256 AA.

RESULT 36
Q9WXT3 PRELIMINARY; PRT: 256 AA.
AC Q9WXT3;
DI 01-NOV-1999 (TrEMBLrel. 12, Created)

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DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE IRON(II) ABC transporter, ATP-binding protein.
GN TM0078.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogaceae; Thermotoga.
CX NCB: TaxID=2336;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10160591;
RA Nelson K.E., Clayton R.A., Gill S.R., Swinn M.D., Dodson R.C.,
RA Haft D.H., Hickey S.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richards D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter C.G., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima".
RL Nature 399:323-329(1999).
DR EMBL: AE001694; AAD35172.1; -.
DR TIGR: TMC078; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transporter.
DR Pfam: PF00005; ABC_tran; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 256 AA; 28723 MW; 725DA5365C84E156 CRC64;

Query Match 65.5%; Score 38; DB 16; Length 256;
Best Local Similarity 80.0%; Pred. No. 37;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLGRPPFFETS 11
DB 62 LLGR:PWETS 71
PRT: 257 AA.

RESULT 37
Q8Y2A0 PRELIMINARY; PRT: 257 AA.
AC Q8Y2A0;
DI 01-MAR-2002 (TrEMBLrel. 20, Created)
DI 01-MAR-2002 (TrEMBLrel. 20; Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein RSC0436.
GN RSC0436 OR RSC3405.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
CC Ralstoniaceae; Ralstonia.
CX NCB: TaxID=305;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandelier M., Choisme N., Claude-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum".
RL Nature 415:497-502(2002).
DR EMBL: AL646059; CAD13964.1; -.
DR InterPro: IPR001173; Glyco_trans_2.
DR Pfam: PF00535; Glycos_transf_2; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 257 AA; 28452 MW; DE8F0AC694C090A25 CRC64;

Query Match 65.5%; Score 38; DB 16; Length 257;
Best Local Similarity 63.6%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Dr 262 11133PPE 272

RESULT 4:

QREV12 PRELIMINARY; PRI. 434 AA.
 AC QREV12; 2003 (11EMBUREL. 23, Created
 DT 01 MAR-2003 (11EMBUREL. 23, Last sequence update)
 DT 01 MAR-2003 (11EMBUREL. 23, Last annotation update)
 DE C4 dicarboxylate transporter.
 GN C2860
 OS Oceanobacillus thuyensis.
 GC Bacillaria; Firmicutes; Bacillales; Oceanobacillus.
 OX NCBI TaxID:182710;
 RN 11;
 RF SEQUENCE FROM N.A.
 RC STRAIN=HTR831 / DSM 14271 / JCM 11109;
 RX NERFLINE=2220267; PubMed=2235376;
 RA Takami H., Takaki Y., Uchiyama I.
 PT "Genome sequence of Oceanobacillus thuyensis isolated from the Itoya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RC environments."
 RL Nucleic Acids Res. 30:3927-3936 (2002).
 DR EMBL; APC04602; BAC14816.1; -.
 KW Complete proteome.
 SQ SEQUENCE 434 AA; 46688 MW; CHDAE650CF85485E CSC64;

Query Match 65.5%; Score 38; DH 16; Length 434;
 Best Local Similarity 77.8%; Pred. No. 63;
 Matches 7; Conservative 17; Mismatches 17; Indels 0; Gaps 0;

QY 3 LORPPPTS 11
 |||
 QB 49 LORPPPTS 57

Search completed: November 14, 2003, 14:55:43
 Job time: 35 secs